Improving longitudinal spinal cord atrophy

measurements for clinical trials in multiple sclerosis by

using the generalised boundary shift integral (GBSI)

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Declaration

I, Marcello Moccia, confirm that the work presented in this thesis is my own. Where information has been derived from other sources, I confirm that this has been indicated.

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Abstract

Spinal cord atrophy is a common and clinically relevant feature of multiple sclerosis (MS), and can be used to monitor disease progression and as an outcome measure in clinical trials. Spinal cord atrophy is conventionally estimated with segmentation-based methods (e.g., cross-sectional spinal cord area (CSA)), where spinal cord change is calculated indirectly by numerical difference between timepoints.

In this thesis, I validated the generalised boundary shift integral (GBSI), as the first registrationbased method for longitudinal spinal cord atrophy measurement. The GBSI registers the baseline and follow-up spinal cord scans in a common half-way space, to directly determine atrophy on the cord edges.

First, on a test dataset (9 MS patients and 9 controls), I have found that GBSI presented with lower random measurement error, than CSA, reflected by lower standard deviation, coefficient of variation and median absolute deviation.

Then, on multi-centre, multi-manufacturer, and multi–field-strength scans (282 MS patients and 82 controls), I confirmed that GBSI provided lower measurement variability in all MS subtypes and controls, than CSA, resulting into better separation between MS patients and controls, improved statistical power, and reduced sample size estimates.

Finally, on a phase 2 clinical trial (220 primary-progressive MS patients), I demonstrated that spinal cord atrophy measurements on GBSI could be obtained from brain scans, considering their quality and association with corresponding spinal cord MRI-derived measurements. Not least, 1-year spinal

cord atrophy measurements on GBSI, but not CSA, were associated with upper and lower limb motor function.

In conclusion, spinal cord atrophy on the GBSI had higher measurement precision and stronger clinical correlates, than the segmentation method, and could be derived from high-quality brain acquisitions. Longitudinal spinal cord atrophy on GBSI could become a gold standard for clinical trials including spinal cord atrophy as an outcome measure, but should remain a secondary outcome measure, until further advancements increase the ease of acquisition and processing.

Impact statement

In this thesis, I have validated the generalised boundary shift integral (GBSI), as the first registrationbased method for quantification of spinal cord atrophy in multiple sclerosis (MS). The GBSI pipeline is based on the latest iteration of the boundary shift integral, and has been specifically designed to overcome limitations of commonly used segmentation-based methods (i.e., spinal cord crosssectional area (CSA)).

Improvements in spinal cord atrophy measurements presented in this thesis can expand research possibilities for future MS projects. In particular, I analysed a multicentre, multi-manufacturer and multi-field strength scan dataset from the Magnetic Resonance Imaging in MS (MAGNIMS) network, and showed that the GBSI has better measurement precision, leading to smaller sample size estimates and stronger clinical correlates, than CSA, suggesting the registration-based method holds promise for future collaborative studies. These results were then confirmed by re-analysing a phase 2 clinical trial, highlighting that the GBSI could become a gold standard for clinical trials including spinal cord atrophy as an outcome measure. I also demonstrated that obtaining spinal cord atrophy measurements from brain scans could represent a viable and clinically meaningful alternative to more technically-challenging spinal cord images, in particular in multi-centre settings where homogenous spinal cord acquisitions are not feasible. For instance, following the results of this thesis, the United Kingdom MS Society Efficient Clinical Trial Platform will be able to include spinal cord atrophy measurements with GBSI among MRI outcome measures to study the neuroprotective potential of different medications. Not least, GBSI could prove useful in many neurological diseases, such as amyotrophic lateral sclerosis and spinal cord injury, where spinal cord volume changes are representative of the most aggressive aspects of the diseases.

Last but not least, results of this thesis are also important to MS patients. Deriving spinal cord atrophy measurements from brain scans would significantly reduce the scan time for MRI and, thus, participants' burden. In addition, spinal cord atrophy on GBSI, but not CSA, can detect early subtle changes in motor function to the upper and lower limbs, as measured by both neurologists (on neurological examination) and MS patients (on patient reported outcome measures). In the future, identifying changes in spinal cord volume could improve monitoring the clinical course of MS and its response to treatment.

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List of abbreviations

- 3D: three-dimensional
- 3D-FFE: three-dimensional gradient-echo fast field echo
- **9HPT**: nine-hole peg test
- 95%CI: 95% confidence intervals
- Ab: antibody
- AQP4: aquaporin-4
- ASM: active surface model
- **AUC**: areas-under-the-curve
- BBB: blood brain barrier
- **BOLD**: blood oxygenation level-dependent
- BPF: brain parenchymal fraction
- BSLs: bright spotty lesions
- BSI: boundary shift integral
- **CIS**: clinically isolated syndrome
- Coeff: coefficients
- CNS: central nervous system
- CSA: cross-sectional area
- CSF: cerebro-spinal fluid
- CUA: combined unique active
- DIR: double inversion recovery
- DIS: dissemination in space
- DIT: dissemination in time

DMTs: disease-modifying treatments DOF: degrees of freedom **DTI**: diffusion tensor imaging **EBV**: Epstein-Barr virus EDSS: expanded disability status scale **FA**: fractional anisotropy fMRI: functional magnetic resonance imaging FSS: Functional System Score **GBSI**: generalised boundary shift integral Glx: glutamate/glutamine **GM**: grey matter ICC: intraclass correlation coefficient IL: interleukin **IVF**: isotropic volume fraction LETM: longitudinally extensive transverse myelitis MAGNIMS: magnetic resonance imaging in multiple sclerosis **MD**: mean diffusivity **MOG**: myelin oligodendrocyte glycoprotein MPRAGE: magnetisation-prepared rapid gradient echo **MRI**: magnetic resonance imaging MRS: magnetic resonance spectroscopy MS: multiple sclerosis MSWS: multiple sclerosis walking scale MTR: magnetisation transfer ratio

MTSat: magnetisation transfer saturation MUCCA: mean upper cervical cord area **NAA**: N-acetyl-aspartate NAA/Cr: N-acetyl-aspartate/ creatinine **NDI**: neurite density index NMOSD: neuromyelitis optica spectrum disorders **NODDI**: neurite orientation dispersion and density imaging **OCT**: optical coherence tomography **ODI**: orientation dispersion index **OR**: odds ratios PBVC: percent brain volume change **PD**: proton density PET: Positron emission tomography **PP**: primary progressive PSIR: phase-sensitive inversion recovery **qMT**: quantitative magnetisation transfer **QSI**: Q-space imaging **RD**: radial diffusivity **RIS**: radiologically isolated syndrome **RNFL**: retinal nerve fibre layer **ROC**: receiver operating characteristics **RRMS**: relapsing-remitting multiple sclerosis SCT: spinal cord toolbox SMT: spherical mean technique

SP: secondary progressive

SIENA: structural image evaluation using normalisation of atrophy

STIR: short-tau inversion recovery

T25FWT: timed 25-foot walking test

UCCA: upper cord cross-sectional area

WM: white matter

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1. Introduction to multiple sclerosis

This thesis concerns a novel method for spinal cord atrophy measurement in multiple sclerosis (MS). In the <u>Chapter 1</u>, I have provided a general background to MS. After briefly mentioning epidemiology and aetiopathogenesis, I will review current MS classification, clinical assessments, diagnostic criteria and prognosis. Finally, I will discuss available treatments, highlighting limitations and future perspectives for development of new drugs.

1.1. Introduction

MS is a chronic inflammatory demyelinating and neurodegenerative disease of the central nervous system (CNS), potentially causing any neurological deficit [1, 2]. Previous studies have implicated a combination of genetic and environmental factors in the aetio-pathogenesis of MS, with chronic inflammation and neurodegeneration mediated by the patient's immune system [3, 4].

1.1.1. Epidemiology

According to the most recent Global Burden of Disease Study estimates (2016), MS is the most common immune-mediated disease of the CNS, with over 2.2 million cases world-wide, corresponding to 10% increased prevalence from 1990 [5]. North America, Western Europe and Australasia hold higher prevalence rate (91-164 cases per 100,000), compared with Africa (2-3 cases per 100,000) [5]. On the contrary, incidence of MS has been relatively stable or slightly increased over the past four to five decades [5]. As such, the rising prevalence mostly reflects improved survival, with a global mortality rate for MS being decreased by 11% between 1990 and 2016 [5].

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Clinical onset is generally in early adult life, though there is increased awareness of presentation in childhood [1]. Prevalence of MS is similar in preteen boys and girls, but, then, progressively increases through lifetime among women, with a 2:1 sex ratio in favour of women in the sixth decade of life [5]. As discussed above, the life expectancy for a person with MS is relatively unimpeded by the disease, with a 5 to 10-year reduction versus non-affected individuals [6]. However, MS is one of the leading causes of disability from CNS disease among young adults, and has a severe impact on quality of life, made further strenuous by a relatively young average age of onset [1, 5].

1.1.2. Aetiology

1.1.2.1. Genetic risk

The possibility of a genetic background to MS was originally explored in family studies, which show up to 33% recurrence rate of MS within affected families. In particular, first-degree relatives have a ten-fold increased risk of MS, whilst second-degree family members have a three-fold increased risk [1, 2, 7, 8]. Sibling and twin studies display similar patterns of increased risk [9, 10].

The first allele to be accurately associated with risk of MS development was the human leukocyte antigen class II haplotype HLA-DRB*1501 [1, 2, 11, 12]. More recently, the development of genomewide association study technology has allowed the identification of more than 200 genetic loci implicated in the risk of MS. These loci include genes encoding for the immune system (such as interleukin (IL)-2 and IL-7 receptors), cytokine pathways, and co-stimulatory molecules [11, 13, 14]. However, genetics alone cannot explain MS aetiology fully.

1.1.2.1. Environmental risk

Multiple environmental factors have been implicated in MS susceptibility. Prevalence and incidence rates of MS have been shown to increase with latitude [2, 15]. Individuals who move to high-risk latitudes during childhood (e.g., from Africa to Northern Europe) have the MS risk profile of their new high-risk area, rather than the risk levels seen in their area of birth, suggesting that environmental risk factors for MS play a role during the developmental process [16]. The association between latitude and MS risk could be at least in part mediated by vitamin D. Indeed, there is an increased risk of MS in relation to early-life deficiency of vitamin D, whose production is primarily enhanced by sunlight exposure and, thus, is generally reduced in high latitude areas [2, 17]. Still, the exact effect of vitamin D supplementation on healthy individuals (or on patients with MS) is currently unknown [13].

A number of infectious agents have been associated with MS susceptibility. Among them, the Epstein-Barr virus (EBV) has the strongest correlates. Individuals who contract EBV during childhood have a 15-fold increased risk of MS, which further soars to 30-fold for those who are infected during or after adolescence [1, 2, 17]. On the contrary, individuals who are seronegative to EBV have almost zero risk of developing MS. However, the exact relationship between EBV and MS pathogenesis remains unclear [18, 19]. Other herpetic infections have also been studied (e.g., Human Herpes virus 6, Cytomegalovirus, Herpes simplex virus), but with less definite results [1, 2, 20].

Other risk factors include tobacco smoking, reproductive factors (e.g., breastfeeding, menopause, contraceptives), dietary consumption of polyunsaturated fatty acid, obesity, and socioeconomic status, but the exact role of these factors in MS pathogenesis remains poorly understood [1, 2, 20].

Overall, multiple environmental interactions with predisposing genotype could be considered as the initial trigger to MS development [2].

1.1.3. Pathology

The most typical pathology sign of MS is the presence of demyelinating lesions in the white matter (WM) and grey matter (GM), in the brain and in the spinal cord [21–25]. Demyelinating lesions generally originate around venules, where accumulation of inflammatory lymphocytes can be observed [26, 27], along with astrocytic response and macrophages/microglia infiltrates to the active injury site, eventually resulting into gliotic scars [28]. Acute inflammatory demyelination is clinically associated with the acute onset of new neurological symptoms (i.e., clinical relapse) [29–31].

Neuro-axonal loss is another prominent hallmark of MS, and is a key factor of irreversible disability accrual [32]. In the early stages of the disease, axonal loss is generally seen in areas of pathological demyelination, in association with inflammatory infiltrates consisting of macrophages/microglia and lymphocytes [33]. During the course of the disease, axonal loss can occur in areas of prolonged demyelination without active inflammation, suggesting that axonal survival is related to the presence of myelin support [34–38]. Notwithstanding this, the presence of chronically demyelinated axons suggests that demyelination does not necessarily leads to neuro-axonal loss [35, 39, 40]. In advanced MS, axonal loss results into shrinking of the brain parenchyma (i.e., atrophy), and is associated with impaired function of macrophages/microglia and astrocytes, and with increased oxidative stress and mitochondrial damage. In particular, demyelination and subsequently impaired axonal dysfunction increase the energy demand, further contributing to altered metabolism, neuronal dysfunction and, ultimately, axonal loss [41–43]

The mechanisms by which demyelination and axonal loss occur are profoundly heterogeneous and involve a variety of cellular subsets [1, 44, 45]. The sequence of pathological events might include perivenular infiltration of macrophages, CD8+ T lymphocytes, and, CD4+ T lymphocytes and B lymphocytes, with profound blood brain barrier (BBB) leakage, giving rise to classical active demyelinated plaques [45–50]. As the disease progresses, infiltrates of T and B lymphocytes, activation of microglia/macrophages and astrocytes, and mitochondrial dysfunction become obvious throughout the brain parenchyma, also in the absence of major BBB damage [51, 52], with formation of aggregates of inflammatory cells in the form of meningeal follicle-like structures, and expansion of previously-existing WM and GM lesions [42, 43, 45, 46, 53–57]. These changes ultimately lead to progressive demyelination, axonal loss and neurodegeneration in the brain and the spinal cord [42, 43, 45, 54, 57].

Inflammation, demyelination and axonal loss can be measured *in vivo* by using magnetic resonance imaging (MRI) [58]. This will be further discussed in <u>Chapter 2</u>.

1.1.4. Clinical features

At the onset of the disease, the clinical course in most patients is characterised by recurring episodes of neurological deficits (i.e., relapses). A relapse is defined as the acute-subacute occurrence of neurological symptoms lasting at least 24 hours, in absence of infections, fever or other symptoms of systemic disease [59]. On the first relapse, the condition is named clinically isolated syndrome (CIS) or relapsing-remitting MS (RRMS), depending on whether MS pathology is isolated or disseminated in time (DIT) and space (DIS), as further detailed in paragraph 1.1.5 [59–61]. On the occasion of a second clinical relapse, the condition inevitably falls within RRMS [59–61]. In the early phases of MS, patients generally recover from relapses fully, in absence of any treatment, but, later on, disability from relapses can accumulate, resulting in irreversible neurological disability. Following this initial relapsing-remitting course, patients can present with progressive disability accrual, independently from relapses, namely secondary progressive MS (SPMS) [60, 62]. For other patients, gradual disability worsening can occur from the start of the disease, in this case termed primary progressive MS (PPMS) [60]. In recent years, PPMS and SPMS have been reclassified as different parts of the same progressive spectrum (**Table 1.1**) [63, 64]. Of note, patients diagnosed with the progressive form of the disease may also experience periods of symptom remission (and sometimes improvement), within an overall declining trajectory, and, still, can present with inflammatory activity (e.g., relapses or new lesions). As such, progressive MS can be further classified into four categories: active or not active (based on the presence or absence of relapses or new lesions), and with or without symptom progression (based on disability accrual independently from relapses) (**Table 1.1**) [60].

Initial symptoms can consist of nearly any neurological sign, based on the location of the inflammatory demyelinating lesions. In RRMS, most common symptoms at onset are sensorimotor disturbances, visual defects or a combination of multiple symptoms. In PPMS, symptoms at onset generally consist of sensorimotor disturbances, bladder dysfunction, unbalance or a combination of multiple symptoms [65]

Clinical features of MS can be measured with a wide variety of clinical assessments, tests and scales. Functional systems scores (FSS) and the extended disability status scale (EDSS) are the most widely used clinical measures [66]. The FSS measure disability level in various neurological systems on an ordinal scale; the full FSS battery examines disability related to the pyramidal, cerebellar, brainstem, Table 1.1. Classification of MS clinical phenotypes.

Table shows clinical phenotype classification for relapsing and progressive patients. Adapted from Lublin FD et al. Neurology 2014 [60].



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sensory, bowel/bladder, visual, and cerebral systems. Based on these measurements, an overall disability level can be scored with the EDSS, which uses an ordinal scale of increasing severity from 0 (absence of neurological symptoms and signs) to 10 (death related to MS), with 0.5 unit increments [66]. EDSS steps 1.0 to 3.5 indicate unrestricted walking, whilst EDSS steps 4.0 to 7.5 indicate progressive reduction in walking ability [66]; as such, most of the EDSS is highly driven by ambulatory function. Overall, the EDSS is still the internationally accepted primary endpoint in clinical trials, but, considering its documented weaknesses, it is generally combined with other more specific clinical measures [63, 67].

The timed 25-foot walking test (T25FWT) is an objective assessment of ambulatory impairment in MS, wherein patients are measured by the average time they take to walk 25 feet (7.62m), at maximum speed, on two different trials, with a walking aid if necessary [63]. Ambulatory function can also be assessed by MS patients within the so-called patient-reported outcome measures (PROMs) [63]. In particular, the MS walking scale (MSWS) is a 12-item questionnaire showing good correlates with lower limb motor impairment and functional independence [68, 69].

The 9-hole peg test (9HPT) assesses disability of the upper limbs, by measuring the average time for placing nine pegs into nine holes, with dominant and non-dominant hand, in two different trials [63].

More recently, there has been growing attention to cognitive symptoms of MS [70–74]. Among neuropsychological tests, the symbol digit modalities test (SDMT) has shown the best correlates with overall cognitive functioning [75–77]. The SDMT measures information processing speed

through the number of correct digits (1-9) corresponding to a symbol, the patient is able to write or to orally report during a 90-second trial [77].

1.1.5. Diagnosis

Diagnosis of MS requires that clinical and radiological signs of MS are disseminated in both time and space (DIT and DIS), as originally described in the 2001 McDonald criteria and subsequently revised to achieve an earlier and more accurate diagnosis [59, 61, 78–80]. MS diagnosis is currently based on a combination of clinical features (relapses and clinical progression), MRI findings (T2 and T1-Gadolinum enhancing lesions in periventricular, cortical/juxtacortical, infratentorial and/or spinal cord areas), and laboratory measures (oligoclonal bands in the cerebrospinal fluid (CSF)) [61]. In the present thesis, I included populations where diagnosis was performed in accordance with 2010 revision of McDonald criteria, since 2017 revision was presented and published while this work was already ongoing. Possible implications are mainly related to the diagnosis of CIS and will be further discussed in <u>Chapter 5</u>. For comparison purposes, 2010 and 2017 revisions of McDonald criteria are presented in **Table 1.2**.

1.1.6. Prognosis

The prognosis of MS is unpredictable at patient level. However, there are a number of clinical, MRI and laboratory measures that have been shown to be associated with MS prognosis [1, 65].

Age is a main determinant of MS progression across all disease phenotypes [1]. In natural history cohort studies, PPMS and SPMS patients present with similar age at onset of progression, suggesting that disease progression occurs under the dominant influence of age-related pathological

processes, irrespectively of previous relapses [6, 81]. Other demographic factors include female sex, which is associated with higher risk of relapses [1, 82, 83], and genes [84, 85].

At the time of diagnosis, topographic characteristics (non-optic neuritis presentations) and residual disability of relapses are poor prognostic factors [83, 86, 87]. The presence and the number of CSF un-matched oligoclonal bands is another factor associated with poor prognosis and, as such, has been also included in the most recent revision of MS diagnostic criteria [61, 83, 88]. Brain and spinal cord MRI predictors of MS progression will be fully detailed in <u>Chapter 2</u>.

1.1.7. Treatment

No cure is available for MS, and the current therapeutic strategy is aimed at reducing the risk of relapses and disability progression [89]. The rapid advent of disease-modifying treatments (DMTs) in the mid-1990s was heralded by a period of rapid progress in the understanding of MS [90]. In particular, with the support of MRI, new possible treatments have been quickly screened on well selected populations [91], as discussed in <u>Chapter 2</u>.

DMTs can prevent relapses, new brain and spinal cord lesions, and, at least in part, worsening neurological disability [92]. Historically, DMTs have been immunosuppressant or immunomodulatory, meaning that continuous treatment is required to maintain suppression of inflammation (and disease activity). Some more recent DMTs can be given as short courses, with the aim of producing enduring immunological actions (immune reconstitution therapies) [93]. Generally speaking, all DMTs target neuroinflammation and, as such, have a direct effect on the inflammatory component of MS; on the contrary, an indirect (and much less obvious) effect could be expected on neurodegeneration and disability progression [90]. Still, the long-term exposure to

Table 1.2. 2010 and 2017 revisions of McDonald Criteria for MS diagnosis.

Table shows clinical, radiological and laboratory requirements for MS diagnosis in different clinical presentations, according to 2010 and 2017 revisions of McDonald Criteria. Main novelties for the 2017 revision of McDonald Criteria, when compared with 2010 criteria, are inclusion of CSF-specific oligoclonal bands for DIT, evaluation of both cortical and juxtacortical lesions, removal of the differentiation between symptomatic and asymptomatic lesions. Adapted from Thompson AJ et al. Lancet Neurology 2018, and from Polman CH et al. Ann Neurol 2011 [59] [61].

None	None
DIS demonstrated by: \geq 1 T2 lesion in at least 2 of 4 MS-	DIS demonstrated by: \geq 1 T2 lesion in at least 2 of 4 MS-
typical regions, or further relapse implicating a different	typical regions, or further relapse implicating a different
CNS site.	CNS site.
DIT demonstrated by: simultaneous presence of	DIT demonstrated by: simultaneous presence of T1-
symptomatic T1-enhancing and T2 lesions, or a new T1-	enhancing and T2 lesions, or a new T1-enhancing or T2
enhancing or T2 lesions on follow-up, or further relapse.	lesions on follow-up, or further relapse, or CSF-specific
	oligoclonal bands.
	typical regions, or further relapse implicating a different CNS site. DIT demonstrated by: simultaneous presence of symptomatic T1-enhancing and T2 lesions, or a new T1-

1 relapse and objective clinical	DIS demonstrated by: \geq 1 T2 lesion in at least 2 of 4 MS-	DIS demonstrated by: \geq 1 T2 lesion in at least 2 of 4 MS-		
evidence of 1 lesion	typical regions, or further relapse implicating a different	typical regions, or further relapse implicating a different		
(CIS).	CNS site.	CNS site.		
	DIT demonstrated by: simultaneous presence of	DIT demonstrated by: simultaneous presence of T1-		
	symptomatic T1-enhancing and T2 lesions, or a new T1-	enhancing and T2 lesions, or a new T1-enhancing or T2		
	enhancing or T2 lesions on follow-up, or further relapse.	lesions on follow-up, or further relapse, or CSF-specific		
		oligoclonal bands.		
Insidious neurological progression	One-year disease progression and 2 of the following 3	One-year disease progression and 2 of the following 3		
suggestive of MS (PPMS).	criteria:	criteria:		
	1. \geq 1 T2 lesions in periventricular, juxtacortical or	1. ≥1 T2 lesions in periventricular, cortical/juxtacortical		
	infratentorial areas;	or infratentorial areas;		
	2. ≥2 T2 lesions in the spinal cord;	2. \geq 2 T2 lesions in the spinal cord;		
	3. Positive CSF (CSF-specific oligoclonal bands and/or	3. Positive CSF (CSF-specific oligoclonal bands).		
	elevated IgG index).			

DMTs has significantly reduced the risk of severe ambulatory impairment (EDSS 6.0), SP conversion and death in people with relapsing MS, compared with no treatment or placebo [94–96]. Most evidence is coming from Interferon Beta and Glatiramer Acetate studies, whilst few has recently come from newer DMTs [95, 97].

Over ten DMTs have been developed and approved for RRMS and CIS over the last 20 years, whilst only three for progressive MS (Interferon Beta 1b and Siponimod for SPMS, and Ocrelizumab for PPMS) (**Table 1.3**) [98–100]. Indeed, translating medications originally developed for RRMS, to progressive MS has been unsuccessful so far, with several negative trials, including those investigating Fingolimod (INFORMS) [101], Natalizumab (ASCEND) [102], and Rituximab (OLYMPYUS) [103]. This is because clinical and radiological outcome measures for RRMS do not necessarily apply to progressive MS [63, 91]. Also, the poor understanding of the pathological mechanisms in progressive MS makes it challenging to develop targeted therapeutic agents. Thus, the understanding of MS progression and the development of biomarkers could enhance the development of new medications.

Despite the successful development of treatments for MS, a number of clinical trials have failed to show any significant clinical effect [43, 90, 104]. For instance, laquinimod is an immunomodulatory compound downregulating pro-inflammatory T cell responses in the peripheral blood and within the CNS. Furthermore, animal models have suggested neuroprotective effects of laquinimod, exerted through modulation of pathological microglia, with reduced demyelination and axonal damage [104]. Laquinimod consistently showed a positive effect on new or enlarging T2 lesions in both RRMS and PPMS, but did not reach primary clinical endpoints in clinical trials [104, 105], suggesting that clinical effects might require longer time to disclose, when compared with MRI [87], and further highlighting the need of accurate and clinically meaningful MRI outcome measures.

Thus, after providing the reader with a general background to MS and showing its multifaceted pathology and clinical features, in the following <u>Chapter 2</u>, I will review brain and spinal cord imaging outcome measures that have been used in clinical trials and observational studies, specifically mentioning current limitations and possible future perspectives.

Table 1.3. Disease modifying treatments.

Table shows the list of approved DMTs in the United Kingdom, with recommendations for clinical use (adapted from the National Institute for Health and Care Excellence, the National Healthcare System England, and the European Medicine Agency) [98–100]. MRI activity is defined as \geq 1 T1 gadolinium-enhancing lesion or significant increase in T2 lesion load. Inadequate response to previous DMT is defined as \geq 1 relapse in the last year and MRI evidence of disease activity. Rapidly evolving severe RRMS is defined as \geq 2 relapses in the last year and, on brain MRI, \geq 1 T1 gadolinium-enhancing lesion or significant increase in T2 lesion load.

DMT	Administration	Subtype	Additional recommendations
Alemtuzumab	Infusion	RRMS	≥2 relapses in last 1 year and MRI activity;
			RRMS with inadequate response to
			previous DMT.
Beta Interferon 1a	Injection	CIS, RRMS	≥2 relapses in last 2 years;
			≥1 relapse in last 2 years and MRI activity.
Beta Interferon 1b	Injection	CIS, RRMS	≥2 relapses in last 2 years;

			≥1 relapse in last 2 years and MRI activity.
		SPMS	Continuing relapses.
Cladribine	Oral	RRMS	Rapidly evolving severe RRMS;
			RRMS with inadequate response to
			previous DMT.
Dimethyl fumarate	Oral	RRMS	≥2 relapses in last 2 years.
Fingolimod	Oral	RRMS	RRMS with inadequate response to
			previous DMT;
			Alternative to Natalizumab (de-escalation
			strategy in patients at risk of progressive
			multifocal leukoencephalopathy).
Glatiramer Acetate	Injection	CIS, RRMS	≥2 relapses in last 2 years;
			≥1 relapse in last 2 years and MRI activity.
Natalizumab	Infusion	RRMS	Rapidly evolving severe RRMS.
Ocrelizumab	Infusion	RRMS	≥2 relapses in last 2 years;
			≥1 relapse in last 2 years and MRI activity.
		PPMS	Early PPMS with MRI activity.
Siponimod	Oral	SPMS	SPMS with MRI activity.
Teriflunomide	Oral	RRMS	≥2 relapses in last 2 years.
2. Introduction to multiple sclerosis imaging outcome measures

2.1. Introduction

As discussed in <u>Chapter 1</u>, during the last 20 years, over a dozen DMTs received the approval for the treatment of RRMS, being facilitated by screening the anti-inflammatory activity of putative treatments using active MRI lesions as outcomes in phase 2 trials [92, 106]. On the contrary, the paucity of active medications for both PPMS and SPMS is striking [1, 107]. In view of this, the Progressive MS Alliance recently suggested to develop and validate biomarkers of progression that could make clinical trials for progressive MS less time and resource-consuming, when compared with conventional clinical measures [108]. This could be achieved with the identification of reliable, repeatable and sensitive-to change imaging outcomes [91, 109].

Several brain MRI measures are able to reflect the inflammatory and neurodegenerative pathology of MS [110, 111]. Brain lesion count and volume are robust markers of inflammation and demyelination, and are important outcomes in both RRMS and progressive MS trials [63]. Following recent improvements in analysis methods, brain atrophy has gained relevance, in light of its strong association with disability accrual [63, 91]. Advanced brain MRI techniques, such as magnetisation transfer ratio (MTR), diffusion tensor imaging (DTI) and magnetic resonance spectroscopy (MRS), have been included in few trials so far, and hold promise for the future, as they can reflect specific pathological changes targeted by neuroprotective treatments, such as improved myelination measures within lesional tissue, following treatment [91, 112]. Positron emission tomography (PET) and optical coherence tomography (OCT) are also emerging as candidate imaging outcomes of MS progression [91]. More recently, improvements in MRI acquisition protocols and post-processing have overcome some of the limitations associated with imaging the spinal cord, a small and mobile structure at risk of motion artefacts from breathing, cardiac movement, CSF pulsation and blood flow [109, 113]. Conventional spinal cord MRI provides information on focal lesions, which are necessary for the diagnosis and prognosis of MS, and is commonly used in the clinical setting [63, 114]. Spinal cord volume loss is the result of demyelination, neuro-axonal loss, oligodendrocyte damage, and gliosis, ultimately resulting in chronic motor, sensory and autonomic dysfunction [115, 116], and will be at the very centre of this thesis. Advanced spinal cord MRI techniques assess the type and extent of spinal cord abnormalities, but, as discussed below, their use is currently limited to specialised centres for research purposes [109].

Overall, looking at the paradigm of treatment development for PPMS and SPMS, the number of imaging outcomes included in clinical trials has almost doubled from 2.3±1.5 in the decade 1996-2006, to 4.1±2.6 in most recent years (2007 to current) (**Figure 2.1**) [91].

In the present chapter, I will discuss clinical correlates, applications, limitations and future perspectives of brain and spinal cord outcome measures for the study of MS. Methodological and statistical drawbacks will be also discussed.

2.2. Brain outcome measures

2.2.1. Brain lesions

Brain lesions were the first MRI-derived outcome measure for MS clinical trials, and include number of gadolinium-enhancing, new/enlarging T2 lesions, and T1 lesions (or their combination into

Figure 2.1. Clinical trials and imaging outcomes.

Scatter plot shows the number of imaging outcomes used in clinical trials conducted from 1996 up to recent years (the expected conclusion date has been used for on-going clinical trials), independently of trial results (i.e., medication approval or not). Adapted from Moccia M et al. Mult Scler 2017 [91].



combined unique active lesions (CUA)), and their related volumes. Lesion measures are the best biomarker of active inflammation in MS, allowing the screen for early disease activity in phase 2 clinical trials in RRMS [106]. On the contrary, lesion-derived measures play a secondary – but not negligible role in the study of progressive MS. In PPMS, the burden of T2-visible lesion load and of gadolinium-enhancing lesions is low, despite clinical severity, and seems to have only a minimal impact on the disability accrual over time [107, 117]. Still, MRI measures of focal brain lesions are the most common imaging metric in phase 2 and 3 clinical trials in progressive MS [103, 118, 127–136, 119, 137–143, 120–126].

Future clinical trials on progressive MS might include these outcomes if the presence of inflammation is expected and targeted. Indeed, trials might select populations with relatively high inflammatory activity, depending on inclusion/exclusion criteria (e.g., 24.7-27.5% of PPMS patients presented with gadolinium-enhancing lesions at baseline visit of the ORATORIO trial, as expected in the earliest phases of the disease) [64, 120]. However, clinical outcomes might be difficult to predict based on results derived from brain lesions. Indeed, the use of DMTs specifically designed for RRMS in clinical trials in progressive MS can result in a positive effect on lesion count and volume measures, but not on neurodegenerative clinical (e.g. disability progression) and imaging outcomes (e.g. brain and spinal cord atrophy), as occurred in the INFORMS and the ARPEGGIO trials [105, 118, 144]. Similarly, the use of interferon-beta in SPMS was associated with fewer active lesions, but no effect was established on clinical disability [145].

2.2.2. Brain atrophy

Brain atrophy is detectable on MRI scans from the earliest clinical stages of MS, including radiologically isolated syndrome (RIS) and CIS, and is a biomarker of irreversible neurodegenerative processes [146]. Global brain atrophy has been associated with the degree of disability in large cohorts of both RR and progressive MS [147–149]. Besides, improvements in MRI post-processing have allowed segmentation of WM and GM (both cortical and deep) separately, allowing an improved association with clinical features [149–152]. Regional volumes might show a greater change over time, resulting in higher sensitivity and smaller sample size when compared with global measures [124, 153]. Intriguingly, brain atrophy has not been associated with relapse risk in RRMS, suggesting that atrophy is probably driven more by (possibly independent) neurodegenerative changes than inflammatory lesions, which further support the use of this measure in progressive MS [146, 154].

There are several methods to quantify whole brain atrophy. In general, brain tissue volume needs to be normalised for head size, and longitudinal changes can be detected by using registration and segmentation-based techniques. Registration-based methods compare longitudinally acquired images and measure changes in brain surface after registration in a common space; structural image evaluation using normalisation of atrophy (SIENA) is the most popular example. Segmentation-based techniques measure brain volume on a single scan, and, then, determine change over time indirectly, and include brain parenchymal fraction (BPF) (which is the ratio of brain parenchymal volume to the total volume within the brain surface contour) [146, 155]. In comparative analyses, brain atrophy measured with registration-based techniques shows better repeatability, and higher power to detect treatment effect, when compared with segmentation-based [156–158].

Whole brain atrophy has been included in several phase 2 and 3 clinical trials in progressive MS as primary [105, 124, 159–163], or secondary outcome (**Table 2.1**) [103, 118, 136, 138, 142, 143, 164–167, 119, 125, 126, 128–130, 133, 135]. The first trial demonstrating a beneficial effect on global brain atrophy (using simvastatin) was a phase 2 trial study in SPMS [121]. Positive results have been reported also in the phase 3 ORATORIO study in PPMS [120], and the phase 3 EXPAND study in SPMS [143]; future positive results will certainly be available in next years, as a result of the number of on-going trials measuring global brain atrophy (**Table 2.1**).

Regional brain atrophy has been used as secondary outcome in a few trials, where measures were obtained from cortical GM, deep GM, WM [124], putamen, thalamus, and optic nerve [126]. Considering that MS does not affect the brain uniformly, the detection of regional pathology might be predictive of more specific clinical features, when compared with whole-brain measures

Table 2.1. Clinical trials in progressive MS using imaging outcomes.

Table shows phase 2 and 3 clinical trials conducted in PP, SP and mixed populations (PP and SP) of MS patients, with study design, intervention and results on different MRI outcomes (O= ongoing; P= positive treatment effect; N= no effect detected). Adapted from Moccia M et al. Mult Scler 2017 [91].

	Study	Design	Intervention	Brain	Regional	T2	T2	T1	Gadolinum+	CUA	MTR	DTI	fMRI	Spinal	0
				atrophy	brain	lesions	lesion	lesions	lesions	lesions				cord	
					atrophy		volume							atrophy	
۸S	FUMAPMS, 2019	Phase 2	Dimethyl fumarate vs	0	0	0	0	-	0	-	0	0	-	0	
	[125]	N= 90	Placebo	0	U	U	U		0		U	0		0	
	IPPoMS, 2018 [168]	Phase 2	Idebenone	0			·	. <u>.</u>			·	<u>.</u>		<u>.</u>	
		N=85		0											
	ARPEGGIO, 2017	7 Phase 2	Laquinimod vs Placebo												
	[105]	N=374		N	N	Ρ								Ν	
	ORATORIO,	Phase 3	Ocrelizumab 600mg vs	;											
	Montalban et al	. N= 732	Placebo (2:1)	Р		Р	Р								
	New Eng J Med 2017	Duration= 120 weeks		•		•	•								
	[164]														

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INFORMS, Lublin et	Phase 3	Fingolimod 0.5mg vs						•
al. Lancet 2016 [118]	N= 823	Placebo (1:1.5)	Ν	Ρ	F	•	Ρ	Ν
	Duration= 36 months							
OLYMPUS, Hawker	Phase 2/3	Rituximab 1000mg vs					· · · · · · · · · · · · · · · · · · ·	· · · · · · · · · · · · · · · · · · ·
et al. Ann Neurol	N= 439	Placebo	Ν	Ν	N			
2009 [103]	Duration= 96 weeks							
Montalban et al.	Phase 2	Interferon beta-1b	······································	······				
Mult Scler 2009	N= 71	(250µg on alternate						N
[165]	Duration= 24 months	days) vs. Placebo						
PROMISE, Wolinsky	Phase 3	Glatiramer acetate vs						
et al., Ann Neurol	N= 943	Placebo		Ν	N		Ν	
2007 [139]	Duration= 36 months							
Leary et al.	Phase 2	Interferon beta-1a (30µg						
Neurology 2003	N=50	vs. 60µg per week) vs.						N
[166]	Duration= 24 months	Placebo						
Kalkers et al. Mult	Phase 2	Placebo for 12 months						
Scler 2002 [167]	N=16	vs. Riluzole for following						N
	Duration= 24 months	12 months (2x50mg per						Ν
		day)						

EXPAND , 2018 [143]	Phase 3,	Siponimod vs Placebo	Р		Р	Р	Р	Р		
	N= 1651		•		•	•	•	·		
NCT02057159, 2019	Phase 2/3	NeuroVax vs Placebo						•		
[142]								0		
MS-SMART , 2018	3 Phase 2	Amiloride vs Riluzole vs	5							
[163]	N= 445	Fluoxetine vs Placebo	N							
		(1:1:1:1)								
Abili-T , 2017 [161]	Phase 2	Tcelna vs Placebo	0							
	N=183		0							
B7493-W , 2016	5 Phase 2/3	Lipoic acid vs Placebo	•							
[162]	N=54		0							
ASCEND , 2016 [102]	Phase 3	Natalizumab 300mg v								
	N= 889	Placebo	N	Ν	Ν					
MS-STAT, Chataway	/ Phase 2	Simvastatin 80mg v	S							
et al. Lancet 2014	1 N=140	Placebo (1:1)	Ρ	Р	N					
[159]	Duration= 24 months									
NCT00395200,	Phase 2	Autologous								
Connick et al. Lance	t N= 10	mesenchymal stem cells	s N	Р		N	Ν		Ν	
Neurol 2012 [126]	Duration= 20+10 months	transplantation, oper	ı							

	label (before vs after							
	treatment)							
MAESTRO, Phase 3	MBP8298 500mg vs							
Freedman et al. N= 612	Placebo N N N N							
Neurology 2011 Duration= 2 years								
[133]								
Lamotrigine trial, Phase 2	Lamotrigine 400mg vs							
Kapoor et al. Lancet N=120	Placebo (1:1) N N N N	Ν						
Neurol 2010 [124] Duration=2 years								
ESIMS, Hommes et Phase 3	IVIG vs Placebo (1:1)							
al. Lancet 2004 [119] N=318	P N							
Duration= 27 months								
NA-SPMS, The Phase 3	Interferon beta-1b 250							
North American N=939	μg and 160 μg/m ² vs							
Study Group on Duration= 3 years	Placebo (1:1:1)							
Interferon beta-1b P								
in Secondary								
Progressive MS,								
Neurology 2004								
[131]								

IMPACT, Cohen et	Phase 3	IFN beta-1a 60mcg/week				
al., Neurology 2002		IM vs Placebo	Р	Р		
	Duration= 24 months					
SPECTRIMS, Li et al.	Phase 3	Interferon beta-1a 44µg				
Neurology 2001	N= 618	and 22µg vs Placebo	Ρ	Р		Ρ
[132]	Duration= 3 years					
Cladribine MRI	Phase 2	Cladribine 0.7mg/kg and				
Study Group, Rice et	N= 159	2.1 mg/kg vs Placebo				
al. Neurology 2000	Duration: 24 months		N	Ρ	Р	
[137]						
EU-SPMS, European	Phase 3	Interferon beta-1b vs				
Study Group on	N=718	Placebo (1:1)				
Interferon beta-1b	Duration= 36 months			.		
in Secondary				Ρ		
Progressive MS						
Lancet 1998 [123]						
Karussis et al.	Phase 2	Linomide 2.5mg vs				
Neurology 1996	N= 30	Placebo			Р	Ρ
[141]	Duration= 6 months					

PPMS	SPRINT-MS, Fox et	Phase 2	Ibudilast 100mg v	'S										
and	al. Cont Clin Trials	N= 255	Placebo (1:1)	Р										N
SPMS	2016 [160]	Duration= 96 weeks												
	NCT01144117,	Phase 2	Erythropoietin 48000 U	JI										
	Schreiber et al. Mult	N= 50	vs Placebo	Ν			Ν							
	Scler 2016 [129]	Duration= 24 weeks												
	ACTiMuS, Rice et al.	Phase 2	Early vs Late autologou	S										
	Trials 2015 [169]	N= 80	bone marrow cellula	r O		0					ο	0	0	0
			therapy											
	FLUOX-PMS,	Phase 2	Fluoxetine 40mg v	'S						 				
	Cambron et al. Trials	N= 120	Placebo	ο	ο	0					0			0
	2014 [128]	Duration= 108 weeks												
	NAPMS, Romme et	Phase 2	Natalizumab 300m	g						 		<u>,</u>		
	al. Neurology 2014	N= 24	open label (before v	rs P	Р		Ν		Р	Р	Ρ			
	[130]	Duration= 60 weeks	after treatment)											
	CUPID, Zajicek et al.,	Phase 3	Dronabinol vs. Placeb	0						 				
	Lancet Neurol 2013	N=498	(1:1)	N		Ν		N						
	[138]	Duration= 3 years												

[170, 171]. However, standardisation of software for analysis is needed to made widespread application in clinical trials possible [172].

Overall, measures of global and regional brain atrophy are gaining relevance in clinical trials on progressive MS, reflective of improvements in measurement techniques allowing good repeatability and sensitivity to change. Nevertheless, there are several possible limitations, including changes in magnet, gradients, coils, distortion corrections and image-contrast changes. Patients treated with anti-inflammatory treatments have a slight decrease in the brain volume in the first six to twelve months (pseudoatrophy), compared with placebo, due to the resolution of inflammation and oedema [173, 174]. A possible solution is to re-baseline subjects after 6 months [175, 176], although longer periods may be required for more toxic types of treatment (e.g. chemotherapy during bone marrow transplantation) [177]. However, re-baselining implies reduced time of observation on treatment, with subsequently reduced number of patients reaching study outcomes, and, then, loss of statistical power. In the OPERA II trial (one of the two phase 3 trials for Ocrelizumab in RRMS), statistical significance in brain volume change was lost when analysing data from week 24 to 96, instead of baseline to week 96 [178].

A reversible fluctuation of brain volumes can also occur because of variations in hydration status, which could be affected by disability status and time-of-the-day of MRI acquisition [179, 180].

2.2.3. Advanced brain MRI techniques

Conventional neuroimaging techniques lack specificity with regard to different pathophysiological substrates of MS, and are not able to explain the heterogeneous and long-term clinical evolution of the disease [176, 181–183]. Advanced MRI techniques, such as MTR, DTI and MRS, may provide

higher pathological specificity for the more destructive aspects of the disease (i.e., demyelination and neuroaxonal loss), and be more closely associated with clinical correlates [173, 184]. Moreover, functional MRI (fMRI) is contributing to the definition of the role of cortical reorganisation after MS tissue damage [151].

MTR values reflect the efficiency of the magnetisation exchange between mobile protons in tissue water and those bound to the macromolecules, such as myelin. MTR has been associated with disease progression in PPMS [148, 185]. In view of this, MTR has been included in several clinical trials in progressive MS and has been measured in GM (cortical and deep), WM, T2 lesions, putamen, thalamus and optic nerve [125–127, 130].

DTI measures brain tissue microstructure by the exploitation of the properties of water diffusion. From the tensor, it is possible to calculate the magnitude of diffusion, reflected by mean diffusivity (MD), and diffusion anisotropy, which is a measure of tissue organisation, generally expressed as fractional anisotropy (FA). In line with this, MD is increased and FA is decreased in T2 lesions, WM and GM from MS patients [36, 186]. DTI has been assessed across multiple scanners/platforms and is suitable for multi-centre studies [187–189]. DTI is the most frequently-used advanced MRI metric in phase 2 and 3 clinical trials in progressive MS, so far with demonstrable beneficial effects. MD and FA have been measured in pyramidal tracts, WM, GM and lesions in different trials in progressive MS [125, 127, 128, 130, 136]. More specific measures such as axial and radial diffusivity (RD) can be calculated as measures of the mobility of water along and perpendicular to axons (reflecting axonal density and demyelination respectively) [184]; however, they have not been included in clinical trials in progressive MS so far, due to difficulties in standardised acquisitions between centres. The fMRI provides signal related to brain activation based on blood oxygen consumption and blood flow in the brain, and has only been included in two clinical trials on progressive MS [136, 163].

MRS can measure brain levels of several metabolites [190, 191]. The most commonly measured is total N-acetyl-aspartate (NAA), a marker of axonal loss and metabolic dysfunction [192]. NAA has been included in a few clinical trials in RRMS [193], and one in PPMS [194].

2.2.4. PET

PET is a quantitative imaging technique, which investigates cellular and molecular processes in vivo using positron-emitting molecules, ideally binding a selective target [191, 195, 196]. As MS is a complex and multifactorial disease, various radioligands have been tested. Amyloid tracers, measuring myelin loss and repair, and ¹¹C-Flumazenil, reflecting neuronal integrity, might be of interest for clinical trials on neuroprotective compounds [182, 196–199].

To date, no MS clinical trials have included PET, reflecting its invasive nature and high costs. In the future, the development of standardised procedures might represent a trigger for the application of this technique in phase 1 and 2a clinical trials [119].

2.2.5. OCT

OCT is a non-invasive method to obtain high spatial resolution images of the retina, measuring retinal nerve fibre layer (RNFL) thickness and macular volume.

RNFL is thinner in patients with MS than in healthy controls, even in patients with MS who have not experienced episodes of optic neuritis [200]. Therefore, OCT measures a more diffuse pathological process which better corresponds to overall CNS damage [201, 202].

RNFL and macular volume have been included in a few clinical trials on progressive MS (**Table 2.1**) [126, 128, 136, 160], so far without demonstrable neuroprotective effects.

OCT is a fast, non-invasive, easy-to-use imaging method producing quantitative measures reliably, with great potential in MS for testing neuroprotective strategies over a short time frame [146]. Like brain volume, RNFL is sensitive to biological variations. However, there is the need for high-quality acquisitions and appropriate image processing, performed by trained examiners following specific consensus criteria [203].

2.3. Spinal cord outcome measures

2.3.1. Spinal cord lesions

Spinal cord lesions on MRI correspond to areas of demyelination, oedema/inflammation, neuroaxonal loss and gliosis, affecting spinal cord structure and function [25, 116]. Post-mortem spinal cord studies have described a larger proportion of demyelination in the GM (33%), than in the WM (20%), with lesions involving either both GM and WM, or GM alone [204]. No difference in the extent of GM demyelination was seen between different cord levels, whilst most of WM lesions occur in the cervical cord [204, 205].

2.3.1.1. Characteristics of MS lesions on spinal cord MRI

Spinal cord lesions are visualised as areas of T2 hyperintensity (**Figure 2.2**) and, less commonly, as areas of T1 hypointensity on conventional spin echo sequences. Although T1 hypointensity in the spinal cord is thought to be rare in MS, a recent study using inversion-recovery prepared fast field echo sequence (e.g., heavily T1 weighted sequence) at 3T demonstrated that 87% of patients with MS show T1 hypointense lesions in the spinal cord, and most of the lesions seen on the short-tau inversion recovery (STIR) T2 weighted sequence are hypointense on T1 [206].

After administration of gadolinium, new inflammatory activity of MS lesions, with associated BBB breakdown, allow the MS lesions to appear as areas of T1 hyperintensity; gadolinium enhancement in acute spinal cord lesions is generally nodular and, in 20% of the cases, may have a ring-shape [207–209].

MS lesions often occur in the cervical region (59%), and, less frequently, in the lower thoracic spinal cord (T7-12) (20%) [210]. On sagittal scans, they appear as cylindrical lesions, while on axial images they appear as wedge-shape lesions. In sagittal views, they rarely exceed two vertebral segments in length. On axial scans, MS lesions involve less than 50% of the cross-sectional area, occupy preferentially the lateral and posterior WM columns and do not spare the GM. However, spinal cord involvement can be diffuse, as shown by diffuse signal abnormalities on PD images, especially in the progressive forms of MS; diffuse signal abnormalities in RRMS are associated with a poor prognosis [211, 212].

2.3.1.2. Recommended spinal cord MRI protocols

The MRI protocols recommended for spinal cord lesion detection in the clinical setting include both sagittal and axial scans [213]. For sagittal imaging, conventional or fast dual-echo (proton density

(PD) and T2-weighted, either in combination or independently) spin-echo sequences are usually considered the gold standard. A recent study at 1.5T suggested that PD fast spin-echo sequence detects cord lesions in patients who have normal T2 fast spin-echo MRI, and should therefore be used as a core sequence at 1.5T [214]. Either the T2 or PD spin-echo sequence can be substituted with a STIR T2-weighted sequence, which improves the visibility of MS lesions [215]. In general, it is

Figure 2.2. Lesions in MS and NMO.

T2 sagittal and axial (inset) spinal cord MRI of a patient with MS and a patient with AQP4-Ab positive NMOSD. In MS (**A**), spinal cord MRI shows a single area of T2 hyperintensity which involves both GM and WM in the lateral-posterior part of the cord, and has cylindric shape on sagittal view and wedge shape on axial view. In AQP4 NMOSD (**B**), there is a longitudinally extensive transverse myelitis from C1 to C5, with preferential involvement of the central area of the spinal cord. Arrows on the sagittal plane indicate the level at which the lesion is presented on the axial plane; arrow-heads indicate additional lesions. Adapted from Moccia M et al. Ther Adv Neurol Disord 2019 [109].



not recommended to use the STIR sequence on its own because of its susceptibility to flow-related artefacts and possible lower observer concordance [216]. An alternative to STIR sequence or to one of the two dual-echo T2-weighted sequences, is a heavily T1-weighted sequence [217], such as phase-sensitive inversion recovery (PSIR) or magnetisation-prepared rapid gradient echo (MPRAGE), which improves the detection of MS lesions in the cervical cord [218]. The three-dimensional (3D) acquisition of the MPRAGE permits multiplanar reconstruction that facilitates the delineation of lesions [219]. A recent 3T study has reported that a 3D double inversion recovery (DIR) sequence for cervical spinal cord imaging is more sensitive at detecting inflammatory lesions than conventional 2D T2-weighted TSE sequence [220]. However, the DIR sequence of the spinal cord is not widely used in clinical practice because it is strongly affected by artefacts, especially in obese patients, and by magnetic field inhomogeneities, and its coverage capability is currently limited to the cervical spine [220].

For axial imaging, possible sequences are 2D and/or 3D T2-weighted fast spin echo sequences. A full cervical cord axial coverage detects more lesions (9-22%) than sagittal scans alone [210, 221], and can also exclude lesions in cases of equivocal abnormalities on sagittal scans [210, 221, 222].

No significant improvement in lesion detection was found when using 3T field strength compared with 1.5T [223]. Improvements in lesion detection are expected at 7T, although its application and relevance require further studies, especially in the context of new coil designs and optimised acquisition times [224–226].

Although pathological involvement of the spinal cord GM contributes significantly to disability in RRMS and SPMS [227], its assessment with conventional MRI techniques is not achievable because

of insufficient contrast between tissue compartments and low spatial resolution. In the research setting, improved delineation of cervical cord lesions and their involvement of the WM and GM are obtained by using 3D-PSIR in combination with axial 3D gradient-echo fast field echo (3D-FFE) [228], although this MRI protocol requires a long acquisition time and has limited coverage of the cervical cord.

2.3.1.3. Diagnosis of MS supported by spinal cord MRI

The 2017 revised McDonald criteria confirmed that MRI is the most useful paraclinical test to aid the diagnosis of MS, and can be used to establish dissemination of lesions in space (DIS) and time (DIT) [61]. The spinal cord is one of the four areas of the CNS where lesions with characteristics typical of MS are scored to confirm DIS. Prior to the 2017 McDonald criteria, only asymptomatic spinal cord lesions were scored for DIS, which led to the high specificity of the DIS criteria; in order to facilitate the scoring of the criteria, and avoid discussing which lesion is the symptomatic one in cases of multiple lesions occurring in the same CNS location, the 2017 revised criteria do not distinguish anymore between symptomatic and asymptomatic lesions when testing the DIS criteria, as already discussed in <u>Chapter 1</u> [61]. In particular, the inclusion of spinal cord symptomatic lesions for DIS or DIT increases diagnostic sensitivity, with little or no reduction in specificity [80, 229, 230].

Whilst brain MRI is recommended in all patients who are undergoing investigations for the diagnosis of MS, spinal cord MRI is advisable when: (1) The clinical presentation suggests a spinal cord lesion; (2) The clinical presentation is suggestive of PPMS; (3) Brain MRI is normal, but there is a strong clinical suspicion of MS; (4) Brain MRI findings are inconclusive (e.g., age-related vascular changes) [61, 217, 231]. Therefore, spinal cord MRI is generally recommended in patients with spinal cord CIS and in those with non-spinal MS not fulfilling the DIS criteria. It is debated whether all the remaining CIS patients, who have non-spinal MS and fulfil DIS criteria on brain MRI brain, should undergo spinal cord MRI [232].

More recently, patients with clinical features typical of MS, but showing evidence of pathology exclusively in the spinal cord, even with a single lesion, and whose MRI does not fulfil the DIS criteria, have been described as two novel clinical entities: (1) Progressive solitary sclerosis, when insidiously progressive upper motor neuron impairment can be attributed to an isolated demyelinating lesion within the CNS (within the spinal cord in 90% cases) [233]; and (2) Pure spinal MS, when relapsing episodes of short-segment myelitis occur over time, in the absence of typical brain or optic nerve lesions [234]. Progressive solitary sclerosis and pure spinal MS are proposed novel MS phenotypes, characterised by a predominant spinal cord pathology. Myelocortical MS is another suggested pathology subtype of MS where axonal loss in the WM occurs in absence of obvious demyelination, but is still lacking further pathology and clinical validation [39].

2.3.1.4. Differential diagnosis facilitated by spinal cord MRI

MS could be responsible for up to 50% cases of inflammatory myelopathies and, thus, a number of conditions should be considered in the differential diagnosis. These include neuromyelitis optica spectrum disorders (NMOSD), myelin oligodendrocyte glycoprotein-antibody (MOG-Ab) associated disease, sarcoidosis, paraneoplastic syndromes, infectious and post-infectious diseases, and require different treatment and management strategies [235, 236]. Certain lesion characteristics on spinal cord MRI may aid the clinicians to navigate through the differential diagnosis of spinal cord inflammatory pathology [213].

NMOSD is responsible for up 50% cases of longitudinally extensive transverse myelitis (LETM), defined as T2 hyperintense spinal cord lesion extending \geq 3 vertebral levels (**Figure 1.2**) [236]. However, the length of spinal cord lesions in NMOSD depends on timing of MRI with respect to clinical onset [237]. NMOSD can also present with involvement of <3 vertebral segments [238]. Additionally, LETM is not a pathognomonic feature of NMOSD, and other inflammatory demyelinating conditions can cause a LETM.

One of the most important spinal cord MRI features differentiating NMOSD from MS, and other LETM aetiologies, is the presence of bright spotty lesions (BSLs) [239, 240], defined as lesions with signal intensities at least as high as, but not higher than, that of the surrounding CSF on a T2-weighted image, and not as low as that of the surrounding CSF on a T1-weighted image. Bright spotty lesions are seen in the majority of patients without LETM, and it is thought that they indicate severe damage to the spinal cord. Other spinal cord distinctive features of NMOSD are lesions occupying ≥50% axial cross-sectional area (transversally-extensive lesion), T1 hypointense lesions, and centrally- or both centrally- and peripherally-located lesions [236]. Gadolinium enhancement is common in NMOSD, but variable in its appearances (frequently irregular and punctuate); ring-enhancement is seen in one-third of NMOSD myelitis episodes and distinguishes NMOSD from other causes of longitudinally extensive myelopathies, but not from MS [209]. Additionally, NMOSD lesions are more frequently located in the cervical and/or dorsal spinal cord, when compared with the lumbar cord [236].

20-40% of NMOSD patients negative for aquaporin-4 antibody (AQP4-Ab), are instead MOG-Ab positive [241, 242]. The LETM of MOG-Ab-associated disease is virtually indistinguishable from that of NMOSD AQP4 positive disease.

Spinal cord sarcoidosis is an under-recognised cause of LETM, and can precede symptoms of systemic and pulmonary sarcoidosis. Linear dorsal leptomeningeal enhancement extending ≥ 2 vertebral segments and persisting >2 months differentiates spinal cord sarcoidosis from NMOSD and MS, where gadolinium enhancement is patchy, diffuse or ring-like [243, 244]. When linear dorsal subpial enhancement is combined with central canal enhancement in cases of sarcoidosis, a "trident" sign on axial post-gadolinium sequences has been described [244, 245].

Other important causes of spinal cord lesions are post-infectious myelitis (e.g., cytomegalovirus, herpes simplex virus, varicella zoster, enterovirus, etc), which often present with LETM, and are associated with variable radiological appearances on T2, T1 and post-contrast T1 weighted images.

Non-inflammatory myelopathies include vascular aetiologies (e.g., acute spinal cord infarction), spinal dural arteriovenous fistula, tumours, nutritional deficiencies, infections, and compressive myelopathies. In these cases, timely diagnosis and management is crucial to improve clinical outcomes [235, 246].

Additional clinical (e.g., hyper-acute or gradually progressive onset), radiological (e.g., presence of lesions on brain MRI, abnormalities on chest PET imaging), laboratory (e.g., presence of AQP4 and MOG antibodies) features might be necessary to establish the exact diagnosis of myelopathy [236, 243, 245]. The most striking consequence of a more appropriate and widespread use of spinal cord MRI and additional tests in cases of spinal cord myelopathy is that the recognition of an "idiopathic" transverse myelitis is reducing over time [235].

2.3.1.5. Prognosis of MS using spinal cord MRI

In patients with radiologically isolated syndrome (RIS), the presence of asymptomatic spinal cord lesions is seen in 64% of patients who later develop CIS or MS, and in 100% of patients who later develop PPMS [247].

In patients with CIS, the presence and the number of spinal cord lesions are associated with increased risk of clinical conversion to MS and disability progression, regardless of demographics, clinical features and brain MRI [248–250]. In contrast, the probability of disability progression is very low in the absence of spinal cord lesions [248].

In established MS, spinal cord lesions are associated with a higher risk of relapse [251], disability progression [252, 253], and switching of DMT due to poor treatment response [254]. Also, upper cervical cord lesion load, quantified on PSIR sequences, is greater in progressive forms of MS than in RRMS, and is associated with disability [252]. In SPMS, spinal cord lesions frequently involve at least two spinal cord WM columns and extend to the GM [212]. The main limitation of these studies is that spinal cord coverage was confined to the upper cervical cord, in order to minimise physiologic artefacts and enable high-resolution acquisitions within an acceptable time frame, thus limiting generalizability to clinical practice [212].

2.3.1.6. Monitoring MS with spinal cord MRI

Spinal cord lesions are more likely to be symptomatic and leave residual neurological impairment, due to poor compensatory capacity of the spinal cord, than brain lesions [250, 251]. Despite this, 58% of new spinal cord lesions were reported to be asymptomatic and 25% of RRMS patients develop at least one asymptomatic spinal cord lesion over 1.5 years [255]. When only stable RRMS patients are considered, 10% of them show subclinical spinal cord lesion activity alone [251]. Interestingly, asymptomatic spinal cord lesions predict clinical relapses when combined with asymptomatic brain lesions [251]. Thus, spinal cord MRI could disclose subclinical disease activity in otherwise clinically stable MS, and could enhance a more thorough understanding of the course of MS [114]. Asymptomatic spinal cord lesions may not be restricted to MS patients, as they have also been observed in NMOSD patients [256], but more data in NMOSD are needed.

2.3.1.7. Spinal cord lesion mapping

Recent developments in imaging post-processing have allowed the creation of probability maps of spinal cord lesions, which show probability of each voxel being "lesional". Single-centre studies combining 3D-T1 weighted FFE and the active surface model (ASM), a semi-automated voxel-based analysis of the spinal cord within JIM, showed that SPMS and especially PPMS patients have higher lesion counts and volumes, when compared with RRMS, and that lesions are more frequently located in the posterior cord than in the anterior cord, and in the upper cervical cord than in the lower cord [206, 257]. A larger, multi-centre study, employing fully automated methods based on the Spinal Cord Toolbox (SCT) confirmed that lesions are more frequently located in the posterior columns in all MS subtypes, and that lesion mapping at C3 clearly distinguishes between MS subtypes [258]. In particular, high lesion probability was found in the posterior columns in RRMS, posterior and lateral cord in SPMS and posterior, lateral and central regions in PPMS (Figure 2.3) [258]. High disability levels were associated with lateral and central cord involvement [258].

2.3.2. Spinal cord atrophy

Spinal cord atrophy is a common and clinically relevant aspect of MS. An increasing number of

Figure 2.3. Lesion probability maps in the spinal cord.

Lesion probability maps at the cervical level are shown for different disease subtypes. Adapted from



Eden et al. Brain 2019 [258].

studies have focused on the importance of spinal cord atrophy as a biomarker of disability progression and as an outcome measure in clinical trials.

2.3.2.1. Pathological correlates

Spinal cord atrophy is the consequence of different pathological processes, including axonal transection and associated neuro-axonal loss, demyelination, loss of oligodendrocytes, gliosis, and, ultimately diffuse tissue injury [23, 24, 226, 259–262]. Although these pathological abnormalities occur within focal lesions, extensive tissue abnormalities are also present in the normal-appearing spinal cord of MS patients, and this finding may explain why spinal cord atrophy occurs independently of spinal cord lesions [23–25, 35, 263–266]. Additionally, spinal cord atrophy also occurs, at least in part, independently of brain pathology [225, 264, 267].

2.3.2.2. Advances in spinal cord atrophy measurements

Spinal cord atrophy is generally measured as cross-sectional area at the cervical level, which is least affected by movement artefacts, yields the most reproducible results, and provides the best clinical correlates [268–272]. The most common levels are C1-C2 and C2-C3, but measurements can be also made between C1 and C7 [273].

Atrophy assessment can be done on a variety of sequences, mainly 3D T1-weighted and T2*weighted gradient echo sequences on different MRI scanners (e.g. Philips, Siemens, GE) [115, 274, 275].

In the present thesis, we will use two different methods for spinal cord image segmentation and atrophy calculation: surface-based and image-based methods [276]. The older methods were fully manual, whilst the most recent methods have been semi- or fully-automated. For example, JIM is a surface-based method that semi-automatically outlines the cord, after marking the centre of the spinal cord [277]. Within the JIM tool, the ASM has provided more prompt and reproducible measures of the spinal cord volume, compared with manual methods [278]. The ASM offers a considerable reduction in user interaction time, and can be performed over long spinal tracts. The user needs to identify landmarks at the extremes of the region to study, and, then, mark the centreline of the cord. Sagittally-acquired images are then reformatted to the axial plane to obtain five contiguous 3 mm slices; the program automatically calculates the radius and the centre of each axial slice and, finally, the cross-sectional area is obtained by averaging these contiguous slices [274, 279, 280]. Other semi-automated method is NeuroQLab (an image-based method that segments

the upper cervical cord from surrounding non-spinal cord tissue by using a Gaussian mixture modelling method) [281, 282].

Recent efforts have attempted to develop fully-automated methods, such as the SCT, which is an open-source comprehensive software dedicated to the processing of spinal cord MRI. SCT is built on previously-validated methods and includes motion correction tools, templates and algorithms to segment the spinal cord, allowing standardisation and automation of the processing pipeline [283]. The segmentation tool (*PropSeg*) contained in the first version of SCT (version 3.0) has already been tested on a large cohort of MS patients and healthy controls, and has been used in <u>Chapter 5</u> of the present thesis. This fully-automated surface-based image segmentation method has the same sensitivity as the ASM tool within JIM, but has higher inter-rater reproducibility and is more time-efficient [284]. A newer version of SCT (version 4.0) includes a fully-automated segmentation method based on convolutional neural networks (*DeepSeg*) [285], that has been used in <u>Chapter 6</u> of the present thesis; this version also has a fully-automated framework for intramedullary lesion segmentation, presenting with higher efficiency and reproducibility in lesion count and volume, when compared with manual detection [286].

A recent study has demonstrated that there is a systematic difference in the values of the crosssectional area between methods, with lower values provided by fully-automated methods (SCT) than semi-automated methods (NeuroQLab and JIM) [287, 288]; a good agreement between these two semi-automated techniques was observed [287]. When using these methods for longitudinal spinal cord atrophy calculation, the rate of atrophy is estimated indirectly by numerical subtraction of spinal cord cross-sectional area measurements calculated at different time-points [289].

There has been a recent shift towards calculating spinal cord atrophy using brain volumetric images [282, 290]. A recent collaborative study has confirmed that the spinal cord cross-sectional area, calculated at C1-C2 level using dedicated volumetric MRI of the spinal cord, is similar to that obtained using volumetric brain MRI [287, 290, 291]. <u>Chapter 6</u> will aim to validate this new approach, which has the potential to allow calculation of spinal cord atrophy without acquiring a dedicated cord sequence, thereby saving scanning time, in both clinical trials and observational cohorts.

Few clinical trials in progressive MS have included spinal cord atrophy as outcome measure (**Table 2.1**) [63, 124, 125, 136, 144, 165–167, 213], but yielded inconclusive or negative results. Those disappointing results may be, at least in part, due to the relatively high noise and low reproducibility of the segmentation-based methods [91, 109, 292]. A more widespread use of spinal cord atrophy is currently hampered by challenges to obtain high reproducibility and responsiveness to changes when measuring such a small structure. Small absolute changes in spinal cord area are difficult to detect in a multi-centre setting, where there may be a great variability of imaging protocols and scanners [156]. The acquisition of high-quality spinal cord MRI can be affected by artefacts (e.g. breathing, pulsation of blood and CSF), and this may limit the precision of spinal cord atrophy measurements. As a consequence, sample size estimates obtained for current measurement techniques are fairly large and generally prohibitive, when compared with brain atrophy [144].

2.3.2.3. Spinal cord atrophy in disease phenotypes

Spinal cord atrophy occurs even in early stages of MS, and has been detected in patients with CIS [275, 293–295]. In CIS patients who were followed-up for 5 years after onset, the lowest rate of spinal cord atrophy (-0.1% a year) was observed in those who remained CIS, whilst the highest rate (-1.4% a year) was detected in patients who developed MS and had an EDSS at the last time point equal or greater than 3 [250]. In general, a high rate of spinal cord atrophy is observed in the progressive forms of MS, especially SPMS (-2.2% per year) (Figure 2.4) [226, 273, 294–296]. Overall, in clinically-definite MS, the rate of cord atrophy has been reported to vary between 1 and 5% per year [115, 226, 297–299]. A multicentre study has detected a rate of -1.22% per year in patients with stable MS and -2.01% in patients who deteriorated over time [273]. Interestingly, there is a significant development of spinal cord atrophy in early PPMS patients when compared with healthy controls over only 1-year follow-up, but not in patients with established SPMS, who had a higher disability and more atrophic cord than early PPMS patients [300]. Although the rate of atrophy may vary slightly between studies, because of different cohorts and different methods, it is consistently higher than the rate of brain atrophy, which is known to be around -0.5% per year in MS patients [149]. A recent meta-analysis of twenty-two longitudinal studies assessing spinal cord atrophy in all MS subtypes revealed a pooled rate of spinal cord atrophy of -1.78% per year, that increased to -2.08% per year when considering progressive patients alone [268].

The segmentation of GM areas on PSIR images at 3T allows the evaluation of GM atrophy in MS. Relapsing MS patients show smaller spinal cord GM areas (i.e., higher atrophy) than age- and sexmatched controls, without significant differences in spinal cord WM areas [301]; the GM of progressive MS patients shows the highest degree of atrophy [301].

Figure 2.4. Spinal cord atrophy visible on conventional MRI.

Cervical cord MRI with sagittal and axial views at C2 level (inset, used for spinal cord cross-sectional area measurements) in CIS (**A**) and PPMS (**B**) of same age (40 y.o.) and sex (males). Adapted from Moccia et al. Ther Adv Neurol Disord 2019 [109].



Only few studies have examined cervical cord atrophy in NMOSD, and reported conflicting results. Some studies found more pronounced spinal cord atrophy in AQP4 positive patients than MOG patients [302], and in MS than NMOSD [303], whereas another study found similar reductions of cross-sectional areas in NMOSD and MS [304].

2.3.2.4. Spinal cord atrophy and MS disability

A number of studies have shown associations between: (1) the extent of spinal cord atrophy at a single time point and concurrent disability [305], and (2) the rate of spinal cord atrophy over time and disability progression [250, 275, 295, 306–308]. A recent study has reported that every 1% increase in the annual rate of spinal cord volume loss is associated with a 28% risk of developing

disability progression in the subsequent year [296]. In a longitudinal cohort of non-spinal CIS, upper cord cross-sectional area (UCCA) decrease was associated with 5-year increased disability, measured by EDSS [250]. Overall, spinal cord atrophy can account for 77% of disability progression after 5 years [227, 305, 309]. Within EDSS, the sub-scores that reflect the neurological functions mediated by spinal cord pathways, such as the pyramidal, sensory, bowel and bladder functional scores, correlated with spinal cord atrophy [310]. Higher spinal cord atrophy rate is associated with worsening of more specific measures of motor disability, such as the 9HPT and the T25FWT [296, 305]. Associations between the development of spinal cord atrophy and disability progression are particularly strong in PPMS [311].

2.3.2.5. Spinal cord atrophy in clinical trials

Since spinal cord atrophy rates are two-to-three times higher than brain atrophy (-1.78% vs -0.5% per year), in particular in progressive MS [268, 312], and the spinal cord is a very eloquent site of pathology in MS, spinal cord atrophy has been considered as an exploratory outcome measure in phase 2 and phase 3 clinical trials, especially in patients with progressive MS, although much less frequently than brain atrophy [63]. However, clinical therapeutic trials that incorporated spinal cord atrophy as an outcome measure did not demonstrate beneficial drug effects on this metric [124, 144, 313, 314]. In addition to the possibility that the medications tested were not effective, there may be other reasons for these negative results, related to methodological difficulties of calculating spinal cord atrophy; these include: movement artefacts and subsequent image noise; the limited spatial resolution of MRI scanners, which is an important issue, given the small cord size; multicentre design, with inter-site variability related to the use of different scanners with different acquisition settings; and inter-study variability related to the use of different methods to calculate spinal cord area [156, 315]. Also, spinal cord normalisation using the intracranial volume, which aims to reduce

the effect of biological conditions unrelated to the disease, has been suggested [269, 270, 316], but it is not always performed.

There have been encouraging results from a recent, single-centre, study employing spinal cord atrophy [300, 315]. If patients at the early stage of PPMS, with mild disability and a non-atrophic cord are selected, the sample size necessary to run a trial over only 1 year is achievable [300].

2.2.3. Advanced spinal cord MRI techniques

Advanced spinal cord imaging techniques are currently used in exploratory studies to investigate microstructural abnormalities which reflect neurodegeneration, and to develop new targets for therapeutic intervention [91, 191]. These techniques include methods that study neuro-axonal integrity (DTI and new models of diffusion), myelin content (MTR and myelin water imaging), metabolic changes (MRS and functional connectivity on fMRI) (**Table 2.2**). However, advanced MRI techniques remain technically challenging, and results from studies using different acquisition protocols are difficult to compare [317–319]. Hereby, I will focus on the most recent advances in these techniques and their latest applications to MS patients, and refer to other manuscripts for more technical and comprehensive reviews [184, 320, 321].

2.2.4.1. Diffusion based techniques

DTI provides quantitative measures of microstructural abnormalities, which have been found to be abnormal in MS when compared with healthy subjects [322]. Recent studies have reported increased magnitude of diffusion in the direction perpendicular to the main direction of fibre bundles (i.e., RD), and reduced diffusion anisotropy (i.e., FA) in RRMS with acute spinal cord involvement, when compared with healthy controls, and in SPMS, when compared with clinically stable RRMS [227, 318], suggesting reduced myelin and axonal integrity and impaired neuronal fibre coherence [323]. A combination of DTI indices could explain up to 77% of the EDSS variability, suggesting a strong contribution of spinal cord microstructural changes to irreversible disability (**Table 2.2**) [227]. A recent study, which investigated the reproducibility of DTI-derived measures at C1-C6 between different sites, has shown the feasibility of multi-centre spinal cord DTI, with adequate matching of the sequence design across sites, in particular for different manufacturers [324]. The main advantages of spinal cord DTI are that it is simple to acquire and easy to interpret; its main limitation is that the DTI-derived measures are based on model approximations that the biological substrate is likely to violate and have low pathological specificity.

Q-space imaging (QSI) is a model-free technique that determines the voxel wise probability density function of fibre orientation (using apparent diffusion coefficient (ADC), full-width half-maximum (FWHM), and zero displacement probability (PO)), and seems to be more sensitive than conventional DTI measures at detecting MS-related abnormalities [325]. QSI-derived indices of perpendicular diffusivity are increased and indices of parallel diffusivity are decreased in the spinal cord of early PPMS, when compared with controls, possibly reflecting increased movement of water in the direction perpendicular to the long axis of the cord, due to the breakdown of myelin and axonal membranes, even in the absence of a significant degree of spinal cord atrophy [326, 327]. Changes in QSI-derived measures are associated with different measures of clinical disability, suggesting that they reflect pathological abnormalities that contribute to neurological deficits (**Table 2.2**) [326, 327]. The main limitations of QSI include the need to acquire a large number of data points, therefore necessitating long acquisition times, limited directional resolution, and difficulty in interpreting the probability density function.

Neurite orientation dispersion and density imaging (NODDI) is a recently developed multicompartmental diffusion model, providing microstructural indices related to geometrical complexity of neurite architecture (**Figure 2.5**) [328]. This technique applied to the spinal cord has been recently validated by comparison with histology, and a trend toward lower neurite complexity in demyelinated lesions, has been demonstrated [329, 330]. In a pilot study, neurite dispersion index was reduced in the spinal cord of RRMS patients when compared with healthy controls [331], and a recent study has described reduced orientation index in the normal-appearing WM and lesions of the spinal cord from 6 MS patients, when compared with 8 healthy subjects (**Table 2.2**) [332]. The

Figure 2.5. Neurite orientation dispersion and density imaging in the spinal cord.

NODDI provides tissue-specific indices related to geometrical complexity of neurite architecture. Cervical spinal cord NODDI maps (at C2 level) of isotropic volume fraction (IVF) (estimating the amount of free water), neurite density index (NDI) (estimating the amount of neurites), and orientation dispersion index (ODI) (estimating the variability of neurite orientations) are shown from healthy control and MS patients. Courtesy Dr Francesco Grussu, University College London, United Kingdom.



main findings of brain and spinal cord NODDI studies is that for similar value of FA there are different combinations of orientation dispersion index (ODI) and neurite dispersion index, so NODDI is expected to be more pathologically specific than DTI.

Finally, an exploratory study has assessed the feasibility of the spherical mean technique (SMT), which is another multi-compartmental diffusion model, in the spinal cord in 6 MS patients and 8 controls (**Table 2.2**) [333]. SMT, which is feasible on standard MRI scanners, enables mapping of the neurite density and compartment diffusivities, and is sensitive in identifying abnormal changes in MS lesions when compared with healthy WM [333].

An *in vivo* study of the spinal cord, which fits, studies and compares several biophysical models, similar to what has been done in the brain [334], would be important to establish the limitations and the advantages of each model and the clinical potential of the latest models. Reducing the acquisition times, without sacrificing the accuracy of the derived indices, may be possible with the latest techniques [333]. The development of more advanced hardware (high-field MRI scanners), software (localisation, gating, and motion compensation), and coils (multi-channel phased-array coils) will contribute to expand the use of diffusion-derived metrics in MS clinical practice and trials [320].

2.2.4.2. Techniques reflecting myelin content

MTR is a quantitative technique measuring the magnetisation exchange between freely mobile protons and those associated with macromolecules such as myelin, providing an indirect estimate of myelin content, in addition to neuroaxonal integrity and water content. A large study carried out in patients with MS reported lower MTR values in patients with higher EDSS, than those with lower EDSS, independent of lesion load [335], suggesting that this measure can detect clinically relevant differences beyond conventional imaging. Reduced MTR values were found in the cervical spinal cord of 60 patients with early RRMS when compared with 34 age-matched controls, in the absence of spinal cord atrophy [336]. This study also showed that the main contribution to low MTR levels is from the normal-appearing spinal cord tissue, since the effect of the lesions is minimal [336]. In patients, there was a correlation between lower MTR and higher lesion load [336]. Evidence for reduced MTR values was also found in the cervical cord of patients with RIS [317], although this finding requires further confirmation. Of note, the distribution of MTR reduction in the spinal cord supports a spatial pattern of microstructural damage that resembles that in the brain [336, 337], and suggests that MTR abnormalities in a region involving the pia mater and subpial cord occur early in the course of MS and are more marked in those with a progressive course [338]. Clinical correlates of MTR are reported in **Table 2.2**.

Myelin water imaging has been validated as a myelin marker [339, 340], but it has been applied to the spinal cord in only a few studies. Myelin water fraction varies along the spinal cord proportionally to the WM area fraction [341]. In patients with cervical spondylotic myelopathy, myelin water imaging shows high specificity in detecting impaired spinal cord conduction, when compared with conventional imaging (e.g., T2 signal intensity), which only provides a measurement of the extent of spinal cord compression [342]. In MS, spinal cord myelin water fraction decreased by 11% in PPMS, but not in healthy subjects [343], and was associated with disability scores (**Table 2.2**) [344], suggesting progressive demyelination and neuro-axonal loss in this disease subtype, that is related to progressive disability accrual. Cervical spinal cord myelin water volume fraction progressively decreases in MS, but not in NMOSD, in the absence of clinical relapses, suggesting that
neurodegenerative and demyelinating processes occur continuously in MS, but not in NMOSD where inflammation might dominate [345].

MTR and myelin water imaging appear to provide complementary information. Although MTR is not pathologically specific, it is commonly available and fast to acquire, whilst myelin water imaging is more specific as a myelin marker, but requires more complicated post-processing and is not a sequence product.

A recent paper investigated the role of spinal cord quantitative MT saturation technique (MTSat), minimally affected by T1 relaxation and field inhomogeneity, and demonstrated that MTSat correlates with disability more strongly than MTR, suggesting higher sensitivity to tissue damage for future clinical applications (**Table 2.2**) [346].

Finally, quantitative magnetisation transfer (qMT) applied at 3T with reasonable acquisition time showed excellent grey/white contrast and sensitivity to MS pathology (lesions) [347].

2.2.4.3. Metabolic imaging techniques

¹H-MRS estimates levels of metabolites, as long as they are available in relatively high concentrations [191, 348, 349]. The most commonly estimated metabolites are total NAA (a marker of neuronal metabolism and, more in general, of neuronal integrity); NAA/Cr (NAA values normalised by voxel creatinine (Cr)); glutamate and its precursor glutamine (Glx) (whose reduction indicates chronic neuro-axonal degeneration); and *myo*-inositol (a marker of glial cell activation and proliferation) [191, 349]. A recent investigation of MRS at 3T using *in vivo* and *post-mortem*

experiments reported an extended metabolic profile of the spinal cord, thereby indicating the rich information which can be provided by this technique [350].

When MRS was applied to early PPMS patients, lower NAA, lower Glx, and higher *myo*-inositol, in particular within lesions, were detected in patients compared with normal-appearing tissue in healthy controls [326]. Metabolic changes within the spinal cord occurred in the absence of significant spinal cord atrophy, pointing towards early neuro-axonal loss and tissue remodelling, and were associated with disability measures [326]. When including patients at different disease stages, lower NAA/Cr was associated with spinal cord atrophy and with disability progression during follow-up (**Table 2.2**) [351]. Also, diffuse lesions were characterised by lower NAA/Cr when compared with focal lesions [351].

MRS may assist with the differential diagnosis of myelopathies. It has been used to define the metabolic profile of different spinal cord tumours (e.g., strongly reduced NAA and strongly increased myo-inositol in the ependymoma, or absence of significant metabolic changes in extradural tumours, such as the schwannoma), and traumatic spinal cord injury (reduced NAA) [352].

²³Na-MRS has been investigated in the brains of MS patients in several studies [353, 354], that have shown increased total sodium concentration in the MS lesions and normal appearing tissue in patients when compared with controls, suggesting either an expansion of the extracellular compartment as a consequence of neuro-axonal loss, or an accumulation of sodium in the swollen axonal terminals with ongoing degeneration [191]. Advances in sodium imaging acquisition and

Table 2.2. Pathological specificity of advanced spinal cord MRI and clinical correlates.

Table shows pathophysiologic mechanism of MS that can be studied with different advanced MRI techniques. Changes occurring in different MS subtypes and clinical correlates are presented. Adapted from Moccia M et al. Ther Adv Neurol Disord 2019 [109].

Pathophysiologic	Advanced MRI technique	Changes in MS	Clinical correlates	Reference
mechanisms		(compared with controls)	(if abnormal)	
Neuro-axonal integrity	DTI (FA, RD, MD)	MD, FA = in RIS	EDSS	[227, 317,
		RD $\uparrow\uparrow\uparrow$ in RRMS and SPMS	Upper limb function	318]
		MD $\uparrow\uparrow\uparrow$ in RRMS and SPMS	Lower limb function	
		FA $\downarrow \downarrow \downarrow$ in RRMS and SPMS		
	QSI	ADCxy, FWHMxy, P0xy 个个个 in PPMS	Spasticity	[326, 327]
		ADCz, FWHMz, P0z $\downarrow \downarrow \downarrow$ in PPMS	Postural instability	
			Sensory dysfunction	
	NODDI (v _{in} , ODI)	Intra-neurite volume fraction $\downarrow \downarrow \downarrow$ in RRMS lesions		[331, 332]
		ODI ↑↑↑ in RRMS normal-appearing WM		
		ODI ↑↑↑ in RRMS lesions		

	SMT (V _{ax})	Axonal volume fraction $\downarrow \downarrow \downarrow \downarrow$ in RRMS		[333]
	MRS (NAA/Cr)	$\downarrow \downarrow \downarrow$ in PPMS, RRMS and SPMS	EDSS	[351]
			Upper limb function	
			Lower limb function	
	MRS (NAA)	$\downarrow \downarrow \downarrow$ in PPMS	EDSS	[326]
			Spasticity	
			Postural instability	
			Sensory dysfunction	
	MRS (Glx)	$\downarrow \downarrow \downarrow$ in PPMS	Postural instability	[326]
Myelin content	MTR	\downarrow in RIS	EDSS	[317, 335,
		$\downarrow \downarrow \downarrow$ in RRMS		336]
	Myelin water fraction	$\downarrow \downarrow \downarrow$ in PPMS	EDSS	[343, 345]
		$\downarrow \downarrow \downarrow$ in RRMS	Lower limb function	
	MTSat	n/a	EDSS	[346]
			Lower limb function	

Astrocytic activation and	MRS (Myo-inositol)	↑↑↑ in PPMS lesions	Postural instability	[326]
proliferation				
Functional connectivity	BOLD fMRI	$\downarrow \downarrow \downarrow$ in RRMS lesions		[355]
		↑↑↑ in RRMS peri-lesional area		

analysis have allowed application of this metabolic technique to the spinal cord of healthy subjects [356], and patients with MS [357]; preliminary findings mirror brain results, with higher total sodium concentration in MS patients than healthy subjects.

2.2.4.4. Functional MRI

Very few studies have investigated the resting state blood oxygenation level-dependent (BOLD) signal in the spinal cord on fMRI mainly because its sensitivity and reliability are still suboptimal and technical limitations are significant [358]. In a 7T fMRI study measuring the BOLD signal, spinal cord functional networks were generally intact in RRMS (**Table 2.2**). However, increased connectivity was found at the boundaries of lesions, possibly indicating compensatory changes to demyelination/axonal loss, and/or disruption of inhibitory spinal interneurons [355].

2.3 Design issues

2.3.1. Sample size

Sample size calculation is a pivotal aspect of planning clinical trials and is based on the primary outcome of the study, generally being imaging for phase 2 and clinical for phase 3 trials [359, 360]. Imaging outcome measures are often included as secondary or exploratory variables in all patients in phase 3 clinical trials, even though they might require a smaller sample size to detect significant difference. A caveat though is that the size of the treatment effect may differ between clinical and imaging outcomes; i.e. 30% reduction in rate of brain volume may not equate in 30% reduction in disability progression.

In order to further explore this issue, I have estimated the treatment effect on brain atrophy which could have been detected in populations recruited in phase 3 clinical trials in progressive MS (**Table**

2.3), based on the actual sample size and the measured rates of brain atrophy in the placebo arm (accepting a power of 80% and an α -error of 5%). Most recent studies would have been able to detect 15-30% treatment effects on brain atrophy [118, 120, 138, 143], in line with actual detected statistical effect (percent brain volume change (PBVC) relative difference was 17% in the ORATORIO trial and 15% in the EXPAND trial).

Inclusion criteria can also impact on the sample size. For instance, in RRMS populations, the rate of inflammatory activity is high, and measures of inflammatory activity (new or enlarging T2 lesions, new T1 lesions and Gadolinium-enhancing lesions) can lead towards relatively lower sample sizes, compared with progressive MS [361, 362]. When considering the number of enhancing lesions, the detection of 50% treatment effect for interferon-beta treatment requires about 120 patients per arm in RRMS trials, and a three-fold number in SPMS [363]. By contrast, use of imaging markers more specific for progressive features (e.g., brain atrophy) will reduce the sample size needed in clinical trials in PPMS and SPMS. Advanced MRI techniques, such as MTR, might also require smaller sample sizes [364, 365], in particular when trials with neuroprotective agents are conducted in selected populations.

Sample size can be affected also by variability of imaging outcomes, which is directly related to the standard deviation of the measure, a major determinant of the sample size [158]. Increasing the number of scans performed in clinical trials can reduce measurement variability and, accordingly, sample size. However, at least for brain atrophy, the effect of increasing the number of observations is modest, when compared with the effect of increasing the duration of follow-up [289].

Overall, DMTs can have a specific effect on each MRI outcome and thus the sample size should be estimated depending on the expected efficacy profile in the selected population. As such, MRI may be particularly useful in early-phase clinical studies on novel therapeutic agents, where drugs can be easily screened before they are taken forward to larger-scale studies [366], as is common practice for anti-inflammatory drugs in phase 2 RRMS studies.

2.3.2. Measurement sensitivity

Quantitative MRI measures are strongly dependent not only on acquisition parameters, but also on processing methods, presenting with different sensitivity to change, repeatability and measurement error.

Brain atrophy measures have been a cornerstone in the study of interventions with putative neuroprotective effects [63, 120, 143], because of the application of registration-based methods that provide *direct* estimates of brain atrophy, such as the SIENA [367], and the boundary shift integral (BSI) method [368–370]. Both SIENA and BSI have reduced sample size requirements to detect significant differences between groups or over time, and are nowadays well-established methods to measure longitudinal brain atrophy in clinical trials and in observational studies for neurodegenerative diseases [289]. In particular, clinical trial results can be affected by different analyses [157]. For instance, in a clinical trial of teriflunomide in RRMS, changes were measured by BPF, a segmentation-based technique, and no significant effect was found initially [202]. However, in a post-hoc analysis, the use of a registration-based automated technique (SIENA) revealed that teriflunomide was associated with significant reductions in brain volume loss [371].

Table 2.3. Phase 3 clinical trials in progressive MS evaluating brain atrophy.

Table shows phase 3 clinical trials in progressive MS which included brain atrophy as outcome measure. Characteristics of trials (sample size, duration) and of MRI measures (results and technique applied) are reported. The potentially-detectable effect size has been calculated based on placebo arm results and sample. Adapted from Moccia M et al. Mult Scler 2017 [91].

Clinical trials	Sample size recruited	Volume change	Duration	Methods	Effect size
	(treatment vs placebo)	(treatment vs			potentially
		placebo)			detectable
EXPAND, Kappos et al. Lancet	470 vs 239	PBVC -0.71%±0.77 vs	From baseline to	SIENA	21.6%
2018 [143]	(SPMS)	-0.84%±0.71 (p=0.02)	month 24		
ORATORIO, Montalban et al.	488 vs 244	PBVC -0.90%±1.12 vs	From week 24 to	SIENA	26.7%
New Eng J Med 2017 [164]	(PPMS)	-1.09%±1.15 (p=0.02)	120		
INFORMS, Lublin et al. Lancet	336 vs 487	PBVC -1.49%±1.35 vs	From baseline to	SIENA	15.8%
2016 [118]	(PPMS)	-1.53%±1.35	month 36		
		(p=0.673)			

CUPID, Zajicek et al., Lancet	329 vs 164	PBVC -1.95%±1.51 vs	From baseline to	SIENA	33.5%
Neurol 2013 [138]	(182 vs 91 in the MRI sub-	-1.82%±1.47 (p=0.94)	year 3		
	study population)				
	(PPMS and SPMS)				
OLYMPUS, Hawker et al. Ann	292 vs 147	Volume change	From baseline to	BPF	>99%
Neurol 2009 [103]	(PPMS)	-10.8cm ³ ±40.3 vs	week 96		
		-9.9cm ³ ±37.0			
		(p=0.62)			
ESIMS, Fazekas et al. Mult	159 vs 159	PCV -0.62%±0.88 vs	From baseline to	Six-slice	32.5%
Scler 2005 [372]	(SPMS)	-0.88%±0.91	month 27	volume	
		(p=0.0093)			

On the contrary, the current status of spinal cord atrophy measurement is suboptimal. Spinal cord atrophy is conventionally determined indirectly, by numerical subtraction of volume (based on 3D surface fitting) or cross-sectional area (CSA) (based on 2D edge detection on serial images) obtained separately at each time-point, providing *indirect* estimates of atrophy rates [278, 310, 321, 358, 373], that could introduce a lot of noise due to the miss-segmentations. Thus, the development and optimisation of registration-based techniques for spinal cord atrophy may reduce measurement noise and improve its precision [374], and is the main goal of this thesis.

3. Rationale and aims of thesis

3.1. Rationale

As fully discussed in <u>Chapter 1</u>, MS is a common neurological disorder in young adults, with a highly variable clinical course, but potentially leading to chronic disability and poor quality of life [1]. Thus, as mentioned in <u>Chapter 2</u>, identifying reliable imaging outcome measures is a cornerstone for improving the understanding of the disease mechanisms and for monitoring the clinical course of MS and its response to treatment [63, 109]. Progressive MS represents a unique opportunity for studying imaging markers of neurodegeneration, with equal bearing on relapsing forms of the disease. Several imaging candidates hold promise for filling the unmet need of biomarkers in progressive MS, by capturing the effect on neurodegeneration [91].

The study of atrophy looks particularly promising, by the *in vivo* characterisation of most aggressive aspects of MS pathology (e.g., demyelination and neuro-axonal loss). So far, brain atrophy is the best examined and most robust outcome with attainable sample sizes and first positive results, though treatment effects tend to be more modest than those seen for inflammatory MRI markers (i.e., lesions) [91]. Brain volume has already being used as primary outcome measure in phase 2 trials, and as secondary exploratory measure in phase 3 trials in progressive MS [105]. However, spinal cord MRI holds great promise for future trials due to higher rates of atrophy and better sensitivity to change compared with brain volume changes (-1.7%/year spinal cord volume loss vs - 0.6%/year brain volume loss) [149, 268]. As discussed in <u>Chapter 2</u>, robust application of spinal cord atrophy in clinical trials requires implementation of registration-based techniques with lower measurement noise and higher sensitivity to change, when compared with currently available segmentation-based methods.

3.2. Aims

In keep with this background, this thesis will primarily aim to:

- (1) Validate a registration-based method for the quantification of spinal cord atrophy (generalised boundary shift integral (GBSI));
- (2) Evaluate clinical correlates of this novel registration-based method;
- (3) Evaluate possible future implication for the design of clinical trials and observational studies.

The pipeline of the GBSI, along with detailed methods to overcome the limitations posed by current segmentation-based atrophy measurements, and the observational cohorts and clinical trial used for testing and implementing this technique, are fully described in <u>Chapter 4</u>.

In <u>Chapter 5</u>, I preliminarily applied this novel registration-based method to a monocentric test dataset and, then, to a multi-centre cohort acquired across different European sites with specific MRI expertise, within the Magnetic Resonance Imaging in Multiple Sclerosis (MAGNIMS) network. Hereby, I have compared precision and repeatability of spinal cord atrophy measurements obtained with different segmentation methods (e.g., JIM and SCT), and with the novel registration-based method, and, then, explored possible clinical correlates.

In <u>Chapter 6</u>, I re-analysed a phase 2 clinical trial on PPMS to further evaluate clinical correlates and treatment effect of this novel registration-based method, and possible implications for image acquisition and clinical trial design (e.g., measurement precision, image quality, deriving spinal cord atrophy measurements from brain scans).

Finally, in <u>Chapter 7</u>, I have summarised the results, highlighting novel contributions of this thesis to the field and possible future directions in MS research.

4. Methods

In <u>Chapter 4</u>, I report on general methods for the present thesis, including study design, populations and techniques for cross-sectional and longitudinal spinal cord atrophy measurements. In particular, I am hereby presenting general methods, but will leave more specific methods to <u>Chapter 5</u> and <u>Chapter 6</u> (e.g., inclusion and exclusion criteria, demographic and clinical features). Also, I present detailed methods for cross-sectional and longitudinal spinal cord atrophy measurements, but will then discuss specific applications, in relation to different research questions, in <u>Chapter 5</u> and <u>Chapter 6</u>.

Looking at specific contributions to this thesis, I need to acknowledge that the first GBSI pipeline for spinal cord atrophy measurement was developed by Prados and colleagues, as the adaptation of a method used for brain atrophy to measure longitudinal spinal cord atrophy [374, 375]. I have then applied this preliminary pipeline to different cohorts of MS patients and healthy controls (as described in <u>Chapter 5</u> and <u>Chapter 6</u>). While performing spinal cord segmentation, as detailed below, and GBSI pipeline, as from Prados and colleagues [374, 375], I regularly extracted data, and run statistical models and graphical presentations, in order to evaluate overall GBSI performance, and to define possible areas of improvement. Based on this, Dr Prados and I further implemented the pipeline (e.g, we improved definition of the probabilistic XOR masks, we included denoising within the pipeline). As such, the GBSI pipeline presented in <u>Chapter 4</u> is the result of the analyses I run, and subsequent changes in collaboration with Dr Prados.

4.1. Study design

The present thesis is based on retrospective analysis of prospectively collected data from observational studies conducted at the Queen Square MS Centre ([228, 250, 278]MAGNIMS

Collaboration network (www.magnims.eu) [113, 273, 287], and from a phase 2 clinical trial (A Randomized Placebo-controlled trial Evaluating Laquinimod in primary progressive multiple sclerosis, Gauging Gradations In MRI and clinical Outcomes (ARPEGGIO)) [105].

The study was conducted in accordance with the Declaration of Helsinki. Each participant had provided written consent for research within each centre, for the main study and its subsequent analyses, with local ethics committees approval. All scans were pseudo-anonymised, transferred, stored and analysed in accordance with current regulations (EU GDPR 2016/679).

4.2. Populations

4.2.1. London cohorts

London cohorts were composed of three different cohorts with longitudinal spinal cord MRI acquisitions from the Queen Square MS Centre (The London cohorts have been fully reported in previous publications [228, 250, 278], and will be briefly presented below and in subsequent <u>Chapter 5</u>.

4.2.1.1. Test dataset

The test dataset includes spinal cord images from 9 healthy controls and 9 MS patients, who were scanned twice within the same session, with repositioning of the subjects in-between acquisitions [284]. This dataset has been previously used to compare a fully automated spinal cord segmentation method (*PropSeg*), with the semi-automated ASM tool within JIM [284].

Spinal cord MRI was done using a 3T Philips Achieva MRI system with RF dual-transmit technology (Philips Medical Systems, Best, Netherlands) and a 16-channel neurovascular coil. Acquisition protocol is reported in <u>Chapter 5</u>, and further details are available from previous publications [113, 284].

4.2.1.2. CIS cohort

The CIS cohort has been studied at the Queen Square MS Centre in the past 20 years. This cohort includes 131 non-spinal CIS patients who underwent spinal cord MRI at diagnosis (between 1995 and 2004), and after an average period of 5 years; demographic and clinical data were recorded at the two time points [250]. Twenty healthy controls were also included. This cohort has been previously used to study MRI predictors of subsequent MS progression [250].

Spinal cord MRI was done at baseline and follow-up on the same 1.5T Signa scanner (General Electric, WI, USA); there was a scanner upgrade during the study period that, however, in the previous studies, did not seem to affect statistical analyses [250]. Acquisition protocol is reported in <u>Chapter 5</u>, and further details are available from previous publications [113, 250].

4.2.1.3. Spinal cord cohort

The spinal cord cohort includes spinal cord images from 41 MS patients (CIS, RRMS, SPMS, PPMS) and 17 healthy controls, who underwent spinal cord MRI at baseline and after one year; demographic and clinical data were recorded at the two time points [228, 278]. This cohort has been previously used to validate the ASM tool within JIM, and to study possible associations between spinal cord atrophy and other clinical and MRI variables [228, 278].

Spinal cord MRI was done at baseline and follow-up on the same 3T Philips Achieva MRI system with RF multi-transmit technology (Philips Healthcare, Best, the Netherlands), and a 16-channel

neurovascular coil. Acquisition protocol is reported in <u>Chapter 5</u>, and further details are available from previous publications [228, 278].

4.2.2. MAGNIMS cohort

The MAGNIMS is a European network of academics that share a common interest in the study of MS using MRI techniques (www.magnims.eu). Eight MAGNIMS centres have collaborated to acquire spinal cord images from 155 MS patients (CIS, RRMS, SPMS, PPMS) and 59 healthy controls (collected by Professor Mara Rocca and Professor Massimo Filippi, Hospital San Raffaele, Milan); MRIs were acquired at baseline and after one year; demographic and clinical data were recorded at the two time points [113, 273, 287].

MRIs were acquired on multi-producer 3T scans; acquisition protocols are reported in <u>Chapter 5</u>. Inclusion and exclusion criteria have been reported previously [113, 273, 287], and will be better discussed in <u>Chapter 5</u>.

4.2.3. ARPEGGIO clinical trial

The ARPEGGIO trial was a randomised, double-blind, parallel-group, placebo-controlled study. PPMS patients were randomised in a 1:1:1 ratio to receive oral laquinimod 0.6 mg or 1.5 mg, or placebo once daily from January 2015 to April 2016 at 85 sites in 10 countries. Duration of the core study was 48 weeks. The laquinimod 1.5 dose arm was discontinued as of January 1, 2016, due to cardiovascular side effects (patients were followed-up, but no further treatment was given) [105].

All patients underwent brain and cervical spinal cord MRI at baseline, week 24 and week 48, including 3D T1-weighted isotropic images of the brain and spinal cord (1x1x1mm³), within 14 days

of the scheduled clinical visit. MRI scans were collected centrally at the VUmc in Amsterdam and, for the purposes of the present thesis, were then transferred to the NMR Research Unit (. Inclusion and exclusion criteria have been reported previously [105], and will be better discussed in <u>Chapter</u> <u>6</u>.

In the original clinical trial dataset, a number of clinical tests (EDSS, T25FW, 9HPT, SDMT and MSWS), and MRI variables (e.g., number of new T2 lesions, T2 lesion volume change, T1 lesion volume change and PBVC) were included. Full details of acquisitions and processing have been previously reported [105].

4.3. Cross-sectional spinal cord measurements

In the present thesis, we used two different methods for cross-sectional spinal cord image segmentation and atrophy calculation: surface-based and image-based methods [276]. The older methods are fully manual, whilst the most recent methods are semi- or fully-automated.

4.3.1. Spinal cord toolbox

When the work related to this thesis started (<u>Chapter 5</u>), *PropSeg* was the standard segmentation tool within the SCT (SCT version 3.0), after being tested on a large cohort of MS patients and healthy controls [283, 284, 376]. This fully-automated surface-based image segmentation method has the same sensitivity as the ASM within JIM, but has higher inter-rater repeatability and is more time-efficient [284]. The most recent release of the SCT (version 4.0) includes the *DeepSeg* tool, a fully-automated segmentation method based on convolutional neural networks [283, 285], which was used in <u>Chapter 6</u>. The *DeepSeg* also allows automated spinal cord segmentation from brain MRI images, which was not validated on the *PropSeg* [283, 285].

4.3.2. JIM

Within the JIM tool, the ASM is a surface-based method that semi-automatically outlines the cord, after marking the centre of the spinal cord [274, 277]. The ASM has provided more prompt and repeatable measures of the spinal cord volume, compared with manual methods [278]. The ASM offers a considerable reduction in user interaction time, and can be performed over long spinal segments. The user needs to identify landmarks at the extremes of the region to study, and, then, mark the centreline of the cord. Sagittally-acquired images are then reformatted to the axial plane to obtain five contiguous 3 mm slices; the program automatically calculates the radius and the centre of each axial slice and, finally, the cross-sectional area is obtained by averaging these contiguous slices [274].

4.3.3. NeuroQLab

The NeuroQLab is an image-based method that segments the upper cervical cord from surrounding non-spinal cord tissue by using a Gaussian mixture modelling [275, 281, 282]. After definition of the spinal cord subsection to be segmented, watershed segmentation of the spinal cavity and surrounding cerebrospinal fluid is performed, and mean upper cervical cord area (MUCCA) is computed [275, 281, 282].

4.4. Longitudinal spinal cord measurements

4.4.1. Segmentation methods

When using segmentation methods for longitudinal spinal cord atrophy calculation, the rate of atrophy is estimated by numerical subtraction of spinal cord cross-sectional area measurements calculated at different time-points. For instance, percent change of cord area is calculated using the

following formula: Atrophy = 100*(follow-up area - baseline area)/baseline area. Years between baseline and follow-up scans can also be included in the denominator of the formula, if there is variability of the interval between scans [109, 113].

4.4.2. Registration method (GBSI)

The GBSI is applicable to datasets with T1-weighted images, with identical acquisition parameters, ideally using 1 mm isometric voxels, at two time-points for each subject. A graphic overview of the pipeline is presented in **Figure 4.1** and further detailed below.

4.4.2.1. Spinal cord segmentation

The first step is the segmentation of the spinal cord from T1-weighted images [113, 283, 373]. The whole cord is segmented (i.e., WM and GM together), defining the spinal cord boundaries and the cranio-caudal extension of tissue over which the GBSI estimates are required. This segmentation is computed separately and independently for each time-point, over the same spinal cord segments; for instance, in the present thesis I will work on C2-C5 segmentation in <u>Chapter 5</u>, and, then, on C1-2 and C2-5 segmentations in <u>Chapter 6</u>. The segmentation can be obtained manually, semi- or fully-automatically using the wide range of techniques, as detailed above. The extracted spinal cord segmentation can be represented with a hard (binary) or a soft (probabilistic) mask. Considering that the acquired spinal cord extension can vary by a few slices between time-points (e.g., due to positioning of the subject in the scanner), the longitudinal atrophy is computed over the **Figure 4.1. Pipeline for spinal cord longitudinal atrophy measurement using the registration-based technique (GBSI).**

After spinal cord segmentation, baseline and follow-up spinal cord images are denoised, bias-field corrected, straightened and ultimately registered to the halfway space. Intensity changes in the

vicinity of the cord boundaries are estimated for GBSI calculation. Adapted from Prados F, Moccia M, et al. Submitted [374, 375].



intersection of these regions of interest, discarding the pixels that are not covered at both timepoints.

4.4.2.2. Image denoising

The extracted masks are used to compute a ring surrounding the spinal cord to scale the signal intensity of the images accounting for the presence of the noise floor [377]. For this step, the signal intensities in the original T1-weighted images are denoised using a fast version of the adaptive non-local means filter algorithm, using the mask from the segmented spinal cord [378]. To be more precise, the standard deviation of the signal in a ring within the CSF was calculated to compute the root power of the noise, and, then, used to account for the presence of a noise floor (this approach is standard on T1-weighted images, where this can be obtained from regions where the signal from the CSF is suppressed) [377]. Any value of voxels within the extracted ring that were more than 2 standard deviations above the mean were discarded, in order to avoid the inclusion of values from

nerve roots or other spurious signal intensities. Finally, the ring within the CSF was derived by dilation of the spinal cord mask by 2-pixel layers, and, then, by subsequent subtraction of the mask once.

4.4.2.3. Inhomogeneity correction

An intensity inhomogeneity correction is applied to the 3D data using the N4 algorithm [379], within the region determined by the two-time dilatation of spinal cord masks. The following parameters are used: full width at half maximum (FWHM)=0.05, convergence threshold=0.0001, and maximum number of iterations=1000 [370].

4.4.2.4. Spinal cord straightening

To remove any difference in the cord curvature between time-points resulting from positioning in the scanner, straightening of the MRI images is obtained from the previously computed spinal cord segmentation, using a robust and accurate method, freely available as part of the SCT software package [283, 380] This method preserves spinal cord topology, which is essential for measuring subtle changes in spinal cord edges when using GBSI.

4.4.2.5. Half-way space registration

Images are registered to the half-way space using an affine transformation in order to avoid biases that would be introduced if registering one time-point to the other [381–383]. This step is achieved using an inverse-consistent and symmetric algorithm [384]. Once the transformations are obtained, images and corresponding masks for each time-point are linearly resampled to the common halfway space.

4.4.2.6. Differential bias correction

A longitudinal differential bias correction method is used to remove the residual intensity inhomogeneity-derived differences between the baseline and the repeated images (radius=5 voxels) [385]. This step is needed, despite the previous cross-sectional inhomogeneity correction, to avoid artificial atrophy values by the remaining intensity differences from the cross-sectional inhomogeneity correction method.

4.4.2.7. Intensity normalisation

Image intensities are normalised so that the probabilistic area from which GBSI will be computed can be extracted [369, 370]. The intensity normalisation of the baseline and follow-up images is obtained from a linear regression between the average tissue intensity inside the cord and inside the CSF. The tissue intensity values are computed using a k-means algorithm (k=2), which is limited to a region of interest obtained from each input mask (after 2 dilations).

4.4.2.8. Probabilistic XOR

The probabilistic XOR mask is obtained from the half-way linearly-resampled segmentation masks following the same steps already introduced for the brain GBSI calculations (**Figure 4.2**) [370]. This mask identifies the voxels with high probability to be tissue at the edge of the cord.

Figure 4.2. GBSI calculation.

pXOR mask is shown on the left, the intensity profile function that computes the GBSI is shown in the middle and the GBSI results are displayed on the right. Adapted from Prados F, et al. ISMRM 2016 [375].



4.4.2.9. Atrophy computation

The GBSI is computed on a voxel-by-voxel basis as the difference in intensity between baseline and follow-up images within a clipped window [368–370]. The clipped window aims to catch the difference between tissue intensities at the two time-points, by reducing the background influence. The intensity differences are weighted by the probabilistic XOR mask voxel-wise. For the spinal cord GBSI, a predetermined clipping window was used [374, 375]. To increase robustness, the "forward" and "backward" BSI is calculated for each pair of images (i.e., swapping baseline and follow-up images, and repeating the intensity normalisation, probabilistic XOR and atrophy computation steps), and the mean of the results is included. Finally, percent spinal cord volume change is calculated by dividing the GBSI value by the binarised, straightened and registered baseline cord mask volume.

4.4.3. Software

The N4, denoising, differential bias correction, registration and GBSI methods are all freely available as part of NifTK software package at https://cmiclab.cs.ucl.ac.uk/CMIC/NifTK. SCT has been used for spinal cord straightening, and it can be found at https://github.com/neuropoly/spinalcordtoolbox. In this thesis, the GBSI has been implemented using these software packages; however, other software packages offer similar processing options and could be used alternatively.

5. Longitudinal spinal cord atrophy in multiple sclerosis using the generalised boundary shift integral

5.1. Background

As previously discussed in <u>Chapter 2</u>, spinal cord atrophy on MRI is a marker of neurodegeneration in MS [226, 260], and is one of the main substrates of long-term disease progression [109, 213, 227, 250, 296, 305, 308, 311, 386]. Spinal cord atrophy progresses faster than brain atrophy (1.7%/year vs 0.4-0.6%/year), is greater in progressive MS than in the relapsing forms of MS, and predicts disability [268, 305, 312]. It is crucial to obtain an accurate and precise longitudinal measurement of spinal cord atrophy, because it could be used to monitor disease progression and become a primary outcome measure in phase 2 clinical trials with neuroprotective therapies, not only in MS, but also in other neurodegenerative disorders [91, 108, 300, 387].

Spinal cord atrophy is conventionally estimated with segmentation-based methods (e.g., CSA), applied to volumetric spinal cord images [278], that measure cord characteristics at each time point; indirect longitudinal atrophy measurements are obtained by numerical subtraction, with relatively-low repeatability and responsiveness to change [109, 292]. On the contrary, longitudinal brain atrophy measurements are nowadays based on registration-based techniques that significantly reduce measurement noise [289].

As such, in <u>Chapter 5</u>, I have applied the GBSI pipeline fully described in <u>Chapter 4</u> to measure longitudinal spinal cord atrophy in cohorts of MS patients and healthy controls. I have performed spinal cord segmentation, GBSI calculation, and, then, statistical analyses.

5.2. Aims

The present chapter reports on a multicentre, multi-manufacturer and multi-field strength scan analysis, and aims to:

- (1) Evaluate precision and repeatability of spinal cord atrophy measurements obtained with different segmentation methods (e.g., JIM and SCT), and with the registration-based GBSI;
- (2) Compare measurements of spinal cord atrophy obtained using GBSI with those obtained with conventional CSA (semi-automatic segmentation with the SCT);
- (3) Explore associations between GBSI- and CSA-derived spinal cord measurements and MS clinical features;
- (4) Estimate the sample size needed to detect changes in spinal cord atrophy over one year using GBSI and CSA.

5.3. Methods

5.3.1. Study design and population

In this chapter, I performed a retrospective analysis of prospectively collected data from Queen Square MS Centre (MAGNIMS centres. Overall, I included a test dataset composed of 9 healthy controls and 9 MS patients, and a validation dataset composed of 327 MS patients and 96 healthy controls. The London and MAGNIMS cohorts have been reported in previous publications and in <u>Chapter 4</u> [228, 250, 273, 278, 287].

Eligibility criteria were:

(1) Diagnosis of CIS or MS according to the 2010 McDonald Criteria [59], or healthy controls without history of neurological or psychiatric disorders;

- (2) The presence of at least two volumetric MRI scans (interval between scans was collected), acquired with isotropic voxel of 1x1x1mm³;
- (3) Information on: EDSS score at each time point [66], subtype of MS (CIS, RRMS and progressive MS (including both PPMS and SPMS)) [59], age, gender and disease duration (time from clinical onset to baseline MRI).

Each participant had provided a written consent for research within each centre. The final protocol for the analysis of pseudo-anonymised scans, acquired independently and prospectively in each centre, was approved by the European MAGNIMS collaboration and by the local ethics committees.

5.3.2. MRI acquisition and processing

Dedicated cervical spinal cord 3DT1-weighted images (1x1x1mm³) were analysed. Images were acquired in 8 MAGNIMS sites on 1.5T and 3T scanners, from different manufacturers and with different MRI parameters (**Table 5.1**).

In the whole population, for calculating CSA and GBSI, masks of C2-5 spinal cord level were obtained for images acquired at each time point with SCT, using the routine method known as *PropSeg* (version 3.1.1) (**Figure 5.1**), that has been fully explained in <u>Chapter 2</u> and <u>Chapter 4</u> [283]. C2-5 CSA was obtained by averaging all cord cross-sectional areas. For GBSI, I followed the previously described pipeline, which is applicable to datasets with identical image acquisitions (i.e., T1weighted), and similar voxel size, with acquisitions at two time-points for each subject [370, 374, 375]. Briefly, the extracted segmentation masks were used to compute a ring surrounding the spinal cord to scale the signal intensity of the images accounting for the presence of the noise floor [377]. For this step, the whole 3D volume was corrected for signal intensities, using a fast version of the

Site	Number of	Manufacturer, model and field	Acquisition parameters
	included	strength	(TR/TE/TI msec)
	individuals		
Barcelona	21	Siemens Magnetom Trio 3T	2300/3.2/900
Bochum	4	Philips Achieva 3T	8/"shortest"/"shortest"
London	123	GE Signa 1.5T	15.6/4.2/450
	55	Philips Achieva 3T	8/3.7/860
	18	Philips Achieva 3T	8/3.7/860
Lugano	43	Siemens Magnetom Skyra 3T	2300/5.1/1140
Mannheim	14	Siemens Magnetom Skyra 3T	1900/2.6/1000
Milan	49	Philips Achieva 3T	8/"shortest"/"shortest"
Naples	28	General Electric Signa HDtx 3T	7.9/3.2/450
Oxford	15	Siemens Magnetom Prisma 3T	2300/3.59/900

Table 5.1. London and MAGNIMS cohorts and included patients.

adaptive non-local means filter algorithm [378], and, for intensity inhomogeneities, using the N4 algorithm [379]. Spinal cord images were then straightened using a specific software available within the SCT [388], to remove the difference in curvature between time-points due to subject positioning in the scanner. A 3D symmetric and inverse-consistent rigid-only (9 degrees of freedom (DOF)) registration to the half-way space between baseline and follow-up images was performed [384]; masks were resampled to the same space using linear interpolation and registered to the halfway space. To reduce the residual bias field and homogenise the grey scale between both registered time-points, a symmetric differential bias correction was applied [385]. Overall, this method does not generate any bias between the baseline and follow-up images as the exact same

image processing pipeline is applied to both time points. The probabilistic XOR (pXOR) region was adaptively estimated from baseline and follow-up cord segmentations, to calculate the BSI over specific tissue boundaries, excluding voxels in areas that might reduce its sensitivity (e.g., voxels with partial volume with CSF or the centre voxels of the spinal cord). The GBSI was finally computed (**Figure 5.1**).

Percent CSA annual change between time points was calculated using the following formula: 100*[(CSA at follow-up – CSA at baseline)/CSA at baseline)/years between baseline and follow-up scans]. Similarly, percent GBSI annual change was calculated using the following formula: GBSI/ years between baseline and follow-up scans. Of note, spinal cord atrophy based on CSA is measured as the average of the slice-wise 2D edge detection over a fixed cord section/length, hence effectively it is a 3D volume divided by its height; whilst GBSI measures the voxel-by-voxel difference in intensities between the baseline and the follow-up images, as a 3D volume change [113]. I segmented the spinal cord over a fixed cord length (C2-5), and I used the same masks to compute CSA and GBSI, thus making the atrophy measurement effectively computed over the same boundary/region for both measurements [292].

To determine measurement precision and repeatability, I analysed test dataset from 9 healthy controls and 9 MS patients that were re-scanned after having been removed from the scanner and repositioned between the scans during the same visit at the Queen Square MS Centre, [284]. Images of the spinal cord were acquired with 1 mm isotropic voxel using a 3T Philips Achieva MRI system with RF dual-transmit technology (Philips Medical Systems, Best, Netherlands) (**Table 5.1**). I segmented the spinal cord using two different well-established CSA segmentation techniques: a semi-automatic delineation of the CSA using the

Figure 5.1. Spinal cord segmentation and GBSI.

SCT was used for spinal cord segmentation. C2-3, C3-4, and C4-5 reference points were set manually (A). Representative images of semi-automatic spinal cord segmentation output are shown (sagittal and, in the inset, axial views) (B). Afterwards, baseline (C/D) and follow-up (E/F) spinal cord images were straightened, and, ultimately, registered to the halfway space. Intensity changes in the vicinity of the cord boundaries were estimated for generalised boundary shift integral (GBSI) calculation (G/H). Adapted from Moccia M, Prados F et al. Ann Neurol 2019 [113].



ASM within JIM (version 6) [277, 284], and a semi-automatic segmentation method using the *PropSeg* within the SCT (version 3.1.1) (refer to <u>Chapter 2</u> and <u>Chapter 4</u> for further details on these methods). Then, different GBSI measurements were obtained using masks of spinal cord segmentation obtained with JIM and SCT at both time-points (**Figure 5.2**).

Figure 5.2. pXOR masks.

Figure shows pXOR masks obtained from baseline and follow-up segmentations using ASM within JIM, and *PropSeg* within SCT. The semi-automatic delineation using ASM within JIM generated a slightly thinner pXOR mask than the *PropSeg* within the SCT. Adpated from Prados F, Moccia M, et al. Submitted.



5.3.3. Statistical analyses

On the test dataset, to evaluate repeatability of GBSI measurements obtained with different segmentation methods (aim 1), I calculated the intraclass correlation coefficient (ICC) for GBSI obtained from JIM and SCT segmentations. Then, assuming spinal cord atrophy would be expected to be zero in healthy controls and MS patients scanned twice during the same session, measurement error between scans was quantified by the coefficient of variation and the median absolute deviation on GBSI and CSA (SCT segmentation).

On the London and MAGNIMS validation datasets, means, medians and proportions of demographics, clinical features and MRI measures (percentage spinal cord changes obtained with GBSI and CSA) were calculated for patients (and their subgroups) and healthy controls (aim 2). Differences were evaluated with *t*-test, Mann–Whitney test, χ^2 test or Fisher's exact test, as appropriate. GBSI and CSA atrophy progression measurements were compared using a paired t-test.

Linear regression models were employed to estimate spinal cord atrophy changes (with GBSI and CSA) in different disease phenotypes, when compared with healthy controls (used as reference group); age, gender, site of acquisition and disease duration were included as covariates (results are presented as adjusted coefficients (Coeff), 95% confidence intervals (95%CI), and p-values). Then, I used different disease phenotypes as reference group in the linear regression models, to perform direct comparisons between different disease phenotypes (e.g., CIS, RRMS, PMS – including both PPMS and SPMS).

To compare GBSI and CSA in their ability to predict different clinical variables, I employed logistic regression models to estimate associations between percentage spinal cord atrophy change obtained using GBSI and CSA (independent continuous variable), and different binary clinical variables (dependent variable) (e.g., disease subtypes/healthy controls, EDSS progression (which was defined as 1 point change if baseline EDSS \leq 5.5, and 0.5 point if \geq 6.0); age, gender, site of acquisition and disease duration were included as covariates. Results are presented as odds ratios (OR), 95%CI and p-values. Based on this, I obtained areas-under-the-curve (AUC), using GBSI and CSA, in turn, as the main explanatory variables; I used bootstrap resampling (1000 repetitions) to calculate pointwise confidence intervals for the receiver operating characteristics (ROC) curve (aim

3).

Sample sizes required for a hypothetical clinical trial evaluating a neuroprotective medication over one year were estimated using CSA and GBSI. Sample size was computed using the formula $n = \frac{2(Z_{\alpha}+Z_{1-\beta})^2\sigma^2}{A^2}$, where *n* is the required sample size per treatment arm in 1:1 controlled trials, Z_{α} and Z_{1-6} are constant (set at 5% alpha-error and 80% power, respectively), σ is the standard deviation (from each disease phenotype), and Δ is the estimated effect size (aim 4) [289, 300]. Effect size was derived from adjusted beta-coefficients at linear regression models, estimating spinal cord loss in MS patients, when compared with physiologic loss in controls. As such, I assumed that 100% treatment effect is theoretically reached when the spinal cord atrophy change in patients is equal to that observed in healthy controls. From there, with a conservative approach, I hypothesised a number of effect sizes (e.g., 30%, 60% and 90%), that were smaller than the observed difference between MS cases and physiologic spinal cord loss in controls.

Stata 15.0 was used for data processing and analysis. Results were considered statistically significant when associated with p values <0.05.

5.4. Results

5.4.1. Measurement repeatability and error

On the test dataset, I observed similar spinal cord atrophy measurements for GBSI (ICC=0.66), independently of the segmentation technique used as input (GBSI from JIM segmentation=0.38±3.48%; GBSI from SCT segmentation=0.28±3.62%)

Among healthy controls and MS patients scanned twice during the same session, spinal cord atrophy would be expected to be zero. Both GBSI and CSA indeed had overall atrophy rates tending towards

zero (0.28±3.62% and -0.17±5.39%, respectively), indicating no systematic bias. However, GBSI presented with lower random measurement error, when compared with CSA, reflected by a clearly lower coefficient of variation (12.92% and 31.70%) and slightly lower median absolute deviation (0.21% and 0.25%).

5.4.2. Study population

Longitudinal spinal cord scans from 327 MS patients and 96 healthy controls were collected. Fortyfive patients' scans and 14 healthy controls' scans were excluded because of either SCT failure, likely as a consequence of poor contrast (n=13), wrong voxel size (n=26), wrong acquisition parameters (n=10), and artefacts (n=8), or GBSI failure (n=2), mostly from the eldest cohorts acquired using 1.5T scanner (e.g., CIS cohort) (see **Figure 5.3** for the study flow diagram). Therefore, scans from 282 patients and 82 healthy controls acquired in 8 MAGNIMS centres were included in the analysis (see **Table 5.1** for the number of patients per centre and acquisition parameters). The demographic and clinical features of patients and healthy controls are given in **Table 5.2**.

5.4.3. Spinal cord atrophy obtained with CSA and GBSI

On paired t-test, the percentage spinal cord changes obtained with CSA were similar to those obtained with GBSI (p=0.55).

On linear regression models adjusted for age, gender, site of acquisition and disease duration, using CSA as main variable of interest, there was a significant decrease in the percentage spinal cord change over one year between RRMS (-1.74±4.02%) and healthy controls (-0.56±3.77%) (Coeff=-1.45;95%CI=-2.81, -0.10; p=0.03), but not between CIS (-1.19±3.67%) and healthy controls (Coeff=-0.84; 95%CI=-2.49, 0.80; p=0.31), nor between PMS (-1.29±3.20%) and healthy controls (Coeff=-
1.45; 95%CI=-3.70, 0.80; p=0.21) (**Figure 5.4A**). There were no differences in percentage CSA change over one year between CIS and RRMS (Coeff=-0.61; 95%CI=-1.95, 0.72; p=0.37), nor between CIS and PMS (Coeff=-0.60; 95%CI=-2.73, 1.53; p=0.58), nor between RRMS and PMS (Coeff=-0.00; 95%CI=-1.75, 1.73; p=0.99), when adjusted for the same covariates.

When using GBSI, overall, the rates of spinal cord decline were similar (or even higher among PMS) to those obtained with CSA, but the standard deviations of the measurements were smaller. On linear regression models adjusted for age, gender, site of acquisition and disease duration, using

Table 5.2. Demographic and clinical features.

Table shows demographic and clinical features of MS and controls. P-values are shown from *t*-test, Mann–Whitney test, χ^2 test or Fisher's exact test, as appropriate (*p<0.05).

	MS	Controls	p-values
	(n=282)	(n=82)	
Age, years	38.2 ± 11.2	36.6 ± 12.5	0.339
Gender, female	169 (59.8%)	46 (55.7%)	0.590
Interval between scans, years	1.6 ± 1.1	1.2 ± 0.7	0.001*
Disease duration, years	5.9±8.2		
Disease subtype CIS	52 (18.4%)		
RRMS	196 (69.5%)		
PMS	34 (12.1%)		
EDSS at baseline	1.5 (0-7.5)		
EDSS at follow-up	2.0 (0-8.0)		
Patients with EDSS progression	74 (26.2%)		

Figure 5.3. Patient disposition.

Figure shows MS cases and controls from MAGNIMS and UCL Queen Square Institute of Neurology cohorts; scanner filed strength is reported. Exclusion rate from the original cohort is shown, as a consequence of poor contrast, wrong voxel size, wrong acquisition parameters, and artefacts, mostly present in the eldest cohorts acquired using 1.5T scanners (e.g., CIS cohort). Adapted from Moccia M, Prados F et al. Ann Neurol 2019 [113].



GBSI as main variable of interest, there was a significant decrease in the percentage spinal cord change obtained with GBSI between healthy controls (0.02±2.39%) when compared to: CIS (-0.95±2.11%) (Coeff=-1.37; 95%CI=-2.40, -0.33; p=0.01), RRMS (-1.74±2.57%) (Coeff=-1.84; 95%CI=-2.70, -0.99; p<0.01), and PMS (-2.29±2.40%) (Coeff=-2.44; 95%CI=-3.87, -1.02; p<0.01) (**Figure 5.4B**). Similarly to the findings obtained with CSA, no differences were detected in GBSI percent annual reduction between CIS and RRMS (Coeff=-0.48; 95%CI=-1.32/0.37; p=0.27), nor between CIS and PMS (Coeff=-2.43, 0.27; p=0.12), nor between RRMS and PMS (Coeff=0.60; 95%CI=-0.60, 1.70; p=0.28), when adjusted for the same covariates.

Figure 5.4. Box-and-Whisker plot of CSA and GBSI measurements

Box-and-Whisker plot for 1-year percentage change with CSA (**A**) and GBSI (**B**) in healthy controls, CIS, RRMS and progressive MS (PMS) (including both PPMS and SPMS). Coeff and p-values are reported from linear regression models using healthy controls as reference group (age, gender, disease duration and site of MRI acquisition were used as covariates). Standard deviation is also reported for each group. Adapted from Moccia M, Prados F et al. Ann Neurol 2019 [113].



5.4.4. Clinical correlates of CSA and GBSI

On logistic regression models adjusted by age, gender, site of acquisition and disease duration, RRMS had higher probability of spinal cord atrophy progression on CSA, when compared with healthy controls. On GBSI, all MS subtypes (CIS, RRMS and PMS patients) had higher probability of spinal cord atrophy progression, when compared with controls. Also, on GBSI, MS patients with EDSS progression had higher probability of spinal cord atrophy progression, than those without (**Table 5.3**).

Table 5.3. Clinical correlates of spinal cord atrophy with CSA and GBSI.

Table shows associations between spinal cord atrophy (with CSA and GBSI), and different clinical variables. OR, 95%CI and p-values are shown from logistic regression models; age, gender, site of acquisition and disease duration were included as covariates (*p<0.05).

			CSA		GBSI				
	OR	95%CI		p-values	OR	95%CI		p-values	
		Lower	Upper	-		Lower	Upper	_	
CIS vs HC	-0.04	-0.14	0.04	0.33	-0.23	-0.40	-0.07	<0.01*	
RRMS vs HC	-0.07	-0.14	-0.00	0.02*	-0.31	-0.42	-0.19	<0.01*	
PMS vs HC	-0.05	-0.17	0.05	0.32	-0.43	-0.64	-0.23	<0.01*	
EDSS progression	-0.00	-0.07	0.06	0.83	-0.13	0.25	-0.02	0.02*	

CIS patients were better differentiated from controls using GBSI (AUC=0.66; 95%CI=0.57, 0.75), than CSA (AUC=0.53; 95%CI=0.43, 0.63) (p=0.03; **Figure 5.5A**). RRMS patients were better differentiated from controls using GBSI (AUC=0.73; 95%CI=0.66, 0.80), than CSA (AUC=0.59; 95%CI=0.52, 0.66) (p<0.01; **Figure 5.5B**). PMS patients were better differentiated from controls using GBSI (AUC=0.77;

95%CI=0.68, 0.86), than CSA (AUC=0.53; 95%CI=0.45, 0.64) (p<0.01; **Figure 5.5C**). Patients with EDSS progression (n=76) were better differentiated from those without EDSS progression (n=206) using GBSI (AUC=0.59; 95%CI=0.52-0.66) than CSA (AUC=0.50; 95%CI=0.43-0.58) (p=0.04; **Figure 5.5D**).

Figure 5.5. ROC curves for CSA and GBSI in relation to clinical variables.

ROC curves for CSA (solid green line) and GBSI (dashed orange line) in relation to differentiating healthy controls (n=82) from CIS (n=52) (**A**), RRMS (n=196) (**B**), and PMS (n=34) (including both PPMS and SPMS) (**C**), and patients with EDSS progression (n=74), from those without EDSS progression (n=208) (**D**). AUC and p-value are reported. Adapted from Moccia M, Prados F et al. Ann Neurol 2019 [113].



5.4.5. Sample size estimates using GBSI and CSA

The minimum sample sizes per arm required to detect a 60% treatment effect in one year clinical trial (i.e., a 60% reduction in percentage spinal cord change in MS cases when compared with physiologic spinal cord loss in controls, adjusted for age, gender, site of acquisition and disease duration) were lower for GBSI compared with CSA (CIS: 106 vs. 830; RRMS: 95 vs. 335; PMS: 44 vs. 215) (power=80%, alpha=5%). Similar results were obtained when estimating the sample size required to detect different treatment effects (**Figure 5.6**).

5.5. Discussion

5.5.1. Main findings

There have been few clinical trials and observational studies in MS that used spinal cord atrophy as an outcome measure, because of the large sample size required when using the available CSA method [63, 91, 144, 292]. In the present study, I applied a standard semi-automatic pipeline for spinal cord segmentation using the SCT, and, then, a fully automated registration-based technique (GBSI) for spinal cord atrophy to a large, multicentre, multi-manufacturer and multi-field strength scan cohort, derived from longitudinal observational studies. The rates of spinal cord loss over one year obtained with GBSI were similar to those obtained with CSA, but they were associated with lower variability, greater ability to distinguish between MS patients and controls, and more robust clinical correlates, thereby holding promise for future MS research on spinal cord imaging. Use of GBSI yielded increased statistical power to detect treatment changes, suggesting that future treatment trials –particularly those testing neuroprotective agents– could include spinal cord atrophy as a primary outcome measure.

Figure 5.6. Sample size estimates for CSA and GBSI.

Profile plot shows sample size estimates for CSA and GBSI in different disease phenotypes (CIS, RRMS and PMS). For sample size calculation, I included adjusted beta-coefficients from linear regression models, estimating spinal cord loss in MS patients, when compared with physiologic loss in controls, and standard deviation from each disease phenotype. Power was set at 80% and alpha at 5%. Different treatment effects were hypothesised (e.g., 30%, 60% and 90%), that were smaller than the observed difference between MS cases and physiologic spinal cord loss in controls. Adapted from Moccia M, Prados F et al. Ann Neurol 2019 [113].



5.5.2. Interpretation

CSA and GBSI provided similar rates of spinal cord atrophy in each MS subtype, but CSA yielded a larger variability (standard deviation), when compared with GBSI (e.g., in RRMS ±4.02% vs. ±2.57%, respectively), implying that GBSI measurements are more precise. Similarly, when images were acquired with a scan-rescan fashion, GBSI presented with lower coefficient of variation, when compared with CSA, indicating higher precision; the median absolute deviation (0.21%) was similar to what has been previously described in the validation of a registration-based method for brain atrophy (0.15-0.20% for the SIENA) [367]. Spinal cord measurements with GBSI can be repeated using different segmentation methods, with high agreement between techniques (e.g., JIM and SCT). Of note, a higher percentage of spinal cord decline (and a lower standard deviation) was found in PMS when using GBSI than when using CSA (-2.29±2.40% vs -1.29±3.20%), and this was probably due to the relatively small sample in this MS subtype, further highlighting the higher measurement precision of GBSI. A more detailed description of spinal cord atrophy measurements in progressive MS will be done in the following <u>Chapter 6</u>.

The smaller variability in GBSI measurements may be due to the ability of GBSI to derive spinal cord atrophy rates directly from small intensity changes between images at the cord boundaries, accounting for partial volume effects in these regions which are critical for measuring changes. Indeed, partial volume effects can lead to the inclusion of tissue outside of the area of interest with subsequent segmentation errors, and to the variability when calculating the absolute crosssectional areas [368–370]. The use of the probabilistic XOR (pXOR) region for weighting the BSI over specific tissue boundaries, is particularly relevant in the spinal cord where there are extremely closefitting surfaces that can be affected by changes even in a small number of voxels. On the contrary, conventional segmentation-based methods (e.g., CSA) rely on the numerical difference between areas obtained from the hard segmentation at each time-point; this approach provides an indirect estimate of atrophy and can introduce greater variability, especially in acquisitions with large voxel sizes or between scans with different intensity scales.

I found that GBSI allowed a four-fold smaller (and therefore achievable) sample size than that obtained with CSA. In a recent review of previous clinical trials in MS [213], differences between treated and untreated patients ranged from 0.4% to 1.8%/year spinal cord loss on CSA, in line with a roughly 60% treatment effect (corresponding to 0.7%/year spinal cord loss). Overall, the sample size estimates for spinal cord atrophy measurements with GBSI are of the same order of magnitude as those for brain atrophy obtained with registration-based methods [153, 158, 289, 360]. However, monitoring spinal cord atrophy could be more clinically relevant than brain atrophy, due to its robust clinical correlates [227, 250, 305]. Spinal cord atrophy occurs in the early stages of MS (e.g., CIS), is more obvious in progressive patients than relapsing types of MS, and progresses faster than brain atrophy [227, 250, 305]. The risk of disability progression increases with the rate of spinal cord atrophy [296], accounting for up to 77% of motor disability, as measured by the EDSS [227, 250, 305]. In line with this, the percentage spinal cord decline measured with GBSI was associated with EDSS progression and with disease subtype, and performed better than CSA-derived spinal cord atrophy in detecting more disabled patients. Of note, differentiation between healthy controls and MS patients (especially progressive MS) revealed better performance of GBSI when compared with CSA, whilst differentiation between patients with and without EDSS progression showed similar GBSI and CSA measurements, with CSA tending to random prediction of results (AUC=0.50) and GBSI presenting with statistically higher but not particularly better predictive value (AUC=0.59). The lack of separation in this chapter might be due to the limited proportion of patients presenting with 3month confirmed disability progression over 1-year observation time, and these findings should be confirmed with a longer follow-up in order to avoid false positive and negative results.

5.5.3. Limitations

Limitations of the present study include the short follow-up duration (1.6 years in MS patients), meaning that I could not assess the association between spinal cord atrophy and long-term disability progression. Previous studies have shown that spinal cord atrophy predicts disease progression and conversion from CIS to RRMS over a long follow-up period [307]. However, study duration was a priori set the at 1 year in order to obtain estimates for clinical trials and short-term observational studies; of note, I obtained annualised atrophy rates in line with pooled estimates from 94 studies (1.78%/year) [268], and the number of participants per arm was consistent with that obtained by other similar studies [153, 158, 289]. The present cohort was recruited before presentation and publication of the 2017 revision of McDonald criteria [61], and, thus, diagnosis was performed with the 2010 revision [59]. As such, I cannot exclude that at least some CIS patients would nowadays classify as RRMS [61], possibly determining an (almost) physiological rate of spinal cord atrophy in the remaining CIS population. I segmented the spinal cord using PropSeg within the SCT. The PropSeg tool has already been demonstrated as a robust, accurate and fast segmentation method of the spinal cord in both MS patients and controls, compared with other segmentation methods (e.g., semi-manual ASM within JIM) [284, 376, 388]. Also, the possibility to derive spinal cord GBSI measurements from brain scans needs to be explored [282, 287, 292, 296].

An important caveat of this chapter, is that good quality images (e.g., dedicated spinal cord 3DT1 images with 1mm isotropic voxel) are needed for spinal cord atrophy measurements. I was only able to use 86% of the patients whose scans were originally collected in eight experienced imaging

centres, using slight variations in MRI protocols and field strength. However, there is an initiative to mitigate the problem of setting-up a standard high-quality image protocol for spinal cord MRI (http://www.spinalcordmri.org - Protocols). In this project, a consensus acquisition protocol has been developed and tested in about 30 different sites across the world, for different vendors (GE, Siemens and Philips). This protocol is easy to apply and facilitates the adoption curve of spinal cord MRI acquisitions. Also, latest software improvements, such as machine-learning based segmentation methods (e.g., *DeepSeg* within the SCT), could facilitate the spinal cord image processing and will be further explored in <u>Chapter 6</u>.

5.5.4. Conclusions

In this chapter, I presented results from a longitudinal multicentre, multi-manufacturer and multifield strength scan analysis, and showed that GBSI and CSA provided similar rates of spinal cord atrophy, but the registration-based method (GBSI) was associated with lower variability, providing smaller sample size estimates as well as a higher significance at differentiating between different MS subtypes and patients with disability progression, compared with segmentation-based method (CSA), though still far from perfect. This study provides evidence that GBSI should be considered as a precise and reliable tool for calculating MS-related spinal cord atrophy in clinical trials and in observational datasets.

6. Spinal cord atrophy in a primary progressive multiple sclerosis trial

6.1. Background

As already discussed in <u>Chapter 1</u> and <u>Chapter 2</u>, spinal cord atrophy is a common feature of MS, can be detected *in vivo* using MRI, and is one of the main substrates of disease progression [226, 294, 297, 298]; as such, spinal cord atrophy can be used to monitor disease progression and has been included in clinical trials evaluating medications with putative neuroprotective effects in MS [227, 300, 305, 309].

In <u>Chapter 5</u> [113, 389], I have preliminary applied the GBSI pipeline to cohorts of MS patients and healthy controls. This technique significantly reduced measurement error by providing a direct measure of atrophy based on registration of all images in a common space [113, 289], when compared with indirect measures obtained from numerical subtraction between segmentations at different timepoints [113], being at risk of differences in cord coverage, miss-segmentations and/or changes in cord curvature [109, 292]. Improvements in measurement precision could be particularly relevant to clinical trials, using gold-standard segmentation methods (e.g., CSA), that, so far, have failed to show any significant treatment effect on spinal cord atrophy, especially in progressive MS patients [105, 213], where this outcome measure holds the strongest clinical correlates [109, 213].

Thus, following previous results, I have hereby further implemented the GBSI pipeline in collaboration with Dr Prados. In particular, I have run spinal cord segmentation and GBSI calculation on a large cohort of progressive MS, and evaluated possible correlates to clinical and patient-reported outcomes. Additionally, I obtained registration-based spinal cord atrophy measurements for different levels and also from brain scans.

6.2. Aims

In the present study, I re-analysed a phase 2 clinical trial on PPMS to:

- Compare spinal cord atrophy measurements using segmentation- and registration-based methods, with possible implications for image acquisition and clinical trial design (e.g., measurement precision, image quality);
- (2) Compare spinal cord atrophy measurements obtained from brain (C1-2) and spinal cord MRI
 (C1-2 and C2-5), using segmentation- and registration-based methods;
- (3) Explore possible clinical correlates, also in relation to conventional brain MRI measures;
- (4) Explore possible treatment effect.

6.3. Methods

6.3.1. Study design

This is a secondary analysis on PPMS patients who participated in the ARPEGGIO phase 2 clinical trial. As already discussed in <u>Chapter 4</u>, the ARPEGGIO trial was a randomised, double-blind, parallelgroup, placebo-controlled study. Patients were randomised in a 1:1:1 ratio to receive oral laquinimod 0.6 mg or 1.5 mg, or placebo once daily from January 2015 to April 2016 at 85 sites in 10 countries. Duration of the core study was 48 weeks [105].

6.3.2. Population

Inclusion and exclusion criteria have been reported previously [105]. Briefly, inclusion criteria were:

- (1) Aged 25–55 years;
- (2) Diagnosis of PPMS [59];
- (3) EDSS at baseline from 3.0 to 6.5;

- (4) Documented worsening of clinical disability in the 2 years prior to screening;
- (5) A FSS ≥ 2 for the pyramidal system or gait impairment due to lower limb dysfunction.

Exclusion criteria were:

- (1) Clinical history of any MS exacerbations or relapses;
- (2) Any other progressive neurological disorder (e.g., cervical cord compression, vitamin B12 deficiency);
- (3) Previous use of immunosuppressive/cytotoxic agents, experimental/investigational drugs and/or MS-specific treatments (e.g., fingolimod, dimethyl fumarate, glatiramer acetate, interferon-β, laquinimod).

6.3.3. MRI acquisition and processing

All patients underwent brain and cervical spinal cord MRI at baseline, week 24 and week 48, including 3D T1-weighted isotropic images of the brain and spinal cord (1x1x1mm³), within 14 days of the scheduled clinical visit. MRI scans were collected centrally at the VUmc in Amsterdam. For the purposes of the present study, I included baseline and week-48 MRI.

For the primary analysis of the ARPEGGIO trial, cord area at C1-2 level was determined using the NeuroQLab, a segmentation-based method using a Gaussian mixture modelling [275, 281, 282]. After definition of the spinal cord subsection to be segmented, watershed segmentation of the spinal cavity and surrounding cerebrospinal fluid was performed, and MUCCA was computed [275]. Percent change of cord area was calculated using the following formula: MUCCA = 100*(week 48 MUCCA - baseline MUCCA)/baseline MUCCA.

In the present study, masks of C1-2 and C2-5 levels were obtained from spinal cord MRI acquired at each time point, using the *DeepSeg* tool within the SCT (version 4.0), a fully-automated segmentation method based on convolutional neural networks (**Figure 6.1**) [283, 285]. Similarly, masks of C1-2 level were obtained from brain MRI (**Figure 6.2**). Percent change of CSA was calculated using the following formula: CSA = 100*(week 48 CSA - baseline CSA)/baseline CSA. For GBSI, I followed the pipeline previously described in <u>Chapter 4</u> [113, 389]. The GBSI was finally computed and the percent variation was measured (**Figure 6.1**; **Figure 6.2**).

From the original clinical trial dataset, I extracted the number of new T2-hyperintense lesions, T2hyperintense lesion volume change, T1-hypointense lesion volume change and PBVC, at baseline and week 48 visits. Full details of acquisitions and processing have been previously reported [105].

6.3.4. MRI quality

To classify scans based on their quality, I used the σ (standard deviation of the MR signal), calculated with the following formula: $\sigma = \frac{\sigma_{\eta}}{\sqrt{2-\frac{\pi}{2}}}$, where σ_{η} is the standard deviation of the magnitude–

reconstructed cerebrospinal fluid signal [377]. For the purpose of this chapter, I classified scans based on the median σ for each spinal cord segment.

6.3.5. Clinical variables

Baseline clinical variables were age, gender, disease duration and EDSS. From the original clinical trial dataset, I extracted following clinical variables corresponding to MRI acquisitions: EDSS, T25FW, 9HPT, SDMT, and MSWS. EDSS progression was defined as \geq 1 point from baseline EDSS if EDSS at entry was \leq 5.5 or increase of \geq 0.5 point if EDSS at entry was >5.5. T25FW, 9HPT, SDMT and MSWS progression was defined as \geq 20% increase from baseline score.

Figure 6.1. Spinal cord MRI processing using SCT and GBSI.

Reference points were preliminarily set at C1, C2 and C5 on sagittal scans (**a**). Then, masks of C1-2 (**b**) and C2-5 (**c**) spinal cord levels were obtained from spinal cord images acquired at each time point using the *DeepSeg* tool within the SCT (version 4.0). The probabilistic boundary-shift region-of-interest was then adaptively estimated from baseline and follow-up cord segmentations and the GBSI integral was finally computed for C1-2 (**d** for sagittal plane, **e** for axial plane) and C2-5 (**f** for sagittal plane, **g** for axial plane).



Figure 6.2. Brain MRI processing using SCT and GBSI.

Reference points were preliminarily set at C1 and C2 on sagittal scans (**a**). Then, masks of C1-2 (**b**) levels were obtained from spinal cord images acquired at each time point using the *DeepSeg* tool within the SCT (version 4.0). The probabilistic boundary-shift region-of-interest was then adaptively estimated from baseline and follow-up cord segmentations and the GBSI integral was finally computed for C1-2 (**c** for sagittal plane, **d** for axial plane).



6.3.6. Treatment exposure

Patients were randomised in a 1:1:1 ratio to receive oral laquinimod in a dose of 0.6 mg or 1.5 mg or placebo (once daily). The laquinimod 1.5 dose arm was discontinued as of January 1, 2016, due to cardiovascular side effects (patients were followed-up, but no further treatment was given).

6.3.7. Statistical analyses

Baseline demographics and clinical characteristics are presented as mean (and standard deviation), number (and percent), or median (and range), as appropriate.

To evaluate possible implications of different spinal cord atrophy measurements on image acquisition and clinical trial design (aim 1), I computed the sample size required for a hypothetical clinical trial evaluating a neuroprotective medication over one year. Sample size was computed using the formula $n = \frac{2(Z_{\alpha}+Z_{1-\beta})^2\sigma^2}{\Delta^2}$, where *n* is the required sample size per treatment arm in 1:1 controlled trials, Z_{α} and $Z_{1-\theta}$ are constant (set at 5% alpha-error and 80% power, respectively), σ is the standard deviation (from each spinal cord atrophy measurement), and Δ is the estimated effect size [289, 300]. Effect size was derived from the spinal cord change on each atrophy measurement (MUCCA, CSA at C1-2 level from brain MRI, GBSI at C1-2 level from brain MRI, CSA at C2-5 level from spinal cord MRI, and GBSI at C2-5 level from spinal cord MRI); different treatment effects were simulated (e.g., 30%, 60% and 90%). Sample size estimates were performed on the whole population first and, then, on the subset of scans above the median quality (based on the standard deviation of the MR signal (σ)). As additional estimates of measurement precision, I also computed coefficients of variation and median absolute deviations.

To evaluate the possibility of deriving longitudinal spinal cord atrophy measurements from brain MRI (aim 2), I used linear regression models including spinal cord atrophy measurements from brain MRI (CSA at C1-2 level and GBSI at C1-2 level in turn) and corresponding spinal cord atrophy measurements from spinal cord MRI (CSA at C1-2 and C2-5 levels, and GBSI at C1-2 and C2-5 levels, respectively). Results were presented as Coeff, 95%CI and p-values.

To evaluate possible clinical correlates of each spinal cord atrophy measurement (aim 3), I used different stepwise linear regression models (one for each MRI variable) with backward selection for *p*=0.20 as the critical value for entering clinical variables in the model (EDSS progression, T25FWT progression, 9HPT progression, SDMT progression, and MSWS progression). For the purposes of this analysis, I considered both spinal cord MRI variables (MUCCA, CSA at C1-2 level from brain MRI, GBSI at C1-2 level from brain MRI, CSA at C1-2 level from spinal cord MRI, GBSI at C1-2 level from brain MRI, CSA at C1-2 level from spinal cord MRI, and GBSI at C2-5 level from spinal cord MRI, and GBSI at C2-5 level from spinal cord MRI, and GBSI at C2-5 level from spinal cord MRI, and BSI at C2-5 level from spinal cord MRI, and BSI at C2-5 level from spinal cord MRI, and BSI at C2-5 level from spinal cord MRI, and BSI at C2-5 level from spinal cord MRI, and BSI at C2-5 level from spinal cord MRI, and BSI at C2-5 level from spinal cord MRI, and BSI at C2-5 level from spinal cord MRI), and brain MRI variables (number of new T2 lesions, T2 lesion volume change, T1 lesion volume change and PBVC). Results were presented as Coeff, 95%CI and p-values.

To evaluate differences in spinal cord atrophy between laquinimod 0.6mg and placebo (aim 4), I used linear regression models. Covariates were age, gender, height, country and baseline CSA [270]. Results were presented as Coeff, 95%CI and p-values.

Stata 15.0 was used for data processing and analysis. Results were considered statistically significant when associated with p-values <0.05.

6.4. Results

6.4.1. Patient disposition

Patient disposition and reasons for exclusion are reported in **Figure 6.3**. Overall, among patients with baseline and week 48 visits and with MRI acquisitions suitable for analyses, I was able to include 98.1% of patients for CSA at C1-2 level from brain MRI (211/215), 84.2% of patients for GBSI at C1-2 level from brain MRI (181/215), 67.4% of patients for CSA at C1-2 and at C2-5 level from spinal cord MRI (114/169), and 66.9% of patients for GBSI at C1-2 and at C2-5 level from spinal cord MRI (113/169). Examples of MRI acquisitions not suitable for analyses or resulted into SCT failure, GBSI failure and atrophy rate above what reasonably expected (±5%) are presented in **Figure 6.4**. For comparison, I included 220 patients with MUCCA, number of new T2 lesions, T2 lesion volume change and PBVC from the original clinical trial.

Demographic and clinical features of included patients are reported in Table 6.1.

Table 6.1. Demographics and clinical features.

Baseline demographics and clinical features are reported for included patients.

46.5±6.8
118 (53.6%)
4.5 (3.0-6.5)
3.4±3.2
172.0±9.8
10

Figure 6.3. Patient disposition.

Patient disposition flow diagram shows number of included and excluded patients. Reasons for exclusion from the original trial population were early termination, lack of upper spinal cord segments included in brain MRI, lack of dedicated spinal cord MRI, SCT failure, GBSI failure, and >5% atrophy rate on both SCT and GBSI. Total number of patients with each MRI measure is presented.



Figure 6.4. Examples for exclusion.

I excluded brain MRI if acquisition did not include C1-2 spinal cord level (**a**). SCT failure, GBSI failure and atrophy rate above what expected (±5%) were related to noisy images (**b**), artefacts (**c**), and poor contrast (**d**) for both brain and spinal cord MRI.



6.4.2. MRI quality

Scans were classified on the median value of σ (standard deviation of the MR signal) at each spinal cord level. The lowest median standard deviation was found on brain MRI at C1-2 level (σ =43.3), followed by spinal cord MRI at C1-2 level (σ =57.0), and spinal cord MRI at C2-5 level (σ =76.5). Representative images are presented in **Figure 6.5**.

Figure 6.5. MRI quality.

Figure shows sagittal plane of brain and spinal cord images above (upper row) and below (lower row) median quality (axial plane in the inset). Different spinal cord levels are reported (C1-2 from brain MRI, C1-2 from spinal cord MRI, and C2-5 from spinal cord MRI). Standard deviation of the MR signal (σ) is reported for each image.



6.4.3. Spinal cord atrophy

Spinal cord atrophy measurements obtained with GBSI (-1.5±3.4% at C1-2 level from brain MRI; -1.8±3.1% at C1-2 level from spinal cord MRI; -1.5±3.6% at C2-5 level from spinal cord MRI) had a larger effect size and smaller standard deviation when compared with corresponding CSA (-0.9±4.2% at C1-2 level from brain MRI; -1.1±4.1% at C1-2 level from spinal cord MRI; -1.5±4.7% at C2-5 level from spinal cord MRI) and MUCCA (-0.9±3.1%) (**Figure 6.6**), resulting into smaller sample size estimates, smaller coefficients of variation and smaller median absolute deviations (**Table 6.2**).

Table 6.2. Sample size estimates and measurement error.

Table shows sample size estimates using 1-year atrophy rate and standard deviation from each MRI measure for the whole population; power was set at 80% and alpha-error at 5%. Different treatment effects were simulated (30%, 60% and 90%). Coefficients of variation and median absolute deviations are also reported.

	Sample size			Coefficient	Median
	Trea	itment e	effect	of variation	absolute
	30%	60%	90%		deviation
MUCCA	2073	518	230	-3.56	3.06
CSA at C1-2 level from brain MRI	3454	864	384	-4.57	4.13
GBSI at C1-2 level from brain MRI	832	208	92	-2.13	3.26
CSA at C1-2 level from spinal cord MRI	2528	632	281	-3.42	3.86
GBSI at C1-2 level from spinal cord MRI	523	131	58	-1.83	2.83
CSA at C2-5 level from spinal cord MRI	1581	395	176	-3.09	4.86
GBSI at C2-5 level from spinal cord MRI	1027	257	114	-2.37	3.33

Results were confirmed when considering the subset of patients with availability of all measurements (MUCCA, CSA and GBSI at different cord levels from both brain and spinal cord MRI), avoiding the effect of different sample size for computing mean and standard deviation (**Figure 6.7a**), and the MRIs with quality above the median (**Figure 6.7b**).

Figure 6.6. Spinal cord atrophy rates by type of scan and analysis technique.

Box-and-Whisker plots show 1-year spinal cord percent volume change for different measurements (MUCCA, CSA and GBSI at different cord levels from brain and spinal cord MRI). Mean, standard deviation and number of included patients are reported.



Figure 6.7. Spinal cord atrophy rates in patients with all measurements and in high-quality scans. Box-and-Whisker plots show 1-year spinal cord percent volume change for different measurements (MUCCA, CSA and GBSI at different cord levels from brain and spinal cord MRI) in a subset of patients with all measurements (n=73) (a), and in scans above median quality (50% of the original sample, as presented in Figure 6.6), estimated as the standard deviation of the MR signal (σ) (b). Mean, standard deviation, and number of included patients are reported.



6.4.4. Spinal cord atrophy from brain scans

Longitudinal spinal cord atrophy measurements obtained from brain MRI were related to corresponding measurements from dedicated spinal cord MRI for both CSA (**Figure 6.8a-b**) and GBSI (**Figure 6.8c-d**).

Figure 6.8. Spinal cord atrophy longitudinal changes from brain and spinal cord MRI.

Scatter plots show 1-year spinal cord atrophy longitudinal changes obtained from brain scans (CSA at C1-2 level from brain MRI in **a** and **b**; GBSI at C1-2 level from brain MRI in **c** and **d**) in relation to measurements obtained with the same technique but from spinal cord MRI (CSA at C1-2 level and CSA at C2-5 level from spinal cord MRI in **a** and **b**; GBSI at C1-2 level and GBSI at C2-5 level from spinal cord MRI in **a** and **b**; GBSI at C1-2 level and GBSI at C2-5 level from spinal cord MRI in **a** and **b**; GBSI at C1-2 level and GBSI at C2-5 level from spinal cord MRI in **a** and **b**; GBSI at C1-2 level and GBSI at C2-5 level from spinal cord MRI in **a** and **b**; GBSI at C1-2 level and GBSI at C2-5 level from spinal cord MRI in **a** and **b**; GBSI at C1-2 level and GBSI at C2-5 level from spinal cord MRI in **a** and **b**; GBSI at C1-2 level and GBSI at C2-5 level from spinal cord MRI in **a** and **b**; GBSI at C1-2 level and GBSI at C2-5 level from spinal cord MRI in **a** and **b**; GBSI at C1-2 level and GBSI at C2-5 level from spinal cord MRI in **a** and **b**; GBSI at C1-2 level and GBSI at C2-5 level from spinal cord MRI in **a** and **b**; GBSI at C1-2 level and GBSI at C2-5 level from spinal cord MRI in **a** and **b**; GBSI at C1-2 level and GBSI at C2-5 level from spinal cord MRI in **a** and **b**; GBSI at C1-2 level and GBSI at C2-5 level from spinal cord MRI in **a** and **b**; GBSI at C1-2 level and GBSI at C2-5 level from spinal cord MRI in **a** and **b**; GBSI at C1-2 level and GBSI at C2-5 level from spinal cord MRI in **a** and **b**; GBSI at C1-2 level and GBSI at C2-5 level from spinal cord MRI in **a** and **b**; GBSI at C1-2 level and GBSI at C2-5 level from spinal cord MRI in **a** and **b**; GBSI at C1-2 level from spinal cord MRI in **a** and **b**; GBSI at C1-2 level from spinal cord MRI in **a** and **b**; GBSI at C1-2 level from spinal cord MRI in **a** and **b**; GBSI at C1-2 level from spinal cord MRI in **a** and **b**; GBSI at C1-2 level from spinal cord MRI in **a** and **b**; GBSI at C1-2 level from spinal cord MRI in **a** and **b**; GBSI at C1



6.4.5. Clinical correlates

Looking at spinal cord atrophy measurements, patients with T25FWT progression presented with more pronounced spinal cord atrophy on GBSI at C1-2 level from brain MRI (Coeff=-1.24; 95%Cl=-2.30, -0.19; p=0.02), and GBSI at C2-5 level from spinal cord MRI (Coeff=-1.47; 95%Cl=-2.18, -0.75; p<0.01). Patients with 9HPT progression presented with more pronounced spinal cord atrophy on GBSI at C1-2 level from brain MRI (Coeff=-0.92; 95%Cl=-1.33, -0.52; p<0.01). Patients with MSWS progression presented with more pronounced spinal cord atrophy on GBSI at C1-2 level from brain MRI (Coeff=-0.92; 95%Cl=-1.33, -0.52; p<0.01). Patients with MSWS progression presented with more pronounced spinal cord atrophy on GBSI at C1-2 level from brain MRI (Coeff=-1.86; 95%Cl=-2.44, -1.27; p<0.01), and GBSI at C1-2 level from spinal cord MRI (Coeff=-1.73; 95%Cl=-2.38, -1.07; p<0.01). No significant clinical correlates were detected for MUCCA, CSA at C1-2 level from brain MRI, CSA at C1-2 level from spinal cord MRI, and CSA at C2-5 level from spinal cord MRI. Spinal cord atrophy measurements in relation to progression of EDSS, T25FWT, 9HPT, MSWS and SDMT are reported in **Table 6.3**.

Looking at brain measurements, patients with EDSS progression presented with increased number of new T2 lesions (Coeff=2.95; 95%Cl=0.61, 5.29; p=0.01), higher T2 lesion volume change (Coeff=1075.53; 95%Cl=479.09, 1671.97; p<0.01), and more pronounced PBVC (Coeff=-0.40; 95%Cl=-0.54, -0.26; p<0.01). Patients with T25FWT progression presented with higher T1 lesion volume change (Coeff=142.88; 95%Cl=23.78, 261.97; p=0.01). Patients with SDMT progression presented with increased number of new T2 lesions (Coeff=2.66; 95%Cl=0.49, 4.84; p=0.01), higher T2 lesion volume change (Coeff=266.56; 95%Cl=21.54, 511.58; p=0.03), and more pronounced PBVC (Coeff=-0.46; 95%Cl=-0.58, -0.33; p<0.01).

Table 6.3. Spinal cord atrophy longitudinal changes from brain and spinal cord MRI.

Table shows spinal cord atrophy in relation to progression of EDSS, T25FWT, 9HPT, MSWS and SDMT, for different measurements. Results in bold

indicate p<0.05 on stepwise linear regression models.

		MUCCA	Brair	n MRI	Spinal cord MRI					
			C1-2		C1	-2	C2-5			
			CSA	GBSI	CSA	GBSI	CSA	GBSI		
EDSS	Yes	-1.03±3.59	-0.93±4.22	-1.71±3.51	-1.39±4.32	-1.89±3.17	-1.63±4.64	-1.62±3.56		
	No	-0.82±2.94	-0.89±4.31	-1.25±3.18	-0.53±3.56	-0.96±2.72	-1.20±5.27	-1.23±3.83		
T25FWT	Yes	-1.33±3.02	-1.04±4.31	-1.77±3.48	-1.55±4.28	-1.84±3.42	-2.06±4.66	-2.03±4.01		
	No	-0.75±3.10	-0.86±4.22	-1.26±3.36	-1.11±4.16	-1.63±3.00	-1.35±4.82	-1.36±3.50		
9HPT	Yes	-1.16±2.35	-1.65±5.52	-1.68±3.42	-1.27±4.18	-2.15±4.22	-1.52±4.65	-2.69±2.73		
	No	-0.98±3.05	-0.85±4.11	-0.88±3.78	-0.71±5.31	-1.61±3.07	-0.05±7.75	-1.45±3.64		
MSWS	Yes	-0.95±3.19	-1.41±4.06	-1.96±3.46	-1.24±4.37	-2.21±2.93	-1.50±5.58	-2.15±3.42		
	No	-0.51±2.74	-0.55±4.50	-0.72±3.25	-1.20±4.15	-0.51±3.24	-1.50±4.00	-1.22±3.58		
SDMT	Yes	-1.38±3.09	-0.96±4.36	-1.87±3.45	-1.23±4.07	-1.80±2.86	-2.11±5.63	-1.84±2.98		
	No	-0.59±3.07	-0.72±4.02	-1.59±3.47	-1.03±4.74	-1.68±3.21	-1.29±4.58	-1.14±3.75		

6.4.6. Treatment effect

In the original ARPEGGIO analysis, no effect of treatment was seen on clinical or atrophy measures, including brain atrophy (using SIENA) and spinal cord atrophy (using MUCCA) [105]. In this post-hoc analysis, again, no treatment effect was detected with any of spinal cord atrophy measurements (**Table 6.4**).

6.5. Discussion

6.5.1. Main findings

In this chapter, I explored clinical correlates and implications for clinical trials of segmentation- and registration-based measurements of spinal cord atrophy in progressive MS, obtained at different levels from both brain and spinal cord MRI. The registration-based method (GBSI) is a candidate secondary outcome measure for clinical trials in MS, providing clinically meaningful measurements of spinal cord atrophy at relatively-low sample size. In particular, deriving spinal cord atrophy measurements from volumetric brain MRI using the GBSI would allow the use of spinal cord atrophy in multi-centre studies, where acquiring high quality MRI of the spinal cord is difficult to achieve.

6.5.2. Interpretation

Overall, I confirmed that GBSI measurements provide similar spinal cord volume change (1.5-1.8%/year), when compared with CSA (0.9-1.5%/year) [113, 268, 389], but are more precise, with smaller standard deviations, coefficients of variation and median absolute deviations. GBSI boundary contours are indeed less affected by partial volume effects (i.e., inclusion of tissue outside of the area of interest) with subsequent segmentation errors [113, 369, 389]. Also, I confirmed the strong clinical correlates of spinal cord atrophy [213, 309]. In this chapter, 1-year spinal cord atrophy

Table 6.4. Treatment effect on spinal cord atrophy.

Table shows spinal cord atrophy in relation to treatment with placebo or laquinimod 0.6 mg. Coeff, 95%CI and p-values are reported from linear regression models adjusted by age, gender, height, country and baseline CSA.

	Placebo	Laquinimod	Coeff	95%CI		P-values
		0.6 mg		Lower	Upper	
MUCCA	-0.81±3.20	-1.38±3.04	-0.25	-1.13	0.62	0.56
CSA at C1-2 level from brain MRI	-1.08±4.10	-1.14±4.12	-0.19	-1.48	1.09	0.76
GBSI at C1-2 level from brain MRI	-1.28±3.40	-2.14±3.51	-0.78	-1.99	0.41	0.19
CSA at C1-2 level from spinal cord MRI	-0.67±4.56	-1.51±4.25	-0.58	-2.55	1.38	0.55
GBSI at C1-2 level from spinal cord MRI	-1.47±2.56	-1.97±3.39	-0.56	-1.97	0.84	0.42
CSA at C2-5 level from spinal cord MRI	-0.80±4.77	-1.80±4.73	-0.42	-2.51	1.66	0.68
GBSI at C2-5 level from spinal cord MRI	-1.31±4.05	-1.51±2.94	-0.38	-2.09	1.32	0.65

measurements obtained with GBSI, but not with CSA, at different levels (C1-2 and C2-5) and from both brain and spinal cord MRI were associated with upper and lower limb motor function, as measured by neurologists (e.g., walking test, and hand test), and by people with MS (e.g., selfreported scale on walking difficulties). By comparison, brain MRI variables were associated with clinical measures of upper and lower limb motor function, and cognitive disability (e.g., EDSS and SDMT), suggesting they better depict the overall patients' status. Looking at previous longitudinal studies measuring spinal cord atrophy in PPMS, early changes in spinal cord area are associated with clinical changes in the long term (e.g., six to fifteen years) [307, 311, 390], making spinal cord atrophy a useful short term surrogate marker of disease progression, with even stronger clinical correlates in the long term.

This chapter has further highlighted the difficulties in acquiring good quality spinal cord images. Unexpectedly, the noise in the dedicated spinal cord MRI was higher than in spinal cord images derived from brain MRI. By applying an semi-automatic pipeline for spinal cord atrophy calculation, I was able to include from 65 to 95% of scans, depending on the spinal cord level. In the previous chapter on combined MAGNIMS and Queen Square spinal cord cohorts, I was able to include 85% of scans [113]. Overall, failures in SCT and GBSI were related to noise, poor contrast and/or artefacts, that are difficult to account for when operating with semi-automatic methods for spinal cord segmentation and registration. Of note, acquiring good quality images is easier for brain than spinal cord, as demonstrated by the variability of the MR signal (standard deviation increased from 43 on C1-2 level from brain MRI, to 57 and 76 on C1-2 and C2-5 levels on spinal cord MRI, respectively). As such, obtaining spinal cord atrophy measurements from brain scans could represent a viable, efficient and clinically meaningful alternative to more technically-challenging spinal cord images, in particular in multi-centre settings where homogenous spinal cord acquisitions are not feasible. So far, the possibility to derive spinal cord measurements from brain scans has been successfully explored only with a cross-sectional design [282, 292, 296]. In this chapter, notwithstanding the large variability of centres acquiring images with different expertise, protocols and field strength, correlation coefficients were statistically, but minimally, higher for GBSI than CSA (0.3 vs 0.2), suggesting that longitudinal spinal cord atrophy could be better derived from brain scans using GBSI, than conventional segmentation-based methods (e.g., CSA). Differences in quality between brain and spinal cord MRI could explain the partial concordance of measurements, and could be due to the use of different coils, that can affect image quality at C1-2 level. Indeed, more advanced coils, optimised for both brain and spinal cord, can improve image quality, especially at upper cervical cord level, when compared with conventional coils [391]. Unfortunately, the ARPEGGIO dataset did not include coils at different sites to be accounted for in the statistical models.

Sample size estimates with spinal cord GBSI (e.g., 130-250 per treatment arm, for a 60% effect) are two-to-four fold smaller than CSA (e.g., 400-800 per treatment arm, for a 60% effect), and are on the same order of magnitude of brain atrophy (the pooled rate of 1-year brain atrophy in placeboand laquinimod-treated patients from the ARPEGGIO trial (-0.45±1.00%) corresponds to 215 patients per treatment arm for a 60% treatment effect) [91, 105]. In <u>Chapter 5</u> [113], I obtained even smaller estimates for both GBSI (50-100), and CSA (200-800), considering a similar treatment effect and also accounting for physiological spinal cord loss in healthy controls. However, that study was conducted on a much more selected population, using MRIs acquired within the MAGNIMS network [113]. In the present study, I tried to simulate similar conditions by classifying scans on the median quality; however, when including top quality scans, atrophy variability only partly improved, with increased effect size and reduced standard deviation for some measurements. Thus, future clinical trials aiming to use spinal cord atrophy as an outcome measure, rather than simply increase the sample size, could only include sites that apply appropriate acquisition protocols, and/or restrict MRI acquisition to a limited number of sites with possibility to acquire high quality images. A consensus spinal cord acquisition protocol has been recently developed and could be used in future multicentre MRI studies on the spinal cord (http://www.spinalcordmri.org - Protocols), as already discussed in <u>Chapter 5</u>. Alternatively, longer follow-up could also be considered [289]; unfortunately, in the ARPEGGIO trial, no MRI scans were available beyond week 48.

6.5.3. Limitations

Limitations of the present study include the relatively short follow-up duration (48 weeks). On the one hand, this is in line with phase 2 clinical trial requirements in MS where brain atrophy is the primary outcome measure. However, one-year follow-up is relatively short to acquire sufficiently reliable clinical outcomes, that could have been better studied in the long term. Also, I used *DeepSeg* for spinal cord segmentation, which is an automated method with high repeatability, but providing smaller volumes than other methods (e.g., NeuroQLab and JIM) [285, 288]; I previously ruled out the impact of different segmentation methods on longitudinal spinal cord atrophy measurements on GBSI, but cannot exclude results using the segmentation-based method (CSA) were affected [389]. Also, I used the standard deviation of the MR signal to classify scans based on their quality [377], whilst other measures should be considered for future studies; for instance the contrast-to-noise ratio provides information on both functional performance (contrast) and data quality (noise caused by the system and physiology) [392, 393]. Additional limitations are related to the study design, including patients within a specific disability range, and, thus, limiting the possibilities of clinical correlates.

6.5.4. Conclusions

Imaging the spinal cord is challenging, but clinically relevant. Spinal cord atrophy can detect early subtle changes in motor function to the upper and lower limbs, with possible long-term more obvious clinical correlates, as a consequence of tract-specificity of spinal cord anatomy. Improvements in spinal cord acquisition, processing and analysis (e.g., SCT and GBSI), along with the possibility of deriving spinal cord atrophy measurements from brain MRI, can enhance the application of this clinically meaningful imaging outcome measure in multi-centre longitudinal observational studies and clinical trials. Rigorous quality control will be required though, as spinal cord scans (and the resulting measurements) remain more variable than those for brain atrophy. Despite power calculations not being far off from those for brain atrophy in the ARPEGGIO study, spinal cord atrophy is destined to remain a secondary outcome for the moment, given the issues around controlling image quality in the spinal cord, especially when people with more advanced levels of disability are to be included.

7. Conclusions and future directions

7.1. Introduction

In this thesis, I have validated the first registration-based method (GBSI) for quantification of spinal cord atrophy, expanding research possibilities for future MS projects, especially for collaborative multicentre studies and clinical trials. In particular, I have achieved thesis objectives by:

- (1) Developing a registration-based method (GBSI) for quantification of spinal cord atrophy, which proved more precise, when compared with segmentation-based methods (i.e., CSA);
- (2) Demonstrating stronger clinical correlates for this novel registration-based method (GBSI), when compared with segmentation-based methods (CSA), from the perspective of both neurologists and MS patients;
- (3) Evaluating implication for the design and the conduction of future clinical trials and observational studies using the registration-based method (GBSI), especially in terms of sample size estimates and image acquisition.

The major findings presented in this thesis, and relating to each of these objectives, are summarised below, along with future directions.

7.2. Improving longitudinal spinal cord atrophy measurements with GBSI

In <u>Chapter 4</u>, I introduced a new pipeline based on the latest iteration of BSI for computing longitudinal spinal cord atrophy, to overcome limitations of commonly used segmentation-based methods. In following <u>Chapter 5</u> and <u>Chapter 6</u>, I demonstrated that longitudinal spinal cord changes with GBSI hold better measurement precision than CSA.

Overall, GBSI and CSA provided similar rates of spinal cord atrophy, but the registration-based method (GBSI) was associated with lower variability and increased statistical power, providing smaller sample size estimates and stronger clinical correlates. In particular, in <u>Chapter 5</u>, in a longitudinal multicentre, multi-manufacturer and multi-field strength scan setting, I showed better performance of GBSI at differentiating between different MS subtypes and patients with disability progression, compared with segmentation-based method (CSA). Then, in <u>Chapter 6</u>, I confirmed that spinal cord atrophy on GBSI can detect early subtle changes in motor function of the upper and lower limbs. Also, I showed the feasibility of deriving spinal cord atrophy in multi-centre studies, where acquiring high quality MRI of the spinal cord is difficult to achieve.

An important caveat of this thesis is that good quality images (e.g., dedicated spinal cord 3DT1 images with 1mm isotropic voxel) are needed for measuring spinal cord atrophy accurately. Depending on the spinal cord segment, the dataset and the segmentation method, I was able to process from 65% to 95% of scans, suggesting that rigorous quality control would be required for future acquisitions. Thus, for the moment, spinal cord atrophy measurements with GBSI should remain a secondary, but clinically relevant, outcome measure, until issues around controlling image quality are solved, especially when people with more advanced levels of disability are to be included.

7.3. Future directions

Future research will focus on characterising spinal cord pathology in a clinical setting (i.e., measurement of spinal cord atrophy with GBSI on clinical MRI acquisitions). In particular, spinal cord atrophy could be combined to other clinical and brain MRI outcome measures to further improve the surveillance of the clinical course of MS and its response to treatment. Indeed, combined

endpoints have become increasingly common in MS, and are conventionally based on relapses, disability progression, brain lesions, and brain atrophy [394, 395]; as such, the inclusion of spinal cord atrophy could further improve statistical power and clinical correlates.

BSI is a registration method which measures intensity changes and, hence, is currently applicable over T1-weighted images, as mentioned in <u>Chapter 4</u>. Further improvements to the GBSI technique will require the application to other sequences (i.e., PSIR or T2*), pending changes in the integral and in the intensity normalisation steps [396, 397]. The possibility of using PSIR and T2* lesions will allow spinal cord lesion masking and filling, which can make atrophy estimates more precise, as it happened for brain atrophy [398–400].

GBSI will need to be tested on images acquired on ultra-high-field (7T) scanners, which have appeared in recent years. 7T MRI of the spinal cord can potentially overcome limitations of 1.5 and 3T scanners, by improving spatial resolution, increasing the contrast-to-noise ratio, and allowing better characterisation of WM and GM [401, 402]. Preliminary reports have shown increased sensitivity and spatial accuracy in characterizing pathology in the spinal cord than lower field MRI [403]. However, 7T spinal cord MRI remains technically challenging due to motion artefacts and field inhomogeneities, and requires time-consuming acquisition and complex post-processing. New coils that reduce field inhomogeneities and allow whole spine coverage will help to overcome these limitations and develop this exciting tool in MS.

The ultimate validation of the GBSI would require pathology samples of the spinal cord, that could be acquired with a scan-rescan fashion, where atrophy is expected to be zero. As such, we could
evaluate the measurement which actually performs the best, and, not least, the pathology background of spinal cord atrophy [23, 24]

Finally, the GBSI should be considered for measuring spinal cord atrophy in other neurological diseases. Indeed, spinal cord atrophy does not only occur in MS, but also in other inflammatory diseases of the central nervous system, such as NMO [302, 303, 404], and human T- lymphotropic virus 1 (HTLV-1)-associated myelopathy/tropical spastic paraparesis [405]. Not least, spinal cord atrophy is associated with more severe clinical features in amyotrophic lateral sclerosis [406–408], spinal cord injury [409], and Friedreich's ataxia [410], and with worse recovery from spinal cord surgery [411]. There is also preliminary evidence of spinal cord atrophy in Alzheimer's disease [412], and in Huntington disease [413], suggesting that spinal cord atrophy can be part of more widespread neurodegenerative diseases.

7.4. Conclusions

Progressive MS represents a unique opportunity for studying imaging markers of neurodegeneration. Several imaging candidates hold promise for filling the unmet need of biomarkers in progressive MS, and brain atrophy is currently the best examined and most robust outcome, with attainable sample sizes and first positive results in phase 2 and 3 trials.

Imaging the spinal cord is challenging, but clinically relevant. Following the present thesis, improvements in spinal cord processing, along with the possibility of deriving spinal cord atrophy measurements from brain MRI, can enhance the application of this clinically meaningful imaging outcome to multi-centre longitudinal observational studies and clinical trials [109, 414]. For instance, results from this thesis will be particularly helpful to the United Kingdom MS Society

Efficient Clinical Trial Platform [415], to study the impact of different medications on the spinal cord atrophy. Not least, GBSI could prove useful in many neurological diseases where spinal cord volume changes are representative of the most aggressive aspects of the diseases (e.g., spinal cord injury, amyotrophic lateral sclerosis). Thus, accurate and sensitive-to-change monitoring of spinal cord atrophy over time can shed light on the most aggressive aspects of many neurological diseases, and the suggested GBSI pipeline is a suitable endpoint in studies of neuroprotection, also combined with other MRI measures.

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