Supplement

Supplement Table 1. Clinical data of all MS patients (main analysis) and of the short-term analysis in an additional cohort of nine MS patients (subanalysis).

	MS patients Main analysis (n=92)	MS patients Subanalysis (n=9)	p-value (Main analysis *vs* subanalysis)
Sex *(F/M)*	65 / 27	6 / 3	*p = 0.803* [a]
Mean (± SD) age at MRI *(years)*	32.9 ± 9.9	42.9 ± 11.8	*p = 0.012* [b]
Mean (± SD) age at diagnosis *(years)*	31.9 ± 9.8	39.7 ± 13.8	*p = 0.094* [b]
Mean (± SD) disease duration *(months)*	12.1 ± 14.5	40.8 ± 78.9	*p = 0.409* [b]
Median (range) follow-up *(months)*	12.0 (10.0 – 14.0)	11.5 (11.0 – 16.5)	*p = 0.887* [b]
Median (range) EDSS *(at baseline)*	1.0 (0 – 4.0)	1.5 (0 – 2.5)	*p = 0.311* [b]
Median (range) EDSS *(after 12 months)*	1.0 (0 – 4.0)	1.0 (0 – 2.5)	*p = 0.990* [b]
Median (range) LV at baseline *(ml)*	1.9 (0.02 – 33.0)	1.2 (0.04– 14.6)	*p = 0.957* [b]
DMD *(no/yes)*	30/62	3 / 6	*p = 0.965* [a]

a) p-value derived from Pearson's chi-square test

b) p-value derived from Mann-Whitney U test (due to the unequal size of both groups we opted to use a non-parametric test for all continuous variables)

Supplement Table 2a. Disease-modifying drugs (DMD) in MS patients and after subdivision into NEDA and EDA at baseline.

	MS patients (n=92)	NEDA (n=56)	EDA (n=36)	p-value (NEDA *vs* EDA)
DMD *(no/yes)*	30 / 62 (32.6% / 67.4%)	14 / 42 (25.0% / 75.0%)	16 / 20 (44.4% / 55.6%)	*0.052* [c]
Subdivision into no DMD, first-line or second line DMD				
No DMD	30 (32.6%)	14 (25.0%)	16 (44.4%)	*0.071* [c]
First-line [a]	50 (54.3%)	32 (57.1%)	18 (50.0%)	
Second-line [b]	12 (13.0%)	10 (17.9%)	2 (5.6%)	
Subdivision into each DMD				
No DMD	30 (32.6%)	14 (25.0%)	16 (44.4%)	*0.233* [c]
Glatiramer acetate	18 (19.6%)	10 (17.9%)	8 (22.2%)	
Interferon-beta	29 (31.5%)	20 (35.7%)	9 (25.0%)	
Teriflunomide	2 (2.2%)	1 (1.8%)	1 (2.8%)	
Dimethyl fumarate	1 (1.1%)	1 (1.8%)	0 (0%)	
Fingolimod	0 (0%)	0 (0%)	0 (0%)	
Natalizumab	12 (13.0%)	10 (17.9%)	2 (5.6%)	

a) First-line DMD: Glatiramer acetate, Interferon-beta, Teriflunomide, Dimethyl fumarate

b) Second-line DMD: Natalizumab, Fingoliomod

c) p-value derived from Pearson's chi-square test

Supplement Table 2b. Disease-modifying drugs (DMD) in MS patients and after subdivision into NEDA and EDA at follow-up.

	MS patients (n=92)	NEDA (n=56)	EDA (n=36)	p-value (NEDA *vs* EDA)
DMD (no/yes)	82 / 10 (89.1% / 10.9%)	51 / 5 (91.1% / 8.9%)	31 / 5 (86.1% / 13.9%)	0.456 [c)]
Subdivision into no DMD, first-line or second line DMD				
No DMD	10 (10.9%)	5 (8.9%)	5 (13.9%)	0.619 [c)]
First-line [a)]	63 (68.5%)	38 (67.9%)	25 (69.4%)	
Second-line [b)]	19 (20.7%)	13 (23.2%)	6 (16.7%)	
Subdivision into each DMD				
No DMD	10 (10.9%)	5 (8.9%)	5 (13.9%)	0.579 [c)]
Glatiramer acetate	13 (14.4%)	9 (16.1%)	4 (11.1%)	
Interferon-beta	36 (39.1%)	21 (37.5%)	15 (41.7%)	
Teriflunomide	6 (6.5%)	2 (3.6%)	4 (11.1%)	
Dimethyl fumarate	8 (8.7%)	6 (10.7%)	2 (5.6%)	
Fingolimod	4 (4.3%)	2 (3.6%)	2 (5.6%)	
Natalizumab	15 (16.3%)	11 (19.6%)	4 (11.1%)	

a) First-line DMD: Glatiramer acetate, Interferon-beta, Teriflunomide, Dimethyl fumarate

b) Second-line DMD: Natalizumab, Fingoliomod

c) p-value derived from Pearson's chi-square test

Supplement Figure 1. Depiction of the distribution of the 21 density intervals (that were applied to threshold the connection matrix) with (A) posterior predictive distribution at baseline (upper row) and at follow-up (lower row) and (B) the normality distribution. The lack of a discrepancy between the observed data and the posterior predictive distribution indicate that the model performs well.