## Additional file 8: Comparison of predicted treatment effectiveness

Clinical Outcome	Number of Relapses		Occurrence of CDP	
	Sample Size for DMT* Taken	Sample Size when DMT* Not Taken	Sample Size DMT* Taken	Sample Size DMT* Not Taken
Dimethylfumarat	134	307	863	306
Fingolimod	128	112	87	135
Glatirameracetat	-	1	45	238
IF-beta1	2	6	3	14
Natalizumab	234	2182	132	1101
Teriflunomide	-	13	16	179

Table S8.1: Sample sizes for highest ranked therapy

The number of patients for each highest ranked therapy (DMT\*) is listed based on their adherence. Sample sizes are listed based on the mean posterior number of relapses, and based on the mean posterior occurrence of a CDP.

GLM model outputs (svyglm.nb)					
	Coefficients	SE	p-value		
Dimethylfumarat: intercept	-1.0705	0.1385	<0.001		
Dimethylfumarat: slope	-0.6918	0.2892	0.0167		
Fingolimod: intercept	-0.8143	0.1711	<0.001		
Fingolimod: slope	0.0423	0.24	0.86		
Natalizumab: intercept	-0.7421	0.0418	<0.001		
Natalizumab: slope	-0.4376	0.1873	0.0195		

SE: Standard error of the coefficients. Model outputs of the survey-weighted negative binomial GLM svyglm.nb, applied to the observed number of relapses. The survey-weighted GLM was fitted to each therapy in turn. Group membership (subject who received the therapy ranked highest by the predictive model and those who received another therapy) was encoded by an indicator variable and derived from the predictive relapse model.

## Table S8.3: Survey-weighted GLM for the predictive CDP model

GLM model outputs (svyglm)					
	Coefficients	SE	p-value		
Dimethylfumarat: intercept	-2.36254	0.09642	4.18E-107		
Dimethylfumarat: slope	-0.53629	0.243424	0.027783622		
Fingolimod: intercept	-2.59057	0.290462	2.34E-16		
Fingolimod: slope	0.111356	0.422328	0.792290399		
Glatirameracetat: intercept	-2.24036	0.174009	4.15E-30		
Glatirameracetat: slope	-0.53358	0.569995	0.3500183		
Natalizumab: intercept	-2.27615	0.083491	9.42E-129		
Natalizumab: slope	-0.40208	0.482948	0.405249923		
Teriflunomide: intercept	-2.37646	0.223784	3.24E-21		
Teriflunomide: slope	-0.4317	1.249648	0.730108299		

SE: Standard error of the coefficients. Model outputs of the survey-weighted quasi-binomial GLM svyglm, applied to the observed occurrences of CDP. The survey-weighted GLM was fitted to each therapy in turn. Group membership (subject who received the therapy ranked highest by the predictive model and those who did not) was encoded by an indicator variable and derived from the predictive CDP model.