Thousands of algorithms trained for predicting the treatment efficacy of rheumatoid arthritis

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rank	submissionTeamName	submitterUserName	submissionId	submissionName	cor	description
1	GuanLab	fanzhu	2484815	Guanlab_final1	0.39307	syn2368045
2	Lucia	vbellon	2495027	MinMax3000	0.38503	syn2393428
3	teamMI	audmu	2495132	predictions_Q1_1_GEMMA	0.38251	syn2491623
4	tracy	powerset	2491352	tracy2	0.38115	syn2490275
5	STSI	erickramer	2495179	clinical_only	0.37581	syn2491171
6	Outliers	DHidru	2495314	team_submission	0.37479	syn2495286
7	STSI	erickramer	2495163	clinical_and_genetic	0.37229	syn2491171
8	wtwt5237	wtwt5237	2484149	RA_final_2	0.37214	syn2484133
9	WarwickDataScience	RichSavage	2484636	Final submission	0.37213	syn2484634
10	GuanLab	fanzhu	2491412	Guanlab_final2	0.36666	syn2368045
11	icm	mbq	2495074	wod	0.36257	syn2375115
12	teamMI	audmu	2495140	predictions_Q1_1_bemkl	0.35192	syn2491623
13	icm	mbq	2495076	wd	0.34175	syn2375115
14	TNFgen	hmzhan	2495043	final2	0.33892	syn2495026
15	SBI_Lab	javier.garciag	2492709	SBI_Lab_Q1_final_submission2	0.3292	syn2491824
16	SBI_Lab	javier.garciag	2492695	SBI_Lab_Q1_final_submission1	0.27714	syn2491824
17	MtSinaiPrediction	quanlong	2495099	quan_final_Lq	0.21942	syn2444012
18	MtSinaiPrediction	quanlong	2495098	quan_final_Gq	0.20828	syn2444012
19	tau	qzhou	2495281	ra_final	0.10314	syn2491535
20	LabG	YLiu	2495458	out1_phe1_140601.csv	0.0984	syn2495418
21	LabG	YLiu	2495459	out7_phe1_140601.csv	0.09674	syn2495418
22	MCIC	sopiyo	2491761	MCIC_Columbus_1	0.07656	syn2491733
23	rgb	mlux	2493834	final_q1_1	0.04111	syn2384264
24	ky	bamtree87	2495274	RAchallenge_Q1_final_template_pval01.csv	0.01371	syn2495269
25	MCIC	sopiyo	2491762	MCIC_Columbus_2	0.00312	syn2491733
26	ky	bamtree87	2495273	RAchallenge_Q1_final_template_pval005.csv	-0.00239	None
27	Lucia	vbellon	2495069	Linear3000	-0.03881	syn2393428

Leaderboard of the crowdsourced research challenge initial phase, Team MI ranking third.

Rheumatoid arthritis is a chronic inflammatory autoimmune disorder affecting millions of people worldwide. Anti-TNF treatment is a widely used treatment blocking the inflammatory cytokine, but it fails in approximately 1/3 of the patients.

The objective of the wide crowdsourced study was to use algorithms in assessing the efficacy of anti-TNF treatment based on clinic and genetic data, or in identifying the non-responders before the treatment. 73 research teams, altogether hundreds of researchers, worldwide competed in an open challenge using the most comprehensive data available of more than 2700 patients and using a wide range of state-of-the-art modeling methodologies.

The eight teams with the best predictive performances were invited to the final phase. Team MI of Aalto University and Helsinki University Institute for Molecular Medicine Finland (FIMM) were among those eight teams.

"We used both sparse linear regression model and multiple kernel learning model to predict the treatment response based on the genetic and clinic information, describes Lu Cheng," Postdoctoral Researcher at the Department of Computer Science.

Team Outlier, the winner in the final phase, did not use any genetic information in the final round. As a conclusion the currently collected genetic data did not significantly contribute to the prediction of treatment response above the clinical predictors including sex, age and medical information.

"If a limited amount of genetic variants would explain the failure of the treatment in some of the patients, we would have had the prediction model as a result of a vast study like this. Either the amount of the genetic variants is much bigger and their effects respectively much

smaller, or the missing heritability is better explained by genetic variants not included in the study, such as rare variants," tells University Lecturer Pekka Marttinen.

Over the course of the 16-week algorithm training period, 73 teams submitted a total of 4874 predictions for evaluation. The research results have been published in *Nature Communications*.

 More information: Solveig K. Sieberts et al. Crowdsourced assessment of common genetic contribution to predicting anti-TNF treatment response in rheumatoid arthritis, *Nature Communications* (2016). DOI: 10.1038/ncomms12460

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