Personalized Medicine: Redefining Cancer Treatment

Predict the effect of Genetic Variants to enable Personalized Medicine

$15,000 · 449 teams · 2 months to go

Overview

Submissions are evaluated on Multi Class Log Loss between the predicted probability and the observed target.

Submission File

For each ID in the test set, you must predict a probability for each of the different classes a genetic mutation can be classified on. The file should contain a header and have the following format:

```
ID,class1,class2,class3,class4,class5,class6,class7,class8,class9
0,0.1,0.7,0.05,0.05,0.1,0,0,0,0
1,0.7,0.1,0.05,0.05,0.1,0,0,0,0
2,0.05,0.05,0.1,0.7,0.1,0,0,0,0
3,0,0,0,0,0.05,0.05,0.1,0,7,0,1
etc.
```

Leaderboard >

1 Bojan Tunguz
2 Oleg Panichev
3 doitall
4 andrewhz
5 Pandas
6 Bluefool

Kernels >

Personalised Medicine - EDA...
97 votes · 16 days ago

EDA in Python
0 votes · 17 hours ago

Redefining Treatment [0.574...
42 votes · 7 days ago

Brief insight on Genetic varia

58 discussion topics >

When is it foolish to anonymi...
8 replies · 3 hours ago

More info about the machine ...
4 replies · 3 hours ago

Official external data and pre...
37 replies · a day ago

Text feature is messed up

7 Keep Calm

8 Jackling_Gu

50 votes · 19 days ago

Genetic Variants to Protein F...

11 votes · 13 days ago

1 reply · a day ago

Is this the expected scenario ...

3 replies · a day ago

Launch
25 days ago

Close
2 months

449 Teams **477** Competitors

Points **This competition does not award standard ranking points**
Tiers **This competition does not count towards tiers**