

# The Malaria DREAM challenge: team TPOT's sub-challenge 2 write-up

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## Abstract

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Challenge link: <https://www.synapse.org/#!Synapse:syn16924919/wiki/583955>

Objective: Predict the parasite clearance rate of malaria parasite isolates based on in vitro transcriptional profiles.

Data source: [1]

## Methods

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### Data harmonization

For this subchallenge, the training dataset's characteristics were very different compared to those of the test set. Importantly, training set contains *in vivo* transcription as described in [1] while test set contains *in vitro* transcription. Other differences in data collection, synchronization, microarray platforms, preprocessing steps, etc. have been detailed on the [challenge website](#). We first impute the missing data points using the KNN imputation method [2] with  $k = 10$  via the [fancyimpute](#) Python package. Next, to adjust for batch effects between the two datasets, we apply the *ComBat* algorithm [3] from the *sva* R package [4] on the transcription data. We assess the effect of the adjustment by examining the principal component analysis (PCA) plots on the raw and processed data.

### Transcriptional feature selection

Using the STatistical Inference Relief (STIR) algorithm [5], we selected the genes with adjusted STIR P values  $< 0.05$ . Specifically, with the MultiSURF neighborhood, STIR nearest-neighbors to select transcriptional features whose association with an outcome may be due to epistasis.

### Automated machine learning for model training

The Tree-based Pipeline Optimization Tool (TPOT) is a Python Automated Machine Learning (AutoML) tool that uses genetic programming to optimize machine learning pipelines for analyzing biomedical data [6]. However, like other AutoML tools, TPOT currently requires high computational expense when analyzing high dimensional data. Therefore, even though we already manually select features prior to executing TPOT, we also limit the final classifier of TPOT pipelines to [LinearSVC](#) to focus TPOT's effort on identifying the sequence of preprocessors (e.g., [recursive feature elimination](#) or [function transformer](#)). We used balanced accuracy as our scoring function.

### Test sample selection

While there is one single sample per isolate in the training set, there are eight samples for each of the 32 isolates in the test set (most have 2 biological replicates, 2 time points: 6 hours and 24 hours post invasion, perturbed with 5nM DHA (DHA) or perturbed with DMSO (UT)). Therefore, to obtain one prediction per isolate, we need to take caution in selecting which test samples to predict on. First, because the majority of the training samples are estimated at 18 hours post invasion (hpi), we selected test samples at 24 hpi (closer to 18 hpi compared to 6 hpi). Second, we analyze the developmental stage of each biological replicate at separate timepoints. We hypothesize that the group of isolates with asexual stage distribution close to that of the training set will yield the most accurate prediction for each isolate. While the stage of the parasites in the training set was determined by Mok et al. according to [1], transcriptional profiles in the test set were compared against the 3D7 sample from [7]. The Methods section in Mok et al.'s [supplementary material](#)

indicates that the two asexual stage estimation techniques are similar [8], but we carefully investigate the distributions of parasite stages in two datasets before making any specific selection.

## Non-genetic features consideration

Because all samples from the test data were collected from the Thailand-Myanmar border, for now, we ignore the `Country` feature. In the future, however, perhaps we can place more weights on the training samples that are geographically closer to this region. We also ignore the `Kmeans.Grp` feature that is cluster groups corresponding to three types of transcription profile based on parasite developmental stage.

## Availability

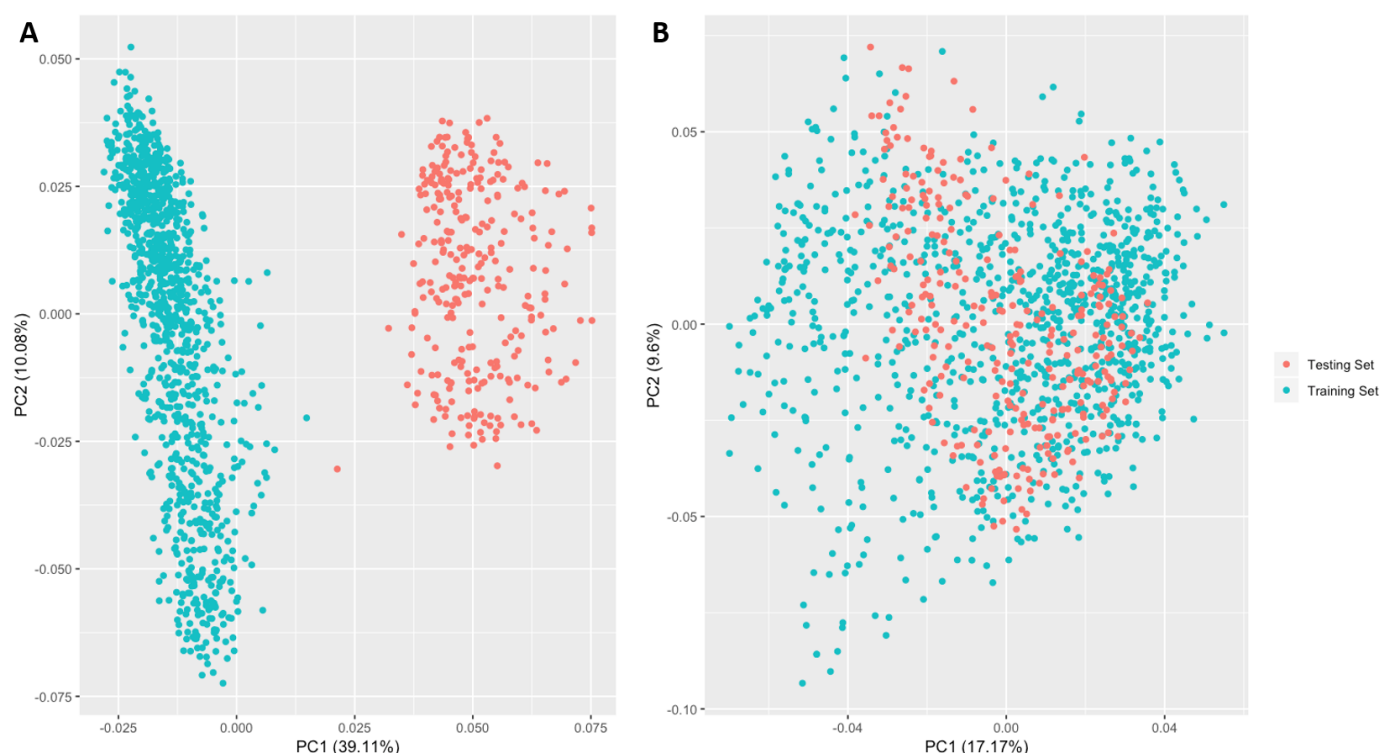
Detailed preprocessing, modeling and analysis code for this study is available at <https://github.com/EpistasisLab/malaria-challenge>.

## Results

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### Batch effect adjustment

Before batch adjustment, the two datasets are clearly separated in the first two principal component dimensions (Fig. 1A). After being adjusted for batch effect, this dataset-specific effect is less evident (Fig. 1B). The amount of variance explained in each component also seems to be more balanced.



**Figure 1:** Principal component analysis plots before (A) and after (B) adjusting for batch effects

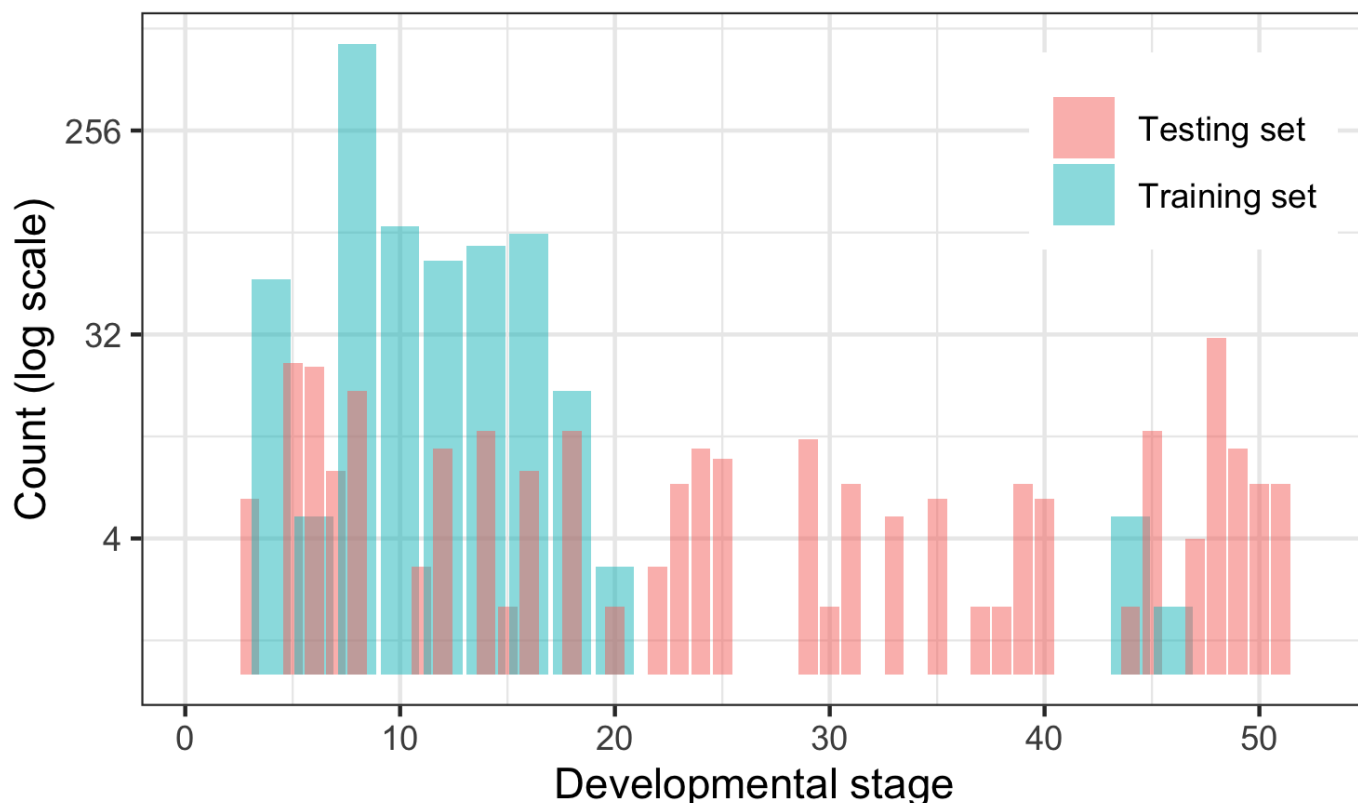
### STIR feature selection and TPOT cross-validated balanced accuracy

The training dataset consists of 1043 in vivo parasite isolates, each with 4952 transcriptomic features, out of which STIR selects 1068.

TPOT [...]

## Test sample selection

In general, the parasite developmental stages in the training set are smaller than those in the test set (Fig. 2). Because of this difference in distribution, we could not use stage of parasites as guideline to select the test samples. Instead, at 24 hpi, we decided to compute the average of the two lowest probabilities per isolate (across two types of treatments and two biological replicates). In other words, setting our goal to be detecting isolates with SLOW parasite clearance rate (SLOW = 1), we want to decrease the false negative rate (SLOW isolates predicted as FAST) by sacrificing some false positives (FAST isolates predicted as SLOW).



**Figure 2:** Developmental stages in training set and testing set

## Conclusion

### Take home

Even with automated machine learning, at the moment, we still need to be clever at preprocessing and integrating the data.

It is surprising to us that there is not a separate holdout set for this challenge. In an attempt to prevent overfitting, the organizers only released the ranking instead of the absolute score of each team's performance. However, a team can still assess the trajectory of their performance compared to other teams and tweak their method in that direction.

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