

# Notes on the GP-Transferability paper

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## 1 Data processing

### 1.1 Description of the different steps and programs for GP transfer paper

- Downsample the brain signals to time series of 350 points.
- Reduce time series to 250 points describing the signal information after the stimulus onset.
- Remove outlier samples from the data.
- For each time series, create 9-feature vector formed by overlapping segments of 50 points with overlaps of 25 points.
- For each segment, compute two features (mean and slope of the segment).
- For each subject, use minimum-redundancy and maximum-relevance feature selection method to select 120 of the 5508 features.
- Feature normalization by subtracting the mean and dividing by the standard deviation.

The results of the preprocessing steps are included in the folder `data`, this folder should be included within the main folder.

### 1.2 Computation of the transfer measures

Using the RuLSIF algorithm<sup>1</sup> proposed by [1] we have computed the transfer measures for each pair of subjects. There are two transference metrics:  $rPE_i$  divergence values and each pair of source and targets  $(s, t)$ , and density ratio of the univariate distributions for each possible value of variable  $X_i$  in the data set  $D_s$ .

The data structures with the divergences and density ratios are included in folder `matlab_data`. To run the optimizers, these two folders should be included within the main folder.

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<sup>1</sup>The implementation is available from <http://www.makotoyamada-ml.com/RuLSIF.html>

## 2 Evolution of the single-objective classifiers

Evolution of the single objective classifiers is done using as objective function the classification accuracy in the train set. The program that implements this optimizer is `./SingleKalimeroTransferMEGGPDeap.py`. It can be called as:

```
./SingleKalimeroTransferMEGGPDeap.py seed nvar 0 subj subj psize  
ngen where nvar = 120, subj is the subject number, and psize and ngen respectively  
represent the population size and number of generations.
```

## 3 Evolution of the MOP classifiers

Evolution of the bi-objective classifiers is done using one of the five bi-objective algorithms described in the paper. The program that implements these optimizers is `./KalimeroTransferMEGGPDeap.py`. It can be called as:

```
./KalimeroTransferMEGGPDeap.py seed nvar Alg subj targetsubj psize  
ngen 1
```

where the input parameters are as in the previous examples, and the parameter (*Alg*) to any of bi-objective algorithms is indicated as:

- 0 : Alg1, (O1,O2) Normal accuracy and transferability
- 1 : Alg2, (O2,O3) Biased accuracy and transferability
- 2 : Alg3, (O1,O3) Normal accuracy and biased accuracy
- 5 : Alg4, (O1,O4) LR (logistic regression) and normal accuracy
- 8 : Alg5, (O3,O4) LR (logistic regression) and biased accuracy

## 4 Evaluation of the other classification approaches

Classical classifiers are evaluated using grid search and 3 possible types of weight transfer for Importance Weighting Cross Validation. The program that runs these classical classifiers requires the instalation of the `libtllda` Python library <sup>2</sup>, which is a library of transfer learners and domain-adaptive classifiers. However, currently this library implements only four classifiers. We extended some of the procedures in the library to deal with other classifiers.

The program `RevisedVersion_MEG_Problem_OtherClassifiers_v1.py` executes all combinations of classifiers, weight methods, and pair-wise transfer experiments. It can be called as:

```
./RevisedVersion_MEG_Problem_OtherClassifiers_v1.py seed 120 3 1  
2 1000 100 2 3
```

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<sup>2</sup><https://github.com/wmkouw/libTLDA>

## References

- [1] M. Yamada, T. Suzuki, T. Kanamori, H. Hachiya, and M. Sugiyama. Relative density-ratio estimation for robust distribution comparison. *Neural computation*, 25(5):1324–1370, 2013.