**Master.rmd**

Large dataset BigData.

Different experiments [i\_exp] to perform on BigData to test the CBDA-SL and Knockoff algorithms.

Each experiment is uniquely identified by a set of input specifications that are read from an argument file.

Input Specifications = [**M , missing values, min\_FSR, max\_FSR, min\_SSR, max\_SSR**], where:

**M**: number of the BigData subsets on which perform Knockoff Filter and CBDA-SL feature mining

**Missing values**: % of missing values to introduce in BigData (just for testing, to mimic real cases)

**min\_FSR** : Lower bound for the % of features/columns sampling

**max\_FSR**: Upper bound for the % of features/columns sampling

**min\_SSR**: Lower bound for the % of subjects/rows sampling

**max\_SSR:** Upper bound for the % of subjects/rows sampling

Sampling ranges for subjects(**SSR -** Subject Sampling Range)and features(**FSR –** Feature Sampling Range) are then defines as follow:

**FSR** = [**min\_FSR, max\_FSR**]

**SSR =** [**min\_SSR, max\_SSR**]

Before each experiment is performed, the necessary data wrangling (e.g., cleaning, harmonization, aggregation and more) is performed on BigData to generate 2 sets of data:

1. data to set aside for validation [Xpred,Ypred]
2. remaining data to be sampled and analyzed by the CBDA-SL and Knockoff algorithms [Xtemp,Ytemp].

Here we refer to X-datasets as datasets of features, while Y-datasets are datasets of outcomes (binomial/multinomial or continuous/Gaussian). A temp workspace is saved to store these 4 datasets.

If BigData is within the order of GBs, alternative strategies can be implemented to avoid loading large datasets before launching the CBDA-SL and Knockoff algorithms. For example, we could generate all the M data subsets and save them in separate RData workspaces, and then load the appropriate ones for each of the M job.

For each j=1:M, we load the temp RData workspace and generate a Xtempj , Xpredj and a Ytempj by sampling Xtemp, Xpred and Ytemp, respectively. FSR and SSR specifications are used to generate kj and nj, which represent the subsets of features/columns and subjects/rows, respectively. kj and nj are then used to generate the matrices Xtempj , Xpredj and a Ytempj to be passed to the Knockoff Filter and CBDA-SL algorithms.

Xtempj and Xpredj are then imputed and normalized. Imputation and normalization can also be done on the BigData, before sampling is performed. A trade-off in computation time can be investigated; however it should be significant only when the original dataset is very large and the FSR/SSR are not small. If FSR/SSR are very small (~5%), an inline/real-time imputation might be more efficient. For imputation we use the function missForest, with max # of iterations ~5-10 for convergence.

**Pseudocode (sort of) of the CBDA-SL algorithm as implemented in the LONI pipeline workflow**

For (row i=1: i\_exp) [# experiments 5-50]

{

for (j=1:M, M~5K-50K) [M is j\_global in the workflow]

{

Knockoff.filter (j)(Xj,Yj,…)

SuperLearner (j)( Xj,Yj,…)

Save results in RData workspaces […….light\_j.RData]

}

}

SuperLearner (j)

{

1. Combines many learners/optimization algorithms [10-30 different algorithms]
2. Performs Cross Validation for each one (~ 10 CV folds)
3. Generate predictions

}

Knockoff.filter(j)

{

1. Combines many learners/optimization algorithms [10-30 different algorithms]

}

{

Returns features selected after passing matrix Xj and outcome Yj

}

The workflow is now parallelized; each j is an independent job. Multiple experiments can be combined in a single pipeline workflow. However we are constrained by the total number of jobs that can be submitted in a single workflow on Cranium (3K).

The latest version of the pipeline workflow combines 3 modules of 3K jobs each for each experiment, for a total of 9K jobs for each experiment.

**Post Optimization process**

**1st Step – Workspaces consolidation**

For (i=1: i\_exp) [# experiments 5-50]

{

for (j=1:M)

{

Load …..Light\_j.RData

}

Save the combine workspace as Exp\_i.RData

}

**2nd Step – MSE Ranking and Feature Mining**

Feature Mining can be performed in 3 ways:

1. By single experiment
2. Combining all the experiments
3. Combining subsets of experiments

The following points are the same across 1, 2 and 3 above for the SuperLearner predictions.

* 1. Calculate Mean Square Error between data to be predicted and the CBDA-SL predictions – MSE\_j
  2. Select the TOP MSEs (TOP=~10-50)
  3. Extract the features kj used for each of the TOP MSEs and build an histogram
  4. Merge all the 9000 features selected by each knockoff.filter(j) and build an histogram
  5. Spikes in the histograms will indicate the features that are most common among the best predictions 🡪 Feature Mining

We are testing the CBDA-Sl and the Knockoff filter on ad hoc datasets to determine their FDRs and LOD (level of detection) of TP (true positive) features. We are still working on determining the rate of convergence of the algorithms under different specs (primarily the # of jobs needed). Preliminary analyses of the results suggest 2-3K as an optimal size for M; however that can be dataset-dependent.

Each job is ~2-10 minutes. If we use the CV.SuperLearner function ~20-100 minutes (still within the limits of XSEDE-OSG – Condor pool optimal scenario, which is 1-2 hrs per job)