

Documentation

Files Directory Tree:

```

./MSSP/src/main
├── MainModule
│   ├── MainBayesianModel
│   │   ├── MainPamDeltaStanLasso.R
│   │   ├── MainPamPercentStanLasso.R
│   │   └── MainRespirationStanLasso.R
│   ├── MainCoefPlot
│   │   ├── MainPamCoefPlot.R
│   │   └── MainRespirationCoefPlot.R
│   ├── MainDataProcess
│   │   ├── MainPamDataProcess.R
│   │   └── MainRespirationDataProcess.R
│   ├── MainMSEVisualization
│   │   └── MainMSEViolinPlot.R
│   ├── MainModelEvaluation
│   │   ├── MainPamDeltaResidualAnalysis.R
│   │   ├── MainPamMCMCDiagnostics.R
│   │   ├── MainPamPercChangeResidualAnalysis.R
│   │   ├── MainRespMCMCDiagnostics.R
│   │   ├── MainRespModelCheck.R
│   │   └── MainRespirationResidualAnalysis.R
│   ├── MainModelSelection
│   │   ├── MainPamDeltaModelSelect.R
│   │   ├── MainPamPercentModelSelect.R
│   │   └── MainRespModelSelect.R
│   └── MainRefitModel
│       ├── MainRefitPamDeltaModel.R
│       ├── MainRefitPamPercentChangeModel.R
│       └── MainRefitRespirationModel.R
├── Visualization
│   ├── Coef-Plot.R
│   └── MSE_violin_plot.R
├── model-evaluation
│   ├── MCMC-Diagnostics.R
│   ├── ModelSelect.r
│   └── ResidualEvaluation.R
├── modeling
│   ├── KFold-CV.R
│   ├── Refit-RStan-Lasso.R
│   └── Rstan-MixEff-Lasso.R
└── prelimEDA
    └── CoralsPamEDA.R

```

Files starts with **Main** are those we are going to execute. Required functions are written in external files located in different folders based on the tasks. The **Main** R scripts will import those functions, and

complete the tasks.

Main Module:

1. **MainDataProcess**: Files in **MainDataProcess** are used to manipulate the dataset, extract columns which will be used in the future analysis, and export the cleaned data.
2. **MainBayesianModel**: Files in **MainBayesianModel** construct the mixed effect regression with Laplace distribution applied, and also using cross validation to output the MSE for each **lambda** (parameter of Laplace dist.) and each fold.
3. **MainModelSelection**: Files in **MainModelSelection** are used to export the information of cross validation result to external markdown files.
4. **MainMSEVisualization**: Files in **MainMSEVisualization** are used to visualize the MSE result from cross validation as violin plots.
5. **MainRefitModel**: Files in **MainRefitModel** are used to refit the mixed effect linear regression after we obtain the **lambda** with the **lowest MSE** from the output of files in **MainBayesModel**.
6. **MainCoefPlot**: Files in **MainCoefPlot** are used to visualize the **posterior mean** and the **95% quantile interval** of the estimation from the mixed effect linear regression estimated in Bayesian approach.
7. **MainModelEvaluation**:
 - **ResidualAnalysis**: Files with **ResidualAnalysis** suffix mean to check the residuals pattern of the model.
 - **MCMCDiagnostics**: Files with **MCMCDiagnostics** suffix mean to diagnose the MCMC sampling, checking if the sampling converge or not.
 - **ModelCheck**: Files with **ModelCheck** suffix mean to compare the result between our estimation and the results from a frequentist approach. If both of them are close enough, then we can state that our estimation is valid.

Usage example:

Take **Respiration Rate** as an example:

Steps:

1. **MainRespirationDataProcess.R**
2. **MainRespirationStanLasso.R**
3. **MainRespModelSelect.R**
4. **MainMSEViolinPlot.R**
5. **MainRefitRespirationModel.R**
6. **MainRespModelCheck.R**
7. **MainRespirationCoefPlot.R**
8. **MainRespirationResidualAnalysis.R**
9. **MainRespMCMCDiagnostics.R**