Microbial Counts Trajectories Infinite Mixture Model Engine (MC-TIMME)
Software for analyzing time-series of microbial counts
Version 1.00
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Source code files included in this release are listed below. MC-TIMME was developed and tested in Matlab^{TM} R2011b (The MathWorks, Natick, MA), and requires the Matlab^{TM} Statistics, Optimization, and Bioinformatics Toolboxes. The free Lightspeed Matlab^{TM} Toolbox by Tom Minka is also required, available at:
<http://research.microsoft.com/en-us/um/people/minka/software/lightspeed/>

See the file `tutorial.pdf` for detailed instructions on how to run MC-TIMME.

Main functions:

```
filterData.m                    - filter refOTUs w/ too few counts
estimateHyperParameters.m       - estimate hyperparameters from data
MCTIMME.m                       - main routine to perform MCMC inference
signatureDiversityScores.m      - compute SD scores from MCMC samples
individualOTUSignatures.m       - individual refOTU signatures from MCMC samples
plotIndividualOTUSignature.m    - plot an individual signature
plotRelaxationTimeDistribution.m - plot Relaxation Time Distribution (RTD)
consensusSignatureGroups.m      - compute CSGs from MCMC samples
generateConsensusSignatures.m   - compute consensus signatures from MCMC samples
plotConsensusSignature.m        - plot a consensus signature
outputCSGInfo.m                 - output files w/ summaries of CSGs
experimentalDesignMatrices.m    - generate information matrices for exp. design
experimentalDesign.m            - generate optimal experimental design
```

Helper functions:

```
loadDethlefsenData.m              - load data from Dethlefsen et al. PNAS 2010
readTimeIntervalFile.m            - read user specified rx/non-rx intervals
expDecayCurve.m                   - exponential decay function for est. hyperparameters
designMatrix.m                    - design matrix for GLM calculations
transformData.m                   - data x-formation for GLM calculations
CSGQualityMeasures.m              - Normalized Mutual Information & Rand Index
findRefOTUsByTaxonomicLabel.m     - get list of refOTUs for given taxonomic label
separateIntervals.m               - separate time intervals into rx/non-rx
```

Object definitions:

```
hyperParameters.m                 - all hyperparameters needed by MC-TIMME
refOTUObject.m                    - reference Operational Taxonomic Units
credibleInterval.m                - credible interval
signatureObject.m                 - signature (both individual & CSGs)
timeIntervalObject.m              - treatment or non-treatment time interval
```