Gamma Mixture Modelling System Requirements:

MATLAB (2018b - v9.5)

Statistics and Machine Learning Toolbox (v11.4)

*Previous versions from 2016a onward have been tested

Installation:

Place the full package into a single directory, and open this directory in MATLAB.

Demo:

Load data (Msh2_Sample or WT_Sample) into a MATLAB variable named 'x'. The gamma mixture-model (MixModel.m) can then be ran (from the current directory) on the sample with the following syntax:

[alpha,beta,weight] = MixModel(x,2,500,0,'kmeans')

This will instantly return the variables:

alpha - estimates for both $\gamma(\alpha)$ values beta - estimates for both $\gamma(\beta)$ values weight - the contribution of each sub-distribution to the overall model (e.g. 0.45 = 45%)

Expected Results:

WT

alpha = [3.1437, 1.0991] beta = [59118, 61354] weight [0.6292, 0.3705] i.e. class I = 62.92%, class II = 37.05%

Msh2

alpha = [3.6782, 0.9058] beta = [31661, 42076] weight [0.8480, 0.1518]

RecombineSim System Requirements:

MATLAB (2018b - v9.5)

Statistics and Machine Learning Toolbox (v11.4)

Signal Processing Toolbox (v8.1)

*Previous versions from 2016a onward have been tested

Installation:

Place the full package into a single directory, and open this directory in MATLAB.

Demo:

Sample event table contains 4 WT (TW), 4 ndt80AR (TN) and 4 $msh2\Delta$ (OM) tetrads, at the 1500bp merging threshold. The following instructions are run in express mode (crossovers only) to reduce runtime.

Syntax:

RecombineSim(eventfile, varfile, output_folder, genotype, threshold, samples, mode, classIlperc, express, alpha, beta)

eventfile: SampleEventTable.txt varfile: VariantTable_SK1.txt

output_folder: a directory or folder name

genotype: 'OM', 'TN' or 'TW'

threshold: 1500

samples: number of cells to simulate

mode: 'Random', 'Hazard' or 'MixModel' (see below)

class/liperc: the % of COs that will form independently of interference

express: 'Y'

alpha: the interfering $\gamma(\alpha)$ values for mixed model simulations beta: the interfering $\gamma(\beta)$ values for mixed model simulations

To run a random simulation (1000 cells, Runtime = ~5-10 minutes):

RecombineSim('SampleEventTable.txt','VariantTable_SK1.txt','Results','OM',1500,1000,'Random',0,'Y')

'OM' can be replaced with 'TN' or 'TW' (as defined above) to simulate a different genotype.

To run an interfering, single (y)-model simulation:

RecombineSim('SampleEventTable.txt','VariantTable_SK1.txt','Results','OM',1500,1000,'Hazard',0,'Y')

To run an interfering, mixed (y)-model simulation:

 $Recombine Sim (`Sample Event Table.txt', 'Variant Table_SK1.txt', 'Results', 'OM', 1500, 1000, 'MixModel', 15, 'Y', [3.53.53, 5], [375003750037500])$

Where:

Class II % = 15 Interfering $\gamma(\alpha) = 3.5$ Interfering $\gamma(\beta) = 37500$

Output Folders:

Event Counts:

1. Event counts for each individual tetrad (e.g. OM-1500bp-EventCount.txt)

Experimental:

- 1. Experimental inter-event distances (IEDs) for each individual tetrad (e.g. OM-1500bp-ExpIED.txt)
- 2. Combined IED datasets (e.g. OM-1500bp-AggregateExpIED.txt) the main dataset used in the manuscript
- 3. Best-fit (γ) -parameters for the experimental data (e.g. OM-1500bp-GammaFit.txt).

Simulations:

- 1. Simulated IED datasets for each individual tetrad (e.g. OM-Random-1500bp-PopAvg.txt)
- 2. Combined simulated IED datasets (e.g. OM-Random-1500bp-AggregateSim.txt) the main dataset used in the manuscript
- 3. Duplication of the above files without event merging (Raw).