

high-dimension-sircovid-MRes/src/vaccine_delay_fits_gradient_transform/orderly.yml

Brief:

Running Hamiltonian Monte Carlo and generate a set of outputs on different values of epsilon. The samples generated from each epsilon will be stored separately as a csv files in outputs folder.

Parameters:

region: Same as the vaccine_delay_fits/orderly.yml.
deterministic: Same as the vaccine_delay_fits/orderly.yml.
short_run: Same as the vaccine_delay_fits/orderly.yml.
method: The type of finite difference method. 'f1' = forward first order, 'b1' = backward first order, 'c1' = central first order, 'f2' = forward second order, 'b2' = backward second order, 'c2' = central second order. Default is 'f1'.
N: number of HMC samples.
start: The starting value of epsilon.
step: The change of epsilon.
ne: Number of different epsilons.
L: Hyper-parameter L in leapfrog integration.
scale: The scaling parameters that used in transformation from parameter space to R^n space.

high-dimension-sircovid-MRes/src/vaccine_delay_fits_gradient_transform/support.R

HMC_parallel:

Parameters:

RnPosterior: The log posterior distribution pdf in R^n space, which also refers to the potential energy function in HMC.
gradient_LP_parallel: Gradient of log posterior distribution.
epsilon: epsilon, hyper-parameter in leapfrog integration.
L: L, hyper-parameter in leapfrog integration.
current_q: current value of q.
filter: filter
filter2: filter for parallel computing
pars: pars variable.
M: Mass Matrix
invM: inver of Mass matrix
method: The type of finite difference method. 'f1' = forward first order, 'b1' = backward first order, 'c1' = central first order, 'f2' = forward second order, 'b2' = backward second order, 'c2' = central second order. Default is 'f1'.