# Parameters

|  |  |  |
| --- | --- | --- |
| **Parameter** | **Default Value** | **Explanation** |
| data |  | n by p matrix of microbiome count data, either quantitative or compositional counts. Each row represents each subject/sample and each column represents each OTU (operational taxonomic unit). |
| quantitative | False | Default is FALSE, which means input "data" is compositional data, which will be normalized using mclr transformation within a function. If TRUE, it means "quantitative" counts are input and no normalization will be applied. |
| method | ‘mb’ | graph estimation methods. Currently, only "mb" method is available. |
| lambda.min.ratio | 0.01 | (Can be seen in SPIEC-EASI) |
| nlambda | 20 | (Can be seen in SPIEC-EASI) |
| lambdaseq | The default sequence has 20 values generated to be equally spaced on a logarithmic scale from 0.6 to 0.006 | A sequence of decreasing positive numbers to control the regularization. Users can specify a sequence to override the default sequence. If user specify as "data-specific", then the lambda sequence will be generated using estimated rank-based correlation matrix from data |
| seed |  | The seed for subsampling |
| ncores | 1 | number of cores to use for subsampling. |
| thresh | 0.1 | threshold for StARS selection criterion. The smaller threshold returns sparser graph. |
| subsample.ratio. | 0.8 | The recommended values are 10\*sqrt(n)/n for n > 144 or 0.8 otherwise. |
| rep.num | 20 | the repetition number of subsampling for StARS eddge stability selection. |
| Rtol | 1e-6 | Desired accuracy when calculating the solution of bridge function in estimateR function. |
| Rmethod |  | The calculation method of latent correlation. Either "original" method or "approx". |

# Explanation