

# Package: SBmedian (via r-universe)

September 5, 2024

**Type** Package

**Title** Scalable Bayes with Median of Subset Posteriors

**Version** 0.1.1

**Description** Median-of-means is a generic yet powerful framework for scalable and robust estimation. A framework for Bayesian analysis is called M-posterior, which estimates a median of subset posterior measures. For general exposition to the topic, see the paper by Minsker (2015) <[doi:10.3150/14-BEJ645](https://doi.org/10.3150/14-BEJ645)>.

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**Encoding** UTF-8

**Imports** Rcpp, Rdpack, expm, stats, utils

**LinkingTo** Rcpp, RcppArmadillo

**RoxygenNote** 7.1.1

**RdMacros** Rdpack

**Repository** <https://kisungyou.r-universe.dev>

**RemoteUrl** <https://github.com/kisungyou/sbmedian>

**RemoteRef** HEAD

**RemoteSha** 8a932f5241344145eaaf5a9611fad15277213860

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mpost.euc*Median Posterior for Subset Posterior Samples in Euclidean Space*

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## Description

mpost.euc is a general framework to *merge* multiple empirical measures  $Q_1, Q_2, \dots, Q_M \subset R^p$  from independent subset of data by finding a median

$$\hat{Q} = \operatorname{argmin}_Q \sum_{m=1}^M d(Q, Q_m)$$

where  $\hat{Q}$  is a weighted combination and  $d(P_1, P_2)$  is distance in RKHS between two empirical measures  $P_1$  and  $P_2$ . As in the references, we use RBF kernel with bandwidth parameter  $\sigma$ .

## Usage

```
mpost.euc(
  splist,
  sigma = 0.1,
  maxiter = 121,
  abstol = 1e-06,
  show.progress = FALSE
)
```

## Arguments

<code>splist</code>	a list of length $M$ containing vectors or matrices of univariate or multivariate subset posterior samples respectively.
<code>sigma</code>	bandwidth parameter for RBF kernel.
<code>maxiter</code>	maximum number of iterations for Weiszfeld algorithm.
<code>abstol</code>	stopping criterion for Weiszfeld algorithm.
<code>show.progress</code>	a logical; TRUE to show iteration mark, FALSE otherwise.

## Value

a named list containing:

**med.atoms** a vector or matrix of all atoms aggregated.

**med.weights** a weight vector that sums to 1 corresponding to med.atoms.

**weiszfeld.weights** a weight for  $M$  subset posteriors.

**weiszfeld.history** updated parameter values. Each row is for iteration, while columns are weights corresponding to weiszfeld.weights.

## References

- Minsker S, Srivastava S, Lin L, Dunson DB (2014). “Scalable and Robust Bayesian Inference via the Median Posterior.” In *Proceedings of the 31st International Conference on International Conference on Machine Learning - Volume 32*, ICML’14, II–1656–II–1664. event-place: Beijing, China.
- Minsker S, Srivastava S, Lin L, Dunson DB (2017). “Robust and Scalable Bayes via a Median of Subset Posterior Measures.” *Journal of Machine Learning Research*, **18**(124), 1–40. <https://jmlr.org/papers/v18/16-655.html>.

## Examples

```
## Median Posterior from 2-D Gaussian Samples
# Step 1. let's build a list of atoms whose numbers differ
set.seed(8128) # for reproducible results
mydata = list()
mydata[[1]] = cbind(rnorm(96, mean= 1), rnorm(96, mean= 1))
mydata[[2]] = cbind(rnorm(78, mean=-1), rnorm(78, mean= 0))
mydata[[3]] = cbind(rnorm(65, mean=-1), rnorm(65, mean= 1))
mydata[[4]] = cbind(rnorm(77, mean= 2), rnorm(77, mean=-1))

# Step 2. Let's run the algorithm
myrun = mpost.euc(mydata, show.progress=TRUE)

# Step 3. Visualize
# 3-1. show subset posterior samples
opar <- par(no.readonly=TRUE)
par(mfrow=c(2,3), no.readonly=TRUE)
for (i in 1:4){
  plot(mydata[[i]], cex=0.5, col=(i+1), pch=19, xlab="", ylab="",
       main=paste("subset",i), xlim=c(-4,4), ylim=c(-3,3))
}

# 3-2. 250 median posterior samples via importance sampling
id250 = base::sample(1:nrow(myrun$med.atoms), 250, prob=myrun$med.weights, replace=TRUE)
sp250 = myrun$med.atoms[id250,]
plot(sp250, cex=0.5, pch=19, xlab="", ylab="",
      xlim=c(-4,4), ylim=c(-3,3), main="median samples")

# 3-3. convergence over iterations
matplot(myrun$weiszfeld.history, xlab="iteration", ylab="value",
        type="b", main="convergence of weights")
par(opar)
```

## Description

SPD manifold is a collection of matrices that are symmetric and positive-definite and it is well known that using Euclidean geometry for data on the manifold is rather inaccurate. Here, we propose a function for dealing with SPD matrices specifically where valid examples include full-rank covariance and precision matrices. Note that  $N_M = \sum_{m=1}^M n_m$ .

## Usage

```
mpost.spd(
  splist,
  sigma = 0.1,
  maxiter = 121,
  abstol = 1e-06,
  show.progress = FALSE
)
```

## Arguments

splist	a list of length $M$ containing $(p \times p)$ matrix or 3d array of size $(p \times p \times n_m)$ whose slices are SPD matrices from subset posterior samples respectively.
sigma	bandwidth parameter for RBF kernel.
maxiter	maximum number of iterations for Weiszfeld algorithm.
abstol	stopping criterion for Weiszfeld algorithm.
show.progress	a logical; TRUE to show iteration mark, FALSE otherwise.

## Value

a named list containing:

- med.atoms** a  $(p \times p \times N_M)$  3d array whose slices are atoms aggregated.
- med.weights** a weight vector that sums to 1 corresponding to med.atoms.
- weiszfeld.weights** a weight for  $M$  subset posteriors.
- weiszfeld.history** updated parameter values. Each row is for iteration, while columns are weights corresponding to weiszfeld.weights.

## Examples

```
## Median Posterior from 5-dimension Wishart distribution
## Visualization will be performed for distribution of largest eigenvalue
## where RED is for estimated density and BLUE is density from all samples.

# Step 1. let's build a list of atoms whose numbers differ
set.seed(8128) # for reproducible results
mydata = list()
mydata[[1]] = stats::rWishart(96, df=10, Sigma=diag(5))
mydata[[2]] = stats::rWishart(78, df=10, Sigma=diag(5))
mydata[[3]] = stats::rWishart(65, df=10, Sigma=diag(5))
mydata[[4]] = stats::rWishart(77, df=10, Sigma=diag(5))
```

```

# Step 2. Let's run the algorithm
myrun = mpost.spd(mydata, show.progress=TRUE)

# Step 3. Compute largest eigenvalues for the samples
eig4 = list()
for (i in 1:4){
  spdmats = mydata[[i]]      # SPD atoms
  spdsizes = dim(spdmat)[3]   # number of atoms
  eigvals = rep(0,spdsizes)    # compute largest eigenvalues
  for (j in 1:spdsizes){
    eigvals[j] = max(base::eigen(spdmat[, , j])$values)
  }
  eig4[[i]] = eigvals
}
eigA = unlist(eig4)
eiglim = c(min(eigA), max(eigA))

# Step 4. Visualize
# 4-1. show distribution of subset posterior samples' eigenvalues
opar <- par(no.readonly=TRUE)
par(mfrow=c(2,3))
for (i in 1:4){
  hist(eig4[[i]], main=paste("subset", i), xlab="largest eigenvalues",
    prob=TRUE, xlim=eiglim, ylim=c(0,0.1))
  lines(stats::density(eig4[[i]]), lwd=1, col="red")
  lines(stats::density(eigA), lwd=1, col="blue")
}

# 4-2. 250 median posterior samples via importance sampling
id250 = base::sample(1:length(eigA), 250, prob=myrun$med.weights, replace=TRUE)
sp250 = eigA[id250]
hist(sp250, main="median samples", xlab="largest eigenvalues",
  prob=TRUE, xlim=eiglim, ylim=c(0,0.1))
lines(stats::density(sp250), lwd=1, col="red")
lines(stats::density(eigA), lwd=1, col="blue")

# 4-3. convergence over iterations
matplot(myrun$weiszfeld.history, xlab="iteration", ylab="value",
  type="b", main="convergence of weights")
par(opar)

```

## Description

Median-of-means is a generic yet powerful framework for scalable and robust estimation. A framework for Bayesian analysis is called M-posterior, which estimates a median of subset posterior measures.

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