Tutorials for the R package mdw

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January 18, 2018

This tutorial illustrates the use of *mdw*. There are three methods for estimating maximum diversity weights. The tree weight method was based on the idea of Gerstein et al. (1994) and was used for constructing immune response scores in Haynes et al. (2012). The maximum entropy weight and the maximum variable weight are described in He and Fong (2018). These three methods are aimed at achieving the same goal, and the following examples compare them numerically.

The first example has three independent variables.

```
require(MASS)
X = mvrnorm(n = 100, mu=rep(0,3), Sigma=diag(3))


# tree.weight
w.tree=tree.weight(cor(X))
# maximum variance weight
w.var=var.weight(X)
# maximum entropy weight
w.ent.1=entropy.weight(X, h=1)
w.ent.2=entropy.weight(X, h=0.1)


cbind(w.tree, w.var, w.ent.1, w.ent.2)
```

Ideally we like to see equal weights, and here are what we get:

	w.tree	w.var	w.ent.1	w.ent.2
1	0.331	0.359	0.352	0.338
2	0.331	0.345	0.344	0.333
3	0.338	0.296	0.304	0.329

Table 1: Example 1

The second example has three variables and two of them are highly correlated, while the third is very weakly correlated with the first two.

```
cor.mat=diag(rep(1,3))
cor.mat[1,2]<-cor.mat[2,1]<-0.9
cor.mat[1,3]<-cor.mat[3,1]<-0.1
cor.mat[2,3]<-cor.mat[3,2]<-0.1
require(MASS); set.seed(1)
X = mvrnorm(n = 100, mu=rep(0,3), Sigma=cor.mat)

# tree.weight
w.tree=tree.weight(cor(X))
# maximum variance weight
w.var=var.weight(X)
# maximum entropy weight
w.ent.1=entropy.weight(X, h=1)
w.ent.2=entropy.weight(X, h=0.1)

cbind(w.tree, w.var, w.ent.1, w.ent.2)
```

The results are shown in Table 2.

	w.tree	w.var	w.ent.1	w.ent.2
1	0.267	0.298	0.295	0.306
2	0.267	0.219	0.230	0.314
3	0.467	0.483	0.475	0.380

Table 2: Example 2.

References

Gerstein, M., Sonnhammer, E.L. and Chothia, C. (1994), "Volume changes in protein evolution," *Journal of Molecular Biology*, 236, 1067–1078.

Haynes, B.F., Gilbert, P.B., McElrath, M.J., Zolla-Pazner, S., Tomaras, G.D., Alam, S.M. et al (2012), "Immune-correlates analysis of an HIV-1 vaccine efficacy trial," *New England Journal of Medicine*, 366, 1275–1286.

He, Z. and Fong, Y. (2018), "Maximum Diversity Weighting for Biomarkers with Application in HIV-1 Vaccine Studies," under review.