

disp2D: R package for 2D Hausdorff and simplex dispersion orderings

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Abstract

This document contains a description of the R package *disp2D* which is an implementation of the Hausdorff and simplex dispersion orderings in the 2D case. A complete description of the procedures implemented in this package can be found in Ayala et al. [2012]. Additional material related with the stochastic orderings considered here appears in López-Díaz [2006].

1 The introduction

First, we load the packages needed later. The package Barber et al. [2012] is required and the package Genz et al. [2012] is used in order to simulate data.

```
> library(disp2D)
> library(geometry)
> library(mvtnorm)
```

In order to illustrate the use of the package, we will use data generated with multivariate normal distribution.

Let us consider the \mathbb{R}^d -valued random vectors \mathbf{X} and \mathbf{Y} with normal distributions, $\mathbf{X} \sim_{st} N(\mu_{\mathbf{X}}, \Sigma_{\mathbf{X}})$ and $\mathbf{Y} \sim_{st} N(\mu_{\mathbf{Y}}, \Sigma_{\mathbf{Y}})$, where $\Sigma_{\mathbf{X}} = AA^t$,

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$A \in M_{d \times d}$ being a matrix whose values are randomly chosen with uniform distribution in the interval $(0, 1)$, the super index t denoting the transpose matrix, and $\Sigma_Y = \Sigma_X + \lambda I_d$, with $\lambda \geq 0$. It is well-known that the eigenvalues of Σ_Y are those of Σ_X plus the value λ . Therefore, it holds that $\mathbf{X} \preceq_{sx} \mathbf{Y}$. Roughly speaking, larger values of λ will produce larger dispersion for the random vector \mathbf{Y} . In keeping with this framework, the following test is proposed

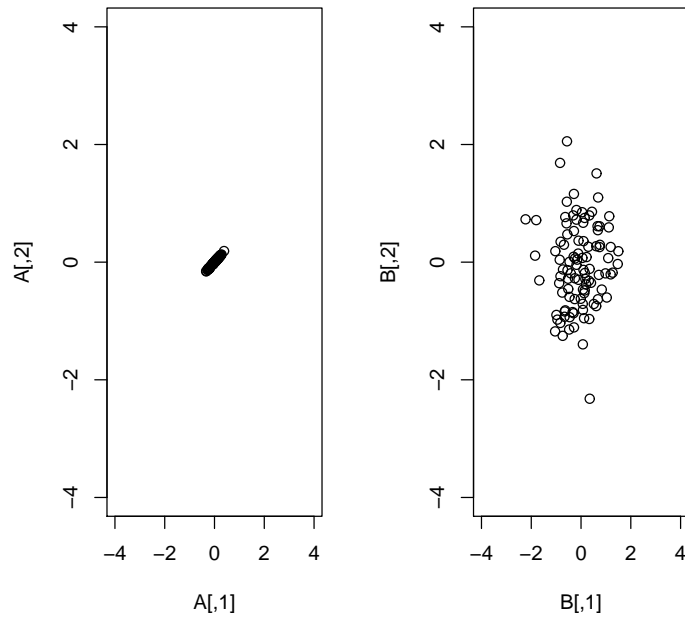
$$H_0 : \mathbf{X} \preceq_{sx} \mathbf{Y} \text{ against } H_1 : \mathbf{X} \not\preceq_{sx} \mathbf{Y}.$$

Let us generate two point sets from the model just considered. The multivariate normal data are generated using the package *mvtnorm* Genz et al. [2012], Genz and Bretz [2009].

```
> d = 2
> n = 100
> mu1 = rep(0,d)
> mu2 = mu1
> lambda = .5
> n1=n2=n= 100
> sigma1 = matrix(runif(d*d),nrow=d,ncol=d)
> sigma1 = t(sigma1) %*% sigma1
> sigma2 = sigma1 + lambda * diag(1,d)
> A = rmvnorm(n1,mean=mu1,sigma=sigma1)
> B = rmvnorm(n2,mean=mu2,sigma=sigma2)
```

Let us see the datasets

```
> par(mfrow=c(1,2))
> plot(A,xlim=c(-4,4),ylim=c(-4,4))
> plot(B,xlim=c(-4,4),ylim=c(-4,4))
> par(mfrow=c(1,1))
```



2 Exact algorithm for the 2D Hausdorff dispersion ordering

The exact version of the Hausdorff dispersion ordering can be evaluated using the following code.

```
> r = .1
> prob = rep(1/n,n)
> HA = exactHausdorff(A,prob,r)
> HB = exactHausdorff(B,prob,r)
```

The following plot displays the two cumulative distribution functions.

```
> plot(ecdf(HA$distance))
> lines(ecdf(HB$distance),lty=2)
```

Finally, we can test the usual stochastic ordering for the empirical distribution of the just evaluated distances by using the Kolmogorov-Smirnov test.

```
> ks.test(HA$distance,HB$distance,alternative="greater")
```

Two-sample Kolmogorov-Smirnov test

```
data: HA$distance and HB$distance
D+ = 0.9226, p-value < 2.2e-16
alternative hypothesis: the CDF of x lies above that of y
```

Other possibilities could be the Wilcoxon test for paired samples.

3 Simplex dispersion ordering

A detailed explanation of this algorithm can be found in Ayala et al. [2012].

If $A = \{\mathbf{x}_1, \dots, \mathbf{x}_{n_1}\}$ and $B = \{\mathbf{y}_1, \dots, \mathbf{y}_{n_2}\}$, let $\{i_1, \dots, i_{d+1}, i_{d+2}, \dots, i_{2(d+1)}\}$ be a sample without replacement from $\{1, \dots, n_1\}$, and $U = d_H(\text{co}(\mathbf{x}_{i_1}, \dots, \mathbf{x}_{i_{d+1}}), \text{co}(\mathbf{x}_{i_{d+2}}, \dots, \mathbf{x}_{i_{2(d+1)}}))$. Therefore, s_1 independent extractions from the set $\{1, \dots, n_1\}$ will produce a

random sample of the corresponding bootstrap distribution u_1, \dots, u_{s_1} . Replacing \mathbf{x} by \mathbf{y} , we obtain v_1, \dots, v_{s_2} , a random sample of the bootstrap distribution associated to the vector \mathbf{y} . Now, these values can be used for the proposed tests.

The function *simplex* provides us a sample of u 's.

```
> d1 = simplex(A,bootstrap=TRUE,nresamples=100)
```

If we consider two different samples we can test the simplex dispersion ordering using

```
> dhx = simplex(A,bootstrap=TRUE,nresamples=10)
> dhy = simplex(B,bootstrap=TRUE,nresamples=10)
> ks.test(dhx,dhy,alternative="greater")
```

Two-sample Kolmogorov-Smirnov test

```
data: dhx and dhy
D^+ = 1, p-value = 4.54e-05
alternative hypothesis: the CDF of x lies above that of y

> ks.test(dhx,dhy,alternative="less")
```

Two-sample Kolmogorov-Smirnov test

```
data: dhx and dhy
D^- = 0, p-value = 1
alternative hypothesis: the CDF of x lies below that of y
```

References

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