Appendix

#description: R script to implement nonparametric estimation of spatial segregation in a multivariate point process for Crossland et al. Task specific preferred retinal loci in macular disease
#
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#acknowledgements: Barry Rowlingson, Lancaster University.
#
#uses packages splancs and spatialkernel
#
#
#comment: read in data for two control subjects (NB and TR)
#comment: read in data for two patients (M5 and M8)
#comment: assumes .csv files (supplementary files) have been copied to C:/ on local computer
#comment: only one example is given here to read in the two files for NB
#comment: this would have to be repeated for TR, M5 and M8
#
#data01<-read.table("c:NBf.csv",header=FALSE,sep="","
#data01<-cbind(data01[,1],-data01[,2])
data01<-cbind(data01,c(rep(1,length(data01)/2)))
data02<-read.table("c:NBr.csv",header=FALSE,sep="",")
data02<-cbind(data02[,1],-data02[,2])
data02<-cbind(data02,c(rep(2,length(data02)/2)))
NB<-rbind(data01,data02)
#
#comment: load required packages
#
library(spatialkernel)
library(splancs)
#
#comment: add Gaussian noise (N(0,2)) to each subjects’ measurements
#
TRnoise<-cbind(TR[,1]+rnorm(length(TR[,1]),0,2),TR[,2]+rnorm(length(TR[,1]),0,2),TR[,3])
NBnoise<-cbind(NB[,1]+rnorm(length(NB[,1]),0,2),NB[,2]+rnorm(length(NB[,1]),0,2),NB[,3])
M5noise<-cbind(M5[,1]+rnorm(length(M5[,1]),0,2),M5[,2]+rnorm(length(M5[,1]),0,2),M5[,3])
M8noise<-cbind(M8[,1]+rnorm(length(M8[,1]),0,2),M8[,2]+rnorm(length(M8[,1]),0,2),M8[,3])
#
#comment: plot measurements. BLACK: fixation task. RED: reading task
#comment: actual measured fixations in top row. Measurements with added noise in bottom row
#comment: segregation still very clear in data added with noise for patients
par(mfrow=c(2,4))
par(mar=c(1,1,1,1))
plot(TR,col=TR[,3],pch=16,asp=1,ylim=c(-24,-12),xlim=c(14,32),cex=0.5)
text(20,-27,"TR",cex=2)
plot(NB,col=NB[,3],pch=16,asp=1,ylim=c(-24,-12),xlim=c(14,32),cex=0.5)
text(20,-27,"NB",cex=2)
plot(M5,col=M5[,3],pch=16,asp=1,ylim=c(-24,-12),xlim=c(14,32),cex=0.5)
text(20,-27,"M5",cex=2)
plot(M8,col=M8[,3],pch=16,asp=1,ylim=c(-24,-12),xlim=c(14,32),cex=0.5)
text(20,-27,"M8",cex=2)
plot(TRnoise,col=TR[,3],pch=16,asp=1,ylim=c(-24,-12),xlim=c(14,32),cex=0.5)
text(20,-27,"TRnoise",cex=2)
plot(NBnoise,col=NB[,3],pch=16,asp=1,ylim=c(-24,-12),xlim=c(14,32),cex=0.5)
text(20,-27,"NBnoise",cex=2)
plot(M5noise,col=M5noise[,3],pch=16,asp=1,ylim=c(-24,-12),xlim=c(14,32),cex=0.5)
text(20,-27,"M5noise",cex=2)
plot(M8noise,col=M8noise[,3],pch=16,asp=1,ylim=c(-24,-12),xlim=c(14,32),cex=0.5)
text(20,-27,"M8noise",cex=2)

# comment: compute the bounding boxes for segregation analysis

polyTR=bboxx(bbox(TRnoise))
polyNB=bboxx(bbox(NBnoise))
polyM5=bboxx(bbox(M5noise))
polyM8=bboxx(bbox(M8noise))

# comment: example of cross-validation test for optimising kernel smoothing bandwidth:
# comment: for one control only (NB) (only shown as an example)
# segTR = spseg(NBnoise[,1:2],NBnoise[,3],opt=1,h=seq(0.1,2,len=20), poly=poly1)
# comment: plot the cv curves with bandwidth:
# plotcv(segNB)
# comment: this suggest h=1 (same for other subjects)

# comment: the monte-carlo test for segregation from spatialkernel
# comment: ntest is the number of resamples
# comment: ntest is set at 20 for illustration.
# comment: ntest=1000 for results in paper, but computation time is long
# comment: p-values will vary because of rnorm values added
# comment: in all cases M5 & M8 return highly significant p-values against the H0 of no segregation
# comment: in all cases TR and NB are not significant

segmcTR =
spseg(TRnoise[,1:2],as.character(TRnoise[,3]),ntest=20,opt=3,h=1, poly=polyTR)
segmcNB =
spseg(NBnoise[,1:2],as.character(NBnoise[,3]),ntest=20,opt=3,h=1, poly=polyNB)
segmcM5 =
spseg(M5noise[,1:2],as.character(M5noise[,3]),ntest=20,opt=3,h=1,
poly=polyM5)
segmcM8 =
spseg(M8noise[,1:2],as.character(M8noise[,3]),ntest=20,opt=3,h=1,
poly=polyM8)
#
#comment: segregation plots (not really required) and only shown for
#TR for illustration
#
#plotmc(segmcTR)
#
#comment: p-values against null hypothesis of no segregation
#comment: these are estimated from ntest=20; the results reported in
#the paper are on ntest=1000
segmcTR$pvalue
segmcNB$pvalue
segmcM5$pvalue
segmcM8$pvalue
#
#end

The generated plot