

Appendix S4: User Code Documentation

This appendix provided details of the R functions provided for practitioners to use on their own data. Five tutorial examples are provided to demonstrate how to implement the code.

INSTALLATION INSTRUCTIONS

Download and unzip the file BlockBootCode. Open R. At the command line, run:
`source("<<file pathname>>\ LoadFunctions.R")`, inserting the path name to the BlockBootCode folder. The CRAN packages dplyr and geoR are required (for variogram fitting).
The R markdown files to run the examples are also provided in the zip file (e.g. Example1.Rmd).
These can be run by opening with RStudio and clicking Knit to Html.

FUNCTIONS PROVIDED

BlockBootApply and **BlockBootID** are two functions to implement the block bootstrap and perform block size selection according the emprirical MSE method ([Lahiri and Zhu, 2006](#)).

select_b_length_off_variogram returns the practical range of a variogram.

CombineBatchesofBootstraps combines **BlockBootApply** objects that may have been submitted in parallel to a cluster computer.

Usage

BlockBootID (x, y, block_Ls, NBoot = 500, Grid_space = NA, shape = "disc", sampling_type = "area")

BlockBootApply (x, y, block_Ls, Stat.function, dat, NBoot = 500, Grid_space = NA, type = "SE")

21 `method.block.length.select = NA, lookuptables.folderpath = NA, subregion_n_x = 3,`
 22 `subregion_n_y = 3, shape = "disc", sampling_type = "area", long_format_required = FALSE, ...)`
 23 **`select_b_length_off_variogram_envelope`** (`x,y, resids, breaks, ini, max.dist, plot = TRUE,...`)
 24 **`CombineBatchsofBootstraps`** (`list_of_boot_batches`)

25 *Arguments to BlockBootID and BlockBootApply*

26 **`x`** vector of the x co-ordinates of sites (in Cartesian co-ords like UTM)
 27 **`y`** vector of the y co-ordinates of sites (in Cartesian co-ords like UTM)
 28 **`block_Ls`** vector of block size parameters to run block bootstrap with. For BlockBootID, only
 29 one block size may be entered.
 30 **`dat`** A dataframe, argument to Stat.function. Each row should be a site.
 31 **`NBoot`** The number of bootstrap replicates to run. Defaults to 500. It is recommended to use a
 32 small NBoot first to test run code.
 33 **`Grid_space`** The space between sampling points. The smaller the space, the more sampling
 34 points there will be available to sample (and the more overlapping blocks may be), but the
 35 longer the resampling algorithm will take. If left blank this is assigned to be 1/3 of the
 36 smallest block length.
 37 **`Stat.function`** Function for a statistic T. This should take a dataframe `dat` as an argument with
 38 sites as rows, and may take unlimited additional arguments. However all site level data
 39 should be contained in `dat` (as this will be resampled).
 40 **`type`** Either "SE" or "Pval". Whether to calculate a Standard error or p-value (one sided, upper
 41 tail) from the bootstrap distribution of the statistic. Raw bootstrap distribution values of the
 42 statistic T are also returned in case of other uses.
 43 **`method.block.length.select`** What method to use to select a block length. May take values
 44 "Lahiri" or NA. IF NA and `block_Ls` is of length 1 the result is given for that block length.

45 **lookuptables.folderpath** A folder pathname for saving “lookup tables”. Saving lookup tables
 46 (tables identifying sites with sampling points, based on the block length) can greatly speed
 47 up resampling time, if the same (x,y) data is going to be resampled multiple times, for
 48 example if submitting batches of resamples in parallel . If this argument is present, the
 49 function looks in the folder to see if a lookup table (for those sites, with that block length)
 50 exists and if it does, uses that table. We recommend supplying this argument.

51 **m_x, m_y** Numbers giving how many subregions to divide the region into for the Lahiri block
 52 length selection method. The region will be divided in m_x horizontally and m_y vertically.
 53 Defaults to 3×3 .

54 **tuning_block_length** Index giving which block length to use as the tuning block length in the
 55 Lahiri block length selection method. E.g. if `tuning_block_length = 2`, the second element
 56 of `block_Ls` is used as tuning block length.

57 **shape** Either “disc”(default) or ”square”. The shape of the block.

58 **sampling_type** Either “area”(default) or “sites”. This gives the stopping criteria to the bootstrap
 59 resampling. i.e. Keep resampling blocks of sites, until the cumulative area of the blocks
 60 sampled is equal to the *area* of the observation region. Alternatively, keep resampling
 61 blocks of sites until the number of sites in the resample is equal to the number of sites in
 62 the observation region. We did check sensitivity of results to this criteria and did not find
 63 this to be an important distinction for our results, but used “area” throughout the results in
 64 this manuscript. However for some applications- e.g. to integrate the block bootstrap with
 65 other software using BlockBootID, the other software may require input as a matrix, in
 66 which case it is desirable to have all resamples contain the same number of sites.

67 **long_format_required** If `dat` (and hence resampled versions of `dat`) needs to be transformed to
 68 long format for a multispecies example, e.g. as in the 4th corner example in this paper, then
 69 set this to `TRUE`.

70 **(...)** Additional arguments to `Stat.function`

Arguments to select_b_length_off_variogram

- 71
- 72 **resids** vector of residuals for variogram
- 73 **breaks** Argument to geoR::variog
- 74 **ini, max.dist** Argument to geoR::variofit
- 75 (...) Additional arguments to variog and variofit

Arguments to CombineBatchesofBootstraps

- 76
- 77 **list_of_boot_batches** A list of **BlockBootApply** objects with the same arguments.

Description

- 78
- 79 **BlockBootID** calculates an ID matrix. The number of rows will be the number of bootstrap
 80 resamples. The number of columns will be the number of sites.
- 81 **BlockBootApply** does lots of stuff...
- 82 **select_b_length_off_variogram_envelope** selects a block length based on a variogram of the
 83 residuals supplied. It first fits an empirical variogram (using geoR::variog), then fits the practical
 84 range of that variogram (using geoR::variofit). It returns a block length equal to the practical
 85 range. This block length can then be used as an argument (to block_Ls or tuning block length) in
 86 BlockBootID or BlockBootApply. It is recommended to check variogram plots and check
 87 sensitivity to breaks, max.dist and ini. See geoR documentation.
- 88 If TestStatFunction takes a while to compute, then it is recommended to do some of the bootstrap
 89 resample computing in parallel. Instead of NBoot = 1000 for example, run 50 lots of NBoot = 20,
 90 submitted in parallel to a cluster computer. One way to estimate running time is to first running
 91 BlockBootApply with a small NBoot (e.g. 2), the time increases approximately proportional to
 92 NBoot. Things that decrease running time: changing (increasing) Grid_space (a very fine grid
 93 space means the lookup tables (which say which sites are within the block associated with those
 94 grid co-ordinates) will take a very long time to calculate); searching over fewer block lengths for

95 the optimal block length; decreasing NBoot; including a pathname to LookupTables so that you
 96 save the table associating sites and grid co-ordinates.

97 *Values of BlockBootApply*

98 **boot.reps.of.Stat.function** A list of length(block_Ls). Each list element contains the bootstrap
 99 distribution of Stat (so a list of length NBoot).

100 **Stat** The Statistic which is being bootstrapped

101 **Lahiri.block.size** If method.block.length.select = "Lahiri", the Lahiri chosen block length

102 **Empirical.MSE** If method.block.length.select = "Lahiri", a table of the Empirical MSE for each
 103 block length (rows). Columns indicate the tuning block length. So for a given tuning block
 104 length the row which contains the minimum value for that column is the block length which
 105 minimises the empirical MSE.

106 **SE.estimate** The Standard Error Estimate of the statistic

107 **sigma_stat_subregion** Vector of estimates of SE(T)- standard error of statistic T, for each block
 108 length in block_Ls, on each subregion

109 **n.in.subregions** The number of sites in each subregion. Singularities will occur if subregions
 110 have zero sites.

111 **sigma_stat_hat** Vector of estimates of SE(T)- standard error of statistic T, for each block length
 112 in block_Ls

113 **block_Ls** Argument supplied to function

114 **tuning_block_length** Argument supplied to function

115

116 **EXAMPLES**

117 These examples are to help users understand the mechanics of how to operate the functions on
 118 their own data.

119 **Example 1** Gets the standard error of a regression coefficient via block bootstrapping
120 (BlockBootApply), selecting the block size using the Lahiri method.

121 **Example 3** As in Example 2 except with block size selection via BlockBootApply, (Lahiri
122 method).

123 **Example 4** Gets the standard error of the AUC of a model via block bootstrapping
124 (BlockBootApply), selecting the block size using the Lahiri method.

125 **Example 5** Demonstrates the use of CombineBatchesofBootstraps. Runs Example 4, and
126 assembles results as if batches of bootstrap resamples have been submitted in parallel to a
127 cluster computer.

Example 1: Standard Error of a Coefficient

Setting Up

First load the data and R functions you need into the R workspace.

```
load("PlayData_for_Examples.RData") ### load the data for the examples
source("LoadFunctions.R") ##### Source the functions required to run the block bootstrap
```

Motivation

Imagine we want to know the standard error of our estimate for β - the coefficient of temperature. First fit the model.

```
set.seed(42)

fit1 = lm (response ~ temperature, data = dat)
summary(fit1)

##
## Call:
## lm(formula = response ~ temperature, data = dat)
##
## Residuals:
##      Min       1Q   Median       3Q      Max
## -3.5766 -0.9687  0.0120  0.9065  5.1925
##
## Coefficients:
##              Estimate Std. Error t value Pr(>|t|)
## (Intercept)  0.03474    0.06584   0.528   0.598
## temperature  1.14190    0.06975  16.372 <2e-16 ***
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
##
## Residual standard error: 1.455 on 498 degrees of freedom
## Multiple R-squared:  0.3499, Adjusted R-squared:  0.3486
## F-statistic: 268 on 1 and 498 DF,  p-value: < 2.2e-16
```

Getting Variogram Practical Range

Fit a variogram on the residuals- notice we can see spatial autocorrelation. Use the variogram practical range as a tuning parameter for the Lahiri method of block selection. Always check the variogram visually. Sometimes you may need to change max.dist, breaks or initial conditions to get a sensible practical range. It is hard to automate this process.

```
ini.vals <- expand.grid(seq(0,10,l=100), seq(0,1,l=100)) #inital values for variofit
variogram_block_length = select_b_length_off_variogram_envelope(x,y,resids = fit1$resid,
max.dist = 0.4, breaks=c(0,0.025,0.05,0.075,0.1,0.15,0.2,0.3,0.4,0.5,0.6,0.7,0.8,1.5),ini=ini.vals)

## variog: computing omnidirectional variogram
```

```
## variofit: covariance model used is matern
## variofit: weights used: cressie
## variofit: minimisation function used: optim
## variofit: searching for best initial value ... selected values:
##          sigmasq phi      tausq kappa
## initial.value "2.02" "0.02" "0"      "0.5"
## status        "est"  "est"  "est"  "fix"
## loss value: 95.7219934941921
varioqram_block_length

## [1] 0.20739591 0.06922791
```

Coding StatFunction argument

Define BetaCoeff a function which will be the *StatFunction* argument to *BlockBootApply*. BetaCoeff gets a coefficient for temperature for inference

```
BetaCoeff = function(dat){
  fit1 = lm ("response-temperature", data=dat)
  Beta = fit1$coefficients["temperature"]
  Beta
}
```

Run Block Bootstrap

First the user should create a folder called e.g. LookupTables in their R working directory. As all the examples below use the same site coordinates they all share the same lookup tables. However if a new analysis is being done on different data (with different site co-ordinates), then a new lookup table needs to be created.

```
lookuptables.folderpathname = "LookupTables/"
```

Run Block Bootstrap, using Lahiri method of block size selection, with the variogram to select the tuning parameter. We search over 4 blocks sizes (0- i.e. IID, 0.05, 0.1, 0.2). BlockBootApply uses the size which minimises the Empirical MSE of $SE(\beta)$. Use 0.2 as tuning block length as per variogram practical range (tuning block length =4).

```
Results = BlockBootApply (x = x ,y = y ,block_Ls = c(0,0.05,0.1, 0.2), Grid_space = 0.01 ,
  dat = dat ,
  Stat.function = BetaCoeff, tuning_block_length = 0.2,
  NBoot = 500, method.block.length.select = "EmpiricalMSE",
  type="SE", lookuptables.folderpath=lookuptables.folderpathname)

## [1] "has foldername, checking for lookupable"
## [1] "file exists"
## [1] "using lookup"
## [1] "has foldername, checking for lookupable"
## [1] "file exists"
## [1] "using lookup"
## [1] "has foldername, checking for lookupable"
## [1] "file exists"
## [1] "using lookup"
## [1] "mutually.exclusive"
## [1] "subregion1"
## [1] "mxy33"
```



```

## [1] "subregion2"
## [1] "mxy33"
## [1] "subregion3"
## [1] "mxy33"
## [1] "subregion4"
## [1] "mxy33"
## [1] "subregion5"
## [1] "mxy33"
## [1] "subregion6"
## [1] "mxy33"
## [1] "subregion7"
## [1] "mxy33"
## [1] "subregion8"
## [1] "mxy33"
## [1] "subregion9"
## [1] "mxy33"
## [1] "subregion1"
## [1] "mxy33"
## [1] "file exists"
## [1] "using existing coords..."
## [1] "subregion2"
## [1] "mxy33"
## [1] "file exists"
## [1] "using existing coords..."
## [1] "subregion3"
## [1] "mxy33"
## [1] "file exists"
## [1] "using existing coords..."
## [1] "subregion4"
## [1] "mxy33"
## [1] "file exists"
## [1] "using existing coords..."
## [1] "subregion5"
## [1] "mxy33"
## [1] "file exists"
## [1] "using existing coords..."
## [1] "subregion6"
## [1] "mxy33"
## [1] "file exists"
## [1] "using existing coords..."
## [1] "subregion7"
## [1] "mxy33"
## [1] "file exists"
## [1] "using existing coords..."
## [1] "subregion8"
## [1] "mxy33"
## [1] "file exists"
## [1] "using existing coords..."
## [1] "subregion9"
## [1] "mxy33"
## [1] "file exists"
## [1] "using existing coords..."
## [1] "subregion1"
## [1] "mxy33"

```

```

## [1] "file exists"
## [1] "using existing coords..."
## [1] "subregion2"
## [1] "mxy33"
## [1] "file exists"
## [1] "using existing coords..."
## [1] "subregion3"
## [1] "mxy33"
## [1] "file exists"
## [1] "using existing coords..."
## [1] "subregion4"
## [1] "mxy33"
## [1] "file exists"
## [1] "using existing coords..."
## [1] "subregion5"
## [1] "mxy33"
## [1] "file exists"
## [1] "using existing coords..."
## [1] "subregion6"
## [1] "mxy33"
## [1] "file exists"
## [1] "using existing coords..."
## [1] "subregion7"
## [1] "mxy33"
## [1] "file exists"
## [1] "using existing coords..."
## [1] "subregion8"
## [1] "mxy33"
## [1] "file exists"
## [1] "using existing coords..."
## [1] "subregion9"
## [1] "mxy33"
## [1] "file exists"
## [1] "using existing coords..."
## [1] "subregion1"
## [1] "mxy33"
## [1] "file exists"
## [1] "using existing coords..."
## [1] "subregion2"
## [1] "mxy33"
## [1] "file exists"
## [1] "using existing coords..."
## [1] "subregion3"
## [1] "mxy33"
## [1] "file exists"
## [1] "using existing coords..."
## [1] "subregion4"
## [1] "mxy33"
## [1] "file exists"
## [1] "using existing coords..."
## [1] "subregion5"
## [1] "mxy33"
## [1] "file exists"
## [1] "using existing coords..."

```

```
## [1] "subregion6"
## [1] "mxy33"
## [1] "file exists"
## [1] "using existing coords..."
## [1] "subregion7"
## [1] "mxy33"
## [1] "file exists"
## [1] "using existing coords..."
## [1] "subregion8"
## [1] "mxy33"
## [1] "file exists"
## [1] "using existing coords..."
## [1] "subregion9"
## [1] "mxy33"
## [1] "file exists"
## [1] "using existing coords..."
```

Check sensitivity to tuning parameter. See that some columns are minimised by block length 0.1, and some columns by 0.05 so tuning block length was important here

```
Results$Empirical.MSE
```

```
##           tuninglength0 tuninglength0.05 tuninglength0.1
## blocklength0      0.0003547597      0.0006171809      0.002031718
## blocklength0.05  0.0008426232      0.0004558952      0.001049705
## blocklength0.1   0.0027512821      0.0015788562      0.001179298
## blocklength0.2   0.0016315219      0.0013584784      0.002096021
##           tuninglength0.2
## blocklength0      0.004278006
## blocklength0.05   0.002573408
## blocklength0.1    0.001828421
## blocklength0.2    0.003746269
```

The block size parameter chosen is:

```
Results$EmpiricalMSE_block_size
```

```
## tuning = 0.2
##           0.1
```

This is the standard error (estimated via block bootstrap to account for spatial autocorrelation) of β

```
Results$SE.estimate.EmpiricalMSE_block_size
```

```
## [[1]]
## [1] 0.1167922
```

Example 2: Community-level Hypothesis Test using BlockBootID with mvabund

Setting Up

First load the data and R packages you need into the R workspace.

```
load("PlayData_for_Examples.RData") ### load the data for the examples
source("LoadFunctions.R") ##### Source the functions required to run the block bootstrap

#Install packages if required
if(!require(mvabund)) { install.packages("mvabund", repos = "http://cran.us.r-project.org");
require(mvabund) }
library(mvabund)
```

Motivation

We want to test an assemblage/ community of species for the significance of a bunch of variables, using “mvabund::summary”.

This example assumes a block size is selected by the user already, from either pilot study or as in Example 3. They can then use **BlockBootID** to generate an ID matrix for input into mvabund.

```
set.seed(42)

lookuptables.folderpathname = "LookupTables/"

##### Get a bootID matrix
BootID.example2 = BlockBootID(x = x ,
                             y = y,
                             block_Ls = 0.1,
                             NBoot = 500,
                             Grid_space = 0.01,
                             lookuptables.folderpath = lookuptables.folderpathname)
```

Run hypothesis test/ summary in mvabund

```
responseMultiSpecies=mvabund(multispecies_dat[,1:20]) #20 species multivariate response
mod.1 = manyglm(responseMultiSpecies~temperature, data = multispecies_dat,family="binomial")
mod.2 = manyglm(responseMultiSpecies~temperature*treatment, data = multispecies_dat,family="binomial")
anova.results = anova(mod.1, mod.2, bootID=BootID.example2, resamp="case")

## Warning in anova.manyglm(mod.1, mod.2, bootID = BootID.example2, resamp =
## "case"): 'montecarlo' or 'pit.trap' should be used for binomial regression.
```

```
## Warning in anova.manyglm(mod.1, mod.2, bootID = BootID.example2, resamp =
## "case"): case resampling with score and LR tests is under development. try
## case resampling with wald test.
```

```
## Using <int> bootID matrix from input.
## Time elapsed: 0 hr 0 min 29 sec
```

```
anova.results
```

```
## Analysis of Deviance Table
```

```
##
```

```
## mod.1: responseMultiSpecies ~ temperature
```

```
## mod.2: responseMultiSpecies ~ temperature * treatment
```

```
##
```

```
## Multivariate test:
```

```
##      Res.Df Df.diff    Dev Pr(>Dev)
```

```
## mod.1      498
```

```
## mod.2      496      2 37.42      1
```

```
## Arguments:
```

```
## Test statistics calculated assuming uncorrelated response (for faster computation)
```

```
## P-value calculated using 500 resampling iterations via case resampling (to account for correlation)
```

The treatment is not significant.

Example 3: Community-level Hypothesis Test using BlockBootID with mvabund, block length selection

Setting Up

First load the data and R packages you need into the R workspace.

```
load("PlayData_for_Examples.RData") ### load the data for the examples
source("LoadFunctions.R") ##### Source the functions required to run the block bootstrap

#Install packages if required
if(!require(mvabund)) { install.packages("mvabund", repos =
"http://cran.us.r-project.org"); require(mvabund) }

library(mvabund)
```

Motivation

```
set.seed(42)
treatment = rbinom(500,1,0.5)
multispecies_dat = data.frame(multispecies_dat,treatment)
```

Coding StatFunction argument

Define MultSpeciesTestStat a function which will be the *StatFunction* argument to *BlockBootApply*.

```
MultSpeciesTestStat = function(dat){
  responseMultiSpecies = mvabund(dat[,1:20])

  null.model = manyglm (responseMultiSpecies~1, data=dat, family="binomial")
  alt.model = manyglm (responseMultiSpecies~temperature*treatment, data=dat, family="binomial")
  Test.stat = sum(alt.model$two.loglike) - sum(null.model$two.loglike)
  ;
  Test.stat
}

MultSpeciesTestStat (multispecies_dat)
```

```
## [1] 10261.29
```

Run Block Bootstrap

Run Block Bootstrap, using Lahiri method of block size selection. We search over 4 blocks sizes (0- i.e. IID, 0.05, 0.1, 0.2). BlockBootApply uses the size which minimises the Empirical MSE of $SE(T)$, where T is the multispecies likelihood ratio test statistic. Use 0.05 as tuning block length, (tuning_block_length =2).

```
lookuptables.folderpathname = "LookupTables/"
```

```
Results.Example3 = BlockBootApply (x = x ,y = y ,block_Ls = c(0,0.05,0.1,0.2), Grid_space = 0.01 ,
dat = multispecies_dat , Stat.function = MultSpeciesTestStat, tuning_block_length = 2, NBoot = 2,
method.block.length.select = "Lahiri", type="SE", lookuptables.folderpath=lookuptables.folderpathname)
```

```
L.example3 = Results.Example3$Lahiri_block_size
#The chosen block size parameter
L.example3
```

```
## [1] 0.1
```

Now make a bootID matrix and feed into mvabund::summary.

```
BootID.example3 = BlockBootID(x = x ,
y = y,
block_Ls = L.example3,
NBoot = 500,
Grid_space = 0.01,
lookuptables.folderpath = lookuptables.folderpathname, shape="disc")

#####

responseMultiSpecies = mvabund(multispecies_dat[,1:20])

mod.full = manyglm(responseMultiSpecies~temperature*treatment, data = multispecies_dat,
family="binomial")

anova(mod.full, bootID = BootID.example3, resamp="case")
```

```
## Warning in anova.manyglm(mod.full, bootID = BootID.example3, resamp =
## "case"): 'montecarlo' or 'pit.trap' should be used for binomial regression.
```

```
## Warning in anova.manyglm(mod.full, bootID = BootID.example3, resamp =
## "case"): case resampling with score and LR tests is under development. try
## case resampling with wald test.
```

```
## Using <int> bootID matrix from input.
## Time elapsed: 0 hr 1 min 22 sec
```

```
## Analysis of Deviance Table
##
## Model: manyglm(formula = responseMultiSpecies ~ temperature * treatment,
## Model:      family = "binomial", data = multispecies_dat)
##
## Multivariate test:
##
## (Intercept)      Res.Df Df.diff    Dev Pr(>Dev)
## temperature      499
## treatment        498      1 10224   0.421
##                  497      1    19   0.990
```

```
## temperature:treatment    496      1    19    0.982
## Arguments:
## Test statistics calculated assuming uncorrelated response (for faster computation)
## P-value calculated using 500 resampling iterations via case resampling (to account for correlation)

#####
```


Example 4: Standard Error of AUC

Setting Up

First load the data and R packages you need into the R workspace.

```
load("PlayData_for_Examples.RData") ### load the data for the examples
source("LoadFunctions.R") ##### Source the functions required to run the block bootstrap

#Install packages if required
if(!require(pROC)) { install.packages("pROC", repos = "http://cran.us.r-project.org"); require(pROC) }

library(pROC)
```

Motivation

Imagine we want to know the standard error of the AUC (area under the ROC curve) of our model. Perhaps we have two models, and we want to see if variation in AUC is explained by sampling error or if it is due to the predictors in the model.

```
set.seed(42)

fit1 = glm (PresAbsresponse ~ temperature, data = dat, family="binomial")

auc(response=dat$PresAbsresponse, predictor= predict(fit1))
```

```
## Area under the curve: 0.7735
```

Coding StatFunction argument

Define getAUC a function which will be the *StatFunction* argument to *BlockBootApply*.

```
GetAUC = function(dat){
  fit1 = glm ("PresAbsresponse~temperature", data=dat, family="binomial")
  AUC = auc(response=dat$PresAbsresponse, predictor= predict(fit1))
  ;
  AUC
}
```

Getting Variogram Practical Range

Fit a variogram on the residuals of fit1- notice we can see spatial autocorrelation. Use the variogram practical range as a tuning parameter for the Lahiri method of block selection. Always check the variogram visually. Sometimes you may need to change max.dist, breaks or initial conditions to get a sensible practical range. It is hard to automate this process.

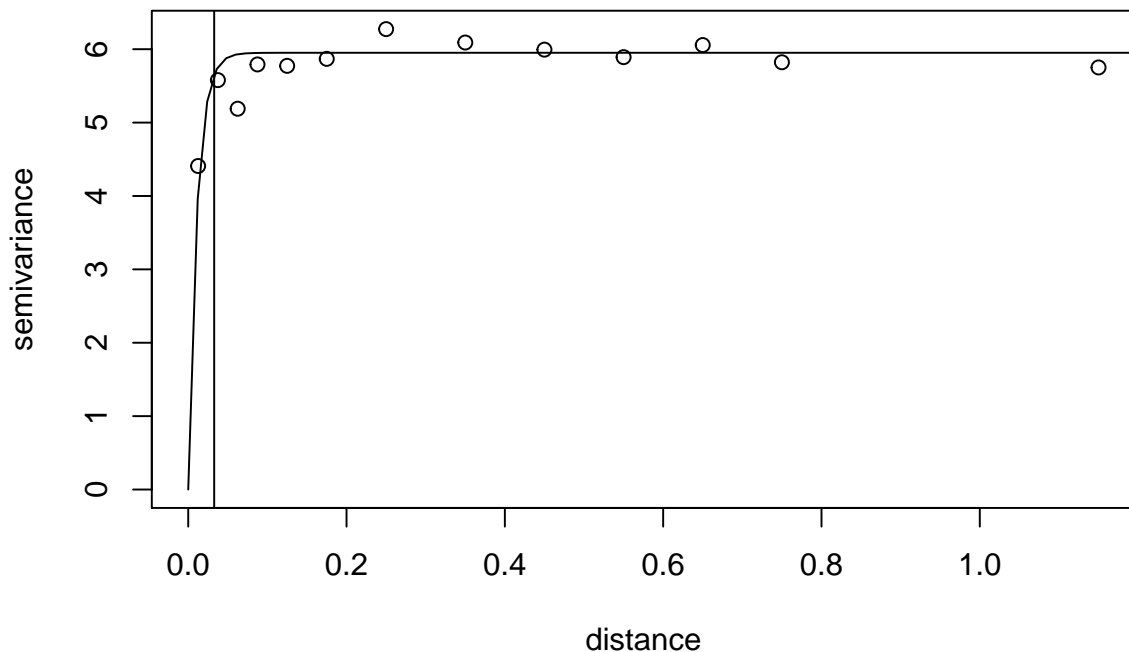
```

ini.vals <- expand.grid(seq(0,10,l=100), seq(0,1,l=100))

variogram_block_length = select_b_length_off_variogram_envelope(x,y,resids = fit1$resid,
max.dist = 1.2, breaks=c(0,0.025,0.05,0.075,0.1,0.15,0.2,0.3,0.4,0.5,0.6,0.7,0.8,1.5),
ini=ini.vals)

## variog: computing omnidirectional variogram
## variofit: covariance model used is matern
## variofit: weights used: npairs
## variofit: minimisation function used: optim
## variofit: searching for best initial value ... selected values:
##          sigmasq phi   tausq kappa
## initial.value "5.96" "0.01" "0"   "0.5"
## status       "est"  "est"  "est"  "fix"
## loss value: 3853.7181489579

```



```
variogram_block_length
```

```
## [1] 0.03280132
```

Run Block Bootstrap

Run Block Bootstrap, using Lahiri method of block size selection, with the variogram to select the tuning parameter. We search over 4 blocks sizes (0- i.e. IID, 0.05, 0.1, 0.2). BlockBootApply uses the size which

minimises the Empirical MSE of $SE(\beta)$. Use 0.05 as tuning block length as per variogram practical range ($tuning_block_length = 2$).

```
lookuptables.folderpathname = "LookupTables/"
```

```
Results.example4 = BlockBootApply (x = x ,y = y ,block_Ls = c(0,0.05,0.1,0.2), Grid_space = 0.01 ,
dat = dat , Stat.function = GetAUC, tuning_block_length = 2, NBoot = 500,
method.block.length.select = "Lahiri", type="SE", lookuptables.folderpath=lookuptables.folderpathname)
```

Check sensitivity to tuning parameter. See that all columns are minimised by block length 0.1, so tuning block length wasn't terribly important here

```
Results.example4$Empirical.MSE
```

```
##           tuninglength0 tuninglength0.05 tuninglength0.1
## blocklength0      0.001626589      0.02305761      0.07962379
## blocklength0.05    0.007378852      0.02219981      0.07119708
## blocklength0.1     0.029063621      0.04260590      0.09013901
## blocklength0.2     0.040642723      0.08243159      0.16230864
##           tuninglength0.2
## blocklength0      0.1593789
## blocklength0.05    0.1441683
## blocklength0.1     0.1617980
## blocklength0.2     0.2629567
```

The block size parameter chosen is:

```
Results.example4$Lahiri_block_size
```

```
## [1] 0.05
```

This is the standard error (estimated via block bootstrap to account for spatial autocorrelation) of the AUC.

```
Results.example4$SE.estimate
```

```
## [1] 0.02576194
```

Example 5: Parallel Computing

Setting Up

First load the data and R packages you need into the R workspace.

```
load("PlayData_for_Examples.RData") ### load the data for the examples
source("LoadFunctions.R") ##### Source the functions required to run the block bootstrap

#Install packages if required
if(!require(pROC)) { install.packages("pROC", repos = "http://cran.us.r-project.org"); require(pROC) }

library(pROC)
```

Motivation

As in Example 4, imagine we want to know the standard error of the AUC (area under the ROC curve) of our model. However we wish to run the bootstrap in parallel on a cluster computer. For $N_{\text{Boot}} = 500$, we could run 10 batches, each with 50 bootstrap resamples. We then assemble the results using the function **CombineBatchesofBootstraps**.

To use **CombineBatchesofBootstraps**, each batch should contain an equal number of bootstrap resamples.

```
set.seed(42)

fit1 = glm (PresAbsresponse ~ temperature, data = dat, family="binomial")
```

Coding StatFunction argument

As in Example 4, define `getAUC` a function which will be the *StatFunction* argument to *BlockBootApply*.

```
GetAUC = function(dat){
  fit1 = glm ("PresAbsresponse~temperature", data=dat, family="binomial")
  AUC = auc(response=dat$PresAbsresponse, predictor= predict(fit1))
  ;
  AUC
}
```

Run Block Bootstrap

First the user should create a folder called e.g. `LookupTables` in their R working directory. As all the batches of bootstraps use the same site coordinates they all share the same lookup tables.

```
lookuptables.folderpathname = "LookupTables/"
```

```
batchID = 1
assign (paste0("Results.example4.batch", batchID ),
      BlockBootApply (x = x ,y = y ,block_Ls = c(0,0.05,0.1,0.2), Grid_space = 0.01 ,
                      dat = dat, Stat.function = GetAUC, tuning_block_length = 2,
                      NBoot = 250, method.block.length.select = "Lahiri",type="SE",
                      lookuptables.folderpath=lookuptables.folderpathname))
```

```
batchID = 2
assign (paste0("Results.example4.batch", batchID ),
      BlockBootApply (x = x ,y = y ,block_Ls = c(0,0.05,0.1,0.2), Grid_space = 0.01 ,
                      dat = dat, Stat.function = GetAUC, tuning_block_length = 2,
                      NBoot = 250, method.block.length.select = "Lahiri",type="SE",
                      lookuptables.folderpath=lookuptables.folderpathname))
```

```
batchIDs=1:2
```

```
list_of_boot_batches = lapply(paste0("Results.example4.batch", batchIDs), get)
```

```
Results.example4.all = CombineBatchesofBootstraps(list_of_boot_batches=
list_of_boot_batches )
```

Check sensitivity to tuning parameter. See that all columns are minimised by block length 0.1, so tuning block length wasn't terribly important here

```
Results.example4.all$Empirical.MSE
```

```
##           tuninglength0 tuninglength0.05 tuninglength0.1
## blocklength0      0.0003802906      0.02173633      0.08486327
## blocklength0.05  0.0093301256      0.02342151      0.07875828
## blocklength0.1   0.0266339887      0.03785125      0.09010597
## blocklength0.2   0.0382523887      0.08122859      0.16753968
##           tuninglength0.2
## blocklength0      0.1325652
## blocklength0.05   0.1225259
## blocklength0.1    0.1323171
## blocklength0.2    0.2269502
```

The block size parameter chosen is:

```
Results.example4.all$Lahiri_block_size
```

```
## [1] 0
```

This is the standard error (estimated via block bootstrap to account for spatial autocorrelation) of AUC

```
Results.example4.all$SE.estimate
```

```
## [1] 0.0194651
```

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LITERATURE CITED

- 144 LAHIRI, S. N. and ZHU, J. (2006). Resampling methods for spatial regression models under a
145 class of stochastic designs. *Ann. Statist.*, **34** 1774–1813.