SpatCourse_SSN1

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Scripts and examples for visualising and analysing Spatial Stream Network models (SSN)

These scripts provide introductory examples on how to deal with .ssn objects in R. We will work with a ready-available .ssn object in .RData format. You can download this from: *https://github.com/stefanolarsen/SpatCourse* The dataset include macroinvertebrates community data across the Adige River network (NE Italy). Environmental descriptors, diversity and feeding-trait metrics are included. For details see: **Larsen et al 2019 - Testing the river continuum concept with geo-statistical stream network models**. *Ecological Complexity.* https://doi.org/10.1016/j.ecocom.2019.100773

Load the key libraries.

```
library(SSN)
library(tidyverse)
#library(gtools)
```

Load the RData with the SSN object (stream invertebrates from Adige River network)

You must first download this .RData object from the *https://github.com/stefanolarsen/SpatCourse*. Then modify the code below to include your path (where you downloaded the file).

```
load("~/Documents/SpatCoursePT/SpatCourse/spat.course.ssn1.RData")

#gitUrl='https://github.com/stefanolarsen/SpatCourse/blob/main/bent.ssn.logit.RData'
```

Create the distance matrices.

These are non-orthodox distance matrices. See help for details. Distance matrix is important for modelling later!

```
createDistMat(spat.course.ssn)
```

```
## Distance matrices already existed while o.write was set to FALSE. Not overwriting existing matrices
```

Now that you have the .ssn object imported, you can explore it.

Spatial objects can be explored with *summary*.

```
summary(spat.course.ssn)
```

```
## Object of class Spatial Stream Network
##
## Object includes observations on 49 variables across 195 sites within the bounding box
##         min       max
## x  601178.4  753197.5
## y 5042879.0 5219401.0
##
## Variables recorded are (found using names(object)):
## $Obs
##  [1] "code"       "X"          "Y"          "richness"   "shannon"
##  [6] "simpson"    "density"    "Star_icmi"  "T_wat"      "pH"
## [11] "Ox_sat"     "Ox_dis"     "N_tot"      "NO3"        "NH4"
## [16] "P"          "T_air"      "upDist"     "h2oArea"    "h2oAgric"
## [21] "h2oWood"    "Z"          "buf_agric_" "buf_wood_a" "mean_slope"
## [26] "afvArea"    "NEAR_FID"   "NEAR_DIST"  "NEAR_X"     "NEAR_Y"
## [31] "NEAR_ANGLE" "rid"        "ratio"      "locID"      "netID"
## [36] "pid"        "PCA1.long"  "LIMeco"     "buf.agr.p"  "buf.wood.p"
## [41] "h2oAgric_p" "h2oWood_p"  "feed_gra"   "feed_xyl"   "feed_shr"
## [46] "feed_gat"   "feed_pff"   "feed_pre"   "feed_oth"
##
## Generic functions that work with this object include names, plot, print, summary, hist, boxplot and c
```

Explore the variables in the data only.

Here there are diversity metrics (richness, shannon). Other descriptors e.g. T_wat (water T), LIMeco (water quality index). Other variables (netID, ratio) come from the process leading to the SSN file, from GIS. ## An important variable is *afvArea* (the additive function based on catchment area), use for weighting the correlation function at river juntions.

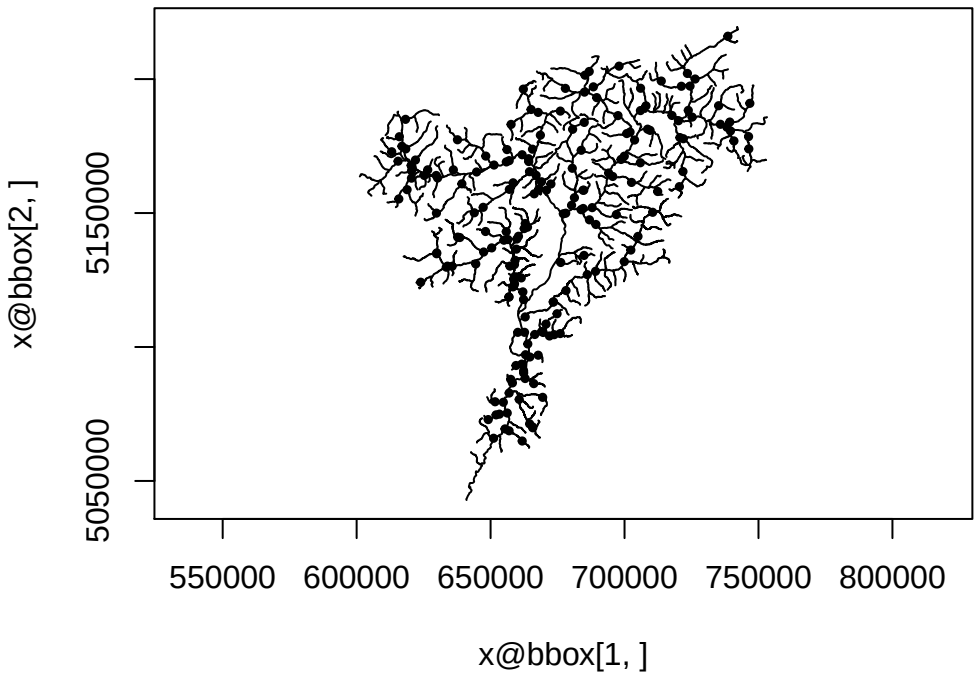
```
names(spat.course.ssn)
```

```
## $Obs
##  [1] "code"       "X"          "Y"          "richness"   "shannon"
##  [6] "simpson"    "density"    "Star_icmi"  "T_wat"      "pH"
## [11] "Ox_sat"     "Ox_dis"     "N_tot"      "NO3"        "NH4"
## [16] "P"          "T_air"      "upDist"     "h2oArea"    "h2oAgric"
## [21] "h2oWood"    "Z"          "buf_agric_" "buf_wood_a" "mean_slope"
## [26] "afvArea"    "NEAR_FID"   "NEAR_DIST"  "NEAR_X"     "NEAR_Y"
## [31] "NEAR_ANGLE" "rid"        "ratio"      "locID"      "netID"
## [36] "pid"        "PCA1.long"  "LIMeco"     "buf.agr.p"  "buf.wood.p"
## [41] "h2oAgric_p" "h2oWood_p"  "feed_gra"   "feed_xyl"   "feed_shr"
## [46] "feed_gat"   "feed_pff"   "feed_pre"   "feed_oth"
```

Explore plotting functions

Simple *plot* function can also work. You see the network and the sampling points.

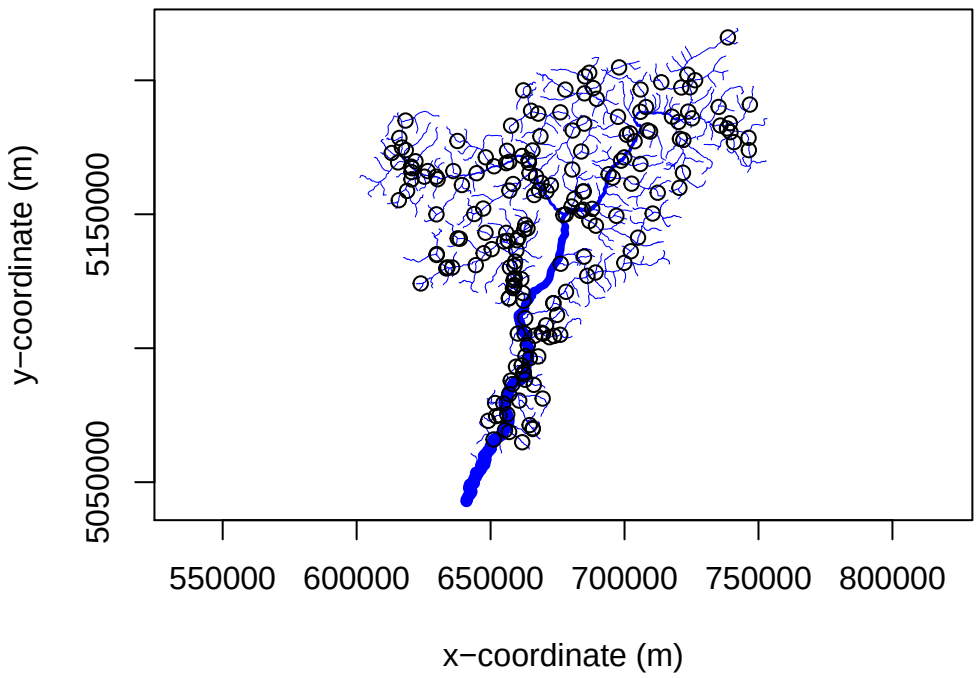
```
plot(spat.course.ssn, asp=1, cex=0.5)
```



Nicer option for plotting; can weight the line width by catchment area.

The option here is: 'lwdLineCol=afvArea'.

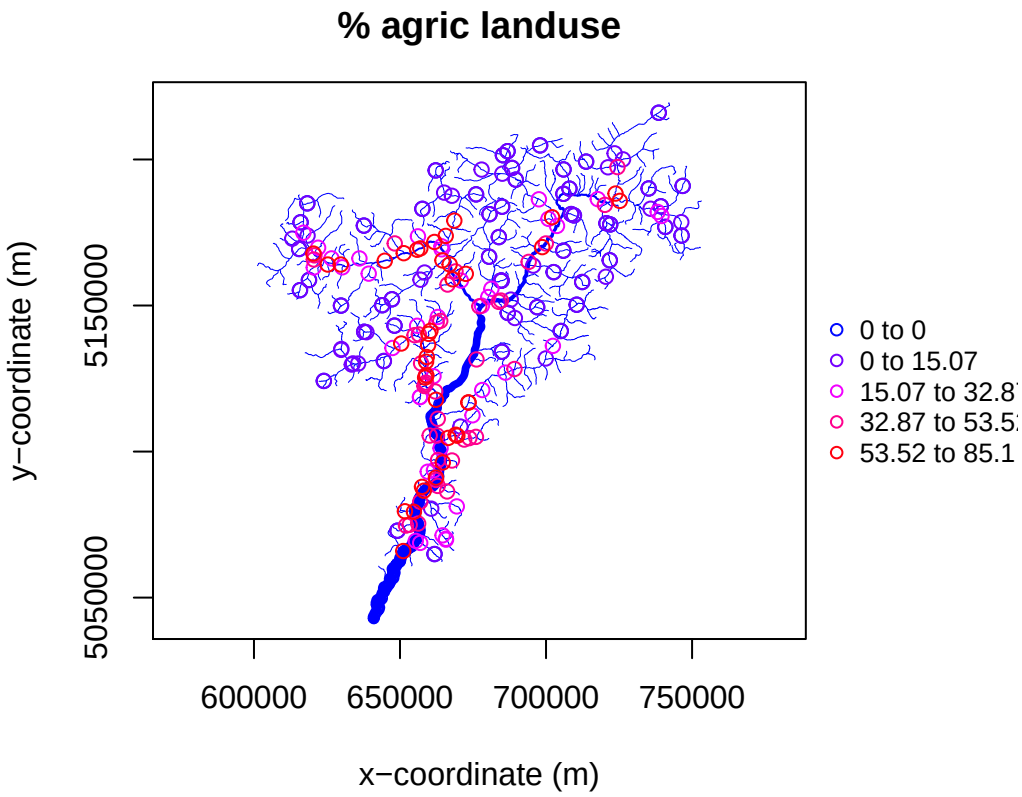
```
plot(spat.course.ssn, lwdLineCol = "afvArea", lwdLineEx = 6, lineCol = "blue",
   pch = 1, xlab = "x-coordinate (m)", ylab = "y-coordinate (m)",
   asp = 1)
```



Exploring patterns in specific variables

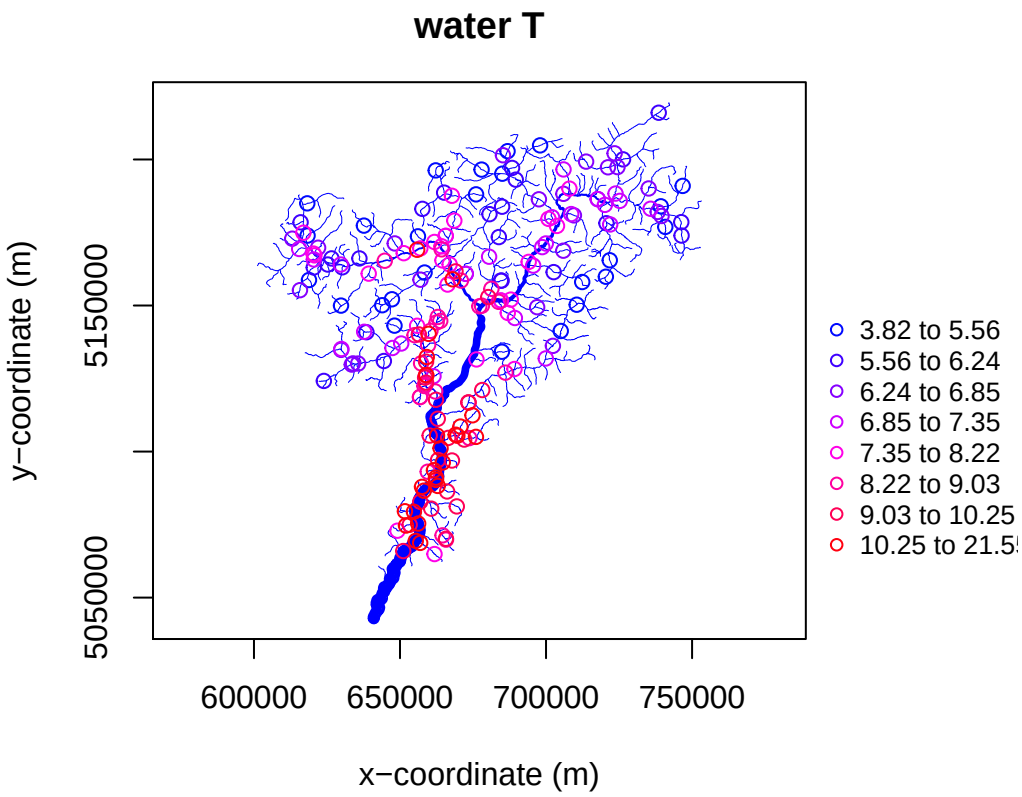
You can also plot specific variable values, with color classes (defined in 'nclasses'). Here e.g. the % of agricultural land-use around each site (buf.agr.p).

```
plot(spat.course.ssn, 'buf.agr.p',, lwdLineCol = "afvArea", lwdLineEx = 6, lineCol = "blue",
     pch = 1, xlab = "x-coordinate (m)", ylab = "y-coordinate (m)",
   asp = 1, nclasses=5, main='% agric landuse')
```



Or plot the water temperature (T_wat).

```
plot(spat.course.ssn, 'T_wat',, lwdLineCol = "afvArea", lwdLineEx = 6, lineCol = "blue",
   pch = 1, xlab = "x-coordinate (m)", ylab = "y-coordinate (m)",
   asp = 1, nclasses=8, main='water T')
```



Manipulate the data frames inside a SSN object

In this example you need to: e.g. Fill NAs in the water quality index: LIMeco Re-transform "logit"-transformed traits to proportions for some traits values.

Extract dataframe from ssn object.

This command extract the data matrix from the ssn object. We can work on it, and then put it back into a ssn object. This is useful if we need to modify or add data to our dataframe.

```
datassn=getSSNdata.frame(spat.course.ssn)
```

Work on the dataframe. Explore structure.

This is now like a standard dataframe in R.

```
str(datassn)
```

```
## 'data.frame':    195 obs. of  49 variables:
##  $ code      : chr  "11104" "11105" "11106" "11107" ...
##  $ X         : num  616913 620774 629715 644783 656953 ...
##  $ Y         : num  5174929 5167246 5164037 5165336 5169574 ...
```

```
##  $ richness  : num  26.6 21 18.8 15.3 17.6 ...
##  $ shannon   : num  10.56 6.35 7.94 4.15 4.93 ...
##  $ simpson   : num  7.31 4.02 5.9 3.1 3.41 ...
##  $ density   : num  1399 1156 523 1528 1661 ...
##  $ Star_icmi : num  1.09 0.993 0.888 0.703 0.869 ...
##  $ T_wat     : num  7.4 8.18 6.86 8.84 7.52 ...
##  $ pH        : num  7.85 8.2 7.89 7.96 7.86 ...
##  $ Ox_sat    : num  112 104 108 107 108 ...
##  $ Ox_dis    : num  11.6 11.2 12 11.6 12.3 ...
##  $ N_tot     : chr  "NA" "NA" "NA" "NA" ...
##  $ NO3       : num  0.93 1.3 NA NA NA ...
##  $ NH4       : num  0.0418 0.105 0.0561 0.0564 0.0425 ...
##  $ P         : num  0.0264 0.0325 0.0359 0.0321 0.0273 ...
##  $ T_air     : chr  "9.546428571" "16" "12.52727273" "13.52142857" ...
##  $ upDist    : num  216962 206978 197260 180683 167066 ...
##  $ h2oArea   : num  232 479 892 1294 1625 ...
##  $ h2oAgric  : num  1.24 8.15 31.96 66.28 95.92 ...
##  $ h2oWood   : num  44.3 87.8 201.1 317.4 394.8 ...
##  $ Z         : num  1302 888 864 602 510 ...
##  $ buf_agric_: num  661581 1430320 1997098 2187835 2640478 ...
##  $ buf_wood_a: num  809991 1098029 195539 0 339981 ...
##  $ mean_slope: num  7.313 0.742 0.1 1.138 0.682 ...
##  $ afvArea   : num  0.0277 0.0539 0.099 0.1339 0.1581 ...
##  $ NEAR_FID  : int  523 517 142 488 219 520 472 259 256 443 ...
##  $ NEAR_DIST : num  6.96e-05 9.99e-05 7.37e-06 1.25e-05 4.98e-05 ...
##  $ NEAR_X    : num  616913 620699 629715 644784 656954 ...
##  $ NEAR_Y    : num  5174929 5167181 5164033 5165332 5169559 ...
##  $ NEAR_ANGLE: num  169.2 -141.7 85.2 103.9 93.4 ...
##  $ rid       : int  522 516 141 487 218 519 471 258 255 442 ...
##  $ ratio     : num  0.5493 0.3346 0.0723 0.7451 0.1208 ...
##  $ locID     : Factor w/ 195 levels "1","100","101",..: 1 101 123 134 144 152 163 174 185 29 ...
##  $ netID     : Factor w/ 1 level "1": 1 1 1 1 1 1 1 1 1 1 ...
##  $ pid       : int  1 2 3 4 5 6 7 8 9 13 ...
##  $ PCA1.long : num  -1.034 -0.429 0.201 0.778 1.015 ...
##  $ LIMeco    : num  0.87 0.85 0.82 0.68 0.865 0.88 0.76 NA NA 0.91 ...
##  $ buf.agr.p : num  21.1 45.5 63.6 69.6 84 ...
##  $ buf.wood.p: num  25.78 34.95 6.22 0 10.82 ...
##  $ h2oAgric_p: num  0.535 1.704 3.584 5.124 5.903 ...
##  $ h2oWood_p : num  19.1 18.3 22.6 24.5 24.3 ...
##  $ feed_gra  : num  0.371 0.517 0.4 0.337 0.346 ...
##  $ feed_xyl  : num  -5.13 -5.65 -5.48 -6.1 -6.05 ...
##  $ feed_shr  : num  0.0886 0.0652 0.1189 0.0398 0.1357 ...
##  $ feed_gat  : num  0.234 0.268 0.28 0.271 0.313 ...
##  $ feed_pff  : num  0.1445 0.0451 0.0895 0.2723 0.0983 ...
##  $ feed_pre  : num  0.1555 0.1013 0.1074 0.0778 0.1044 ...
##  $ feed_oth  : num  -3.66 -3.66 -3.66 -3.66 -3.66 ...
```

```
#some feeding traits proportions are expressed as logit (e.g feed_xyl)
#we can convert it back to proportions if we want.
```

Look for missing values

```
sum(is.na(datassn$LIMeco))
```

```
## [1] 27
```

```
# there are missing values in LIMeco
```

We can fill missing values in LIMeco with overall mean.

```
datassn$LIMeco[is.na(datassn$LIMeco)]<- mean(datassn$LIMeco, na.rm=T)#
```

Just a function to transform logit back to proportion of some feeding traits.

delogit function: convert logit transformed proportions back to proportions

```
delogit=function(x){
  x1=exp(x)
  prop=x1/(1+x1)
  return(prop)
}
```

Convert these traits back to proportions.

```
datassn$feed_oth=delogit(datassn$feed_oth)
datassn$feed_xyl=delogit(datassn$feed_xyl)
```

Then we create a second SSN object with the new modified dataframe.

We can call it the same way for convenience (overwrite the existing one).

```
spat.course.ssn=putSSNdata.frame(datassn, spat.course.ssn)
#save(spat.course.ssn, file='SpatCourse.ssn.RData')
```

To specifically explore the data within a SSN object:access the slots using *@*

```
head(spat.course.ssn@obspoints@SSNPoints[[1]]@point.data)
```

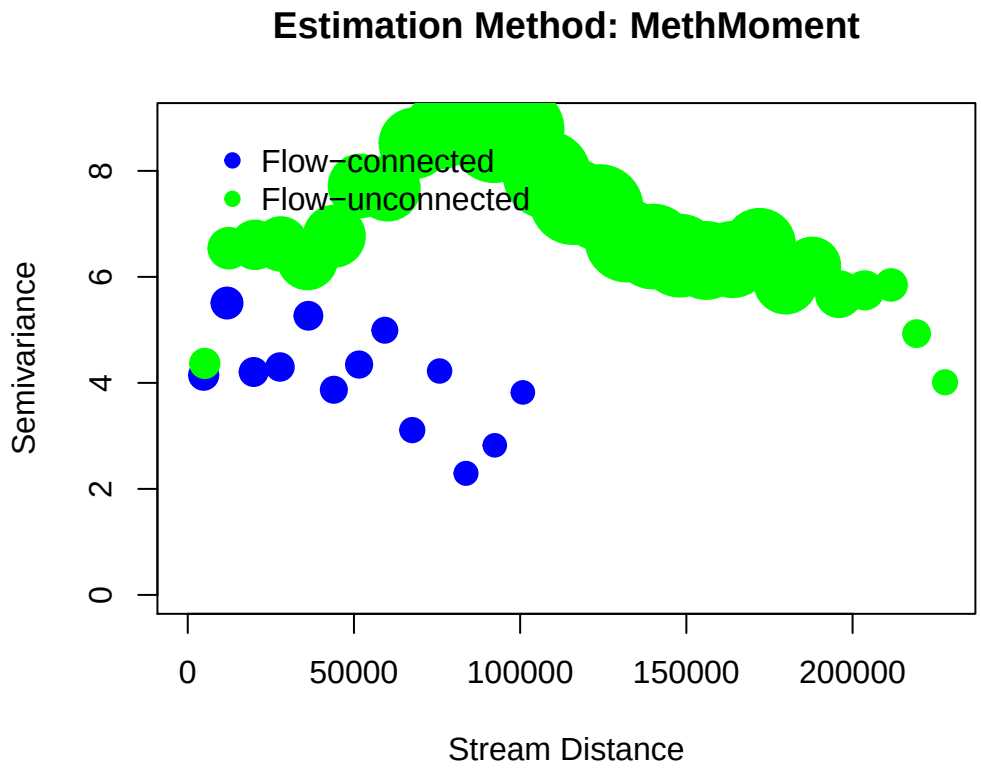
```
##    code        X       Y richness   shannon  simpson   density Star_icmi
## 1 11104 616912.8 5174929 26.55556 10.558511 7.311361 1398.7778 1.0895556
## 2 11105 620773.8 5167246 21.00000  6.349482 4.022947 1156.1667 0.9925090
## 3 11106 629715.1 5164037 18.77778  7.944358 5.899238  523.2222 0.8879836
## 4 11107 644783.1 5165336 15.33333  4.151542 3.096338 1528.2222 0.7025518
## 5 11109 656953.2 5169574 17.55556  4.926763 3.410201 1660.8889 0.8694444
## 6 11110 661774.8 5171761 15.25000  5.554083 4.289583  904.0000 0.8027500
##      T_wat       pH   Ox_sat   Ox_dis N_tot      NO3        NH4          P
## 1 7.403571 7.853571 111.8593 11.57857    NA 0.930000 0.04178571 0.02642857
## 2 8.175000 8.200000 104.0900 11.17500    NA 1.300000 0.10500000 0.03250000
## 3 6.861364 7.890909 108.4798 11.98864    NA       NA 0.05613636 0.03590909
## 4 8.842857 7.964286 107.3411 11.60000    NA       NA 0.05642857 0.03214286
## 5 7.524742 7.861856 107.9668 12.27010    NA       NA 0.04247423 0.02731959
## 6 8.004167 7.991667 107.3012 12.26250    NA 1.804167 0.04166667 0.02875000
```

```
##         T_air   upDist   h2oArea   h2oAgric   h2oWood         Z buf_agric_
## 1 9.546428571 216962.2  232.0061   1.241550  44.34142 1301.8166     661581
## 2          16 206977.5  478.6735   8.154412  87.76638  888.1400    1430320
## 3 12.52727273 197260.4  891.5869  31.958520 201.14650  864.1875    1997098
## 4 13.52142857 180682.9 1293.6352  66.280986 317.37853  601.6891    2187835
## 5 10.95463918 167065.8 1625.0196  95.918329 394.75059  510.3274    2640478
## 6       13.25 161210.9 1702.2652 108.820232 420.01351  352.2998    1694594
##   buf_wood_a mean_slope    afvArea NEAR_FID    NEAR_DIST   NEAR_X  NEAR_Y
## 1   809990.7  7.3127922 0.02774349      523 6.958429e-05 616913.2 5174929
## 2  1098029.0  0.7420453 0.05394963      517 9.985782e-05 620699.3 5167181
## 3   195539.0  0.1000978 0.09902194      142 7.374326e-06 629714.7 5164033
## 4        0.0  1.1382939 0.13388565      488 1.249576e-05 644784.2 5165332
## 5   339981.4  0.6819947 0.15811525      219 4.979581e-05 656954.0 5169559
## 6   558753.6  4.3350407 0.16251227      520 1.658291e-05 661774.9 5171761
##   NEAR_ANGLE rid      ratio locID netID pid  PCA1.long LIMeco buf.agr.p
## 1  169.24863 522 0.54934191     1     1   1 -1.0340673  0.870  21.05877
## 2 -141.68478 516 0.33461351     2     1   2 -0.4285926  0.850  45.52848
## 3   85.16966 141 0.07233777     3     1   3  0.2011001  0.820  63.56959
## 4  103.92335 487 0.74509422     4     1   4  0.7775352  0.680  69.64093
## 5   93.35882 218 0.12080495     5     1   5  1.0154177  0.865  84.04901
## 6 -100.84065 519 0.59876641     6     1   6  1.3097225  0.880  53.94058
##   buf.wood.p h2oAgric_p h2oWood_p  feed_gra    feed_xyl   feed_shr  feed_gat
## 1  25.782801   0.535137  19.11218 0.3712922 0.005875961 0.08863374 0.2342132
## 2  34.951344   1.703544  18.33533 0.5172471 0.003505701 0.06517135 0.2676625
## 3   6.224199   3.584454  22.56050 0.3996249 0.004156538 0.11885428 0.2804388
## 4   0.000000   5.123623  24.53385 0.3365782 0.002229260 0.03977609 0.2711229
## 5  10.821943   5.902595  24.29205 0.3464179 0.002363468 0.13569226 0.3128262
## 6  17.785677   6.392672  24.67380 0.3350684 0.005149049 0.05198261 0.2312810
##     feed_pff  feed_pre   feed_oth
## 1 0.14450043 0.1554770 0.02500710
## 2 0.04509914 0.1012767 0.02503563
## 3 0.08946262 0.1074478 0.02501434
## 4 0.27234322 0.0778204 0.02512339
## 5 0.09827923 0.1044210 0.02500000
## 6 0.26211074 0.1144082 0.02500000
```

Exploring variograms for river networks. the *Torgegram*

Explore default *torgegrams*. SSN package offers this default plots for exploring variograms. It shows the variance for flow-connected and flow-unconnected observation pairs. The size of the spots reflect the #observation pairs for each distance lag. Here an example of torgegram for 'shannon diversity'. *Clearly different spatial patterns for flow-connected and unconnected locations.*

```
tor.shn=Torgegram(spat.course.ssn, 'shannon', nlag = 50, maxlag = 400000)
plot(tor.shn)
```



Let's see how the torgegram object looks like.

It shows the distance lags, the variance ('gam') and the n. of observation pairs within the lag ('np'). And it does so for flow-connected and unconnected locations.

```
tor.shn
```

```
## $distance.connect
##  [1]   4788.988  11824.163  19830.945  27750.220  36303.389  43957.028
##  [7]  51547.647  59295.204  67544.649  75759.661  83708.374  92369.460
## [13] 100813.985
##
## $gam.connect
##  [1] 4.144887 5.506717 4.205762 4.300243 5.266434 3.870225 4.346274 4.993600
##  [9] 3.109768 4.224341 2.294015 2.822745 3.820626
##
## $np.connect
##  [1] 114 141  97  89  94  67  69  51  40  28  22  15  15
##
## $distance.unconnect
##  [1]   5132.361  12348.225  20231.462  28030.915  36001.415  44093.875
```

```
##  [7]  51847.018  60120.128  68193.509  76080.959  84185.824  92101.997
## [13] 100062.904 108060.507 115917.945 124009.023 132043.921 140025.045
## [19] 148057.577 155961.784 163934.849 172010.235 179866.338 187863.722
## [25] 195893.623 203638.621 211588.487 219258.639 227831.461
##
## $gam.unconnect
##  [1] 4.367907 6.541150 6.604840 6.621026 6.323810 6.767396 7.714934 7.668727
##  [9] 8.520837 8.749968 8.922053 8.576814 8.779165 7.925553 7.420135 7.306521
## [17] 6.685355 6.571591 6.401043 6.309791 6.328198 6.614536 5.900969 6.215039
## [25] 5.674788 5.746042 5.848463 4.929490 4.011468
##
## $np.unconnect
##  [1] 116 287 405 480 565 594 620 642 725 796 880 931 974 976 953 953 906 936 906
## [20] 833 807 742 620 515 367 249 150  79  39
##
## $call
## $call$object
## spat.course.ssn
##
## $call$ResponseName
## [1] "shannon"
##
## $call$maxlag
## [1] 4e+05
##
## $call$nlag
## [1] 50
##
##
## attr(,"class")
## [1] "Torgegram"
```

Variograms can be better examined including the three distance types.

Exploring the shapes of variograms over the Euclidean, flow-unconnected and flow-connected dimensions provide more insight into the main spatial patterns of the data.

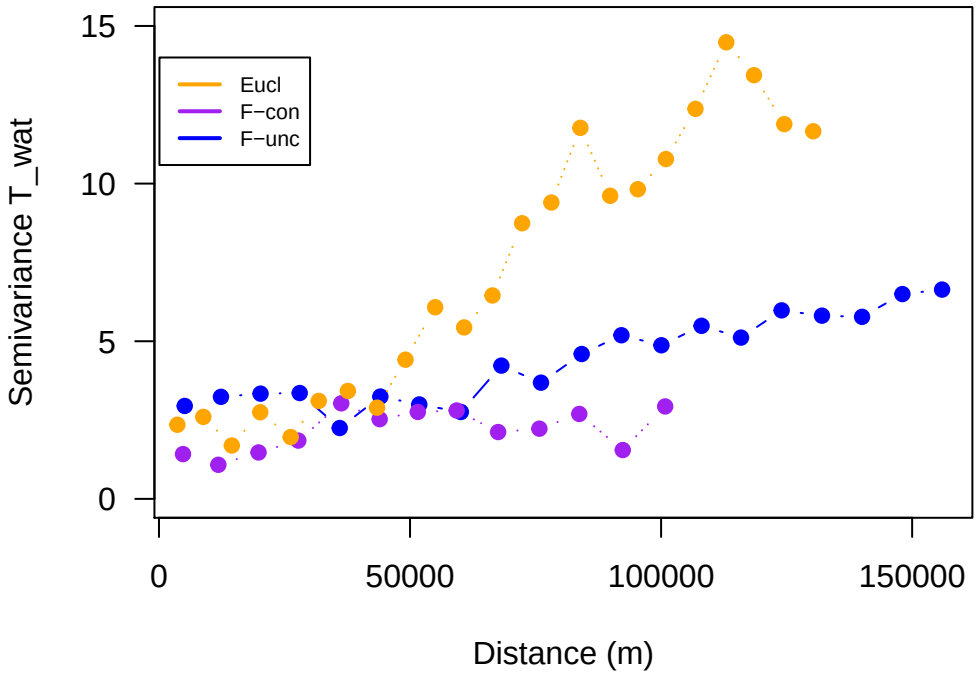
Let's examine the variogram for water T, along the three distances.

```
# first the classic variogram over Euclidean dist
emp.var.wt=EmpiricalSemivariogram(spat.course.ssn, 'T_wat', nlag = 30, maxlag = 200000)
#then the torgegram for flow-connected and unconnected dist
tor.wt=Torgegram(spat.course.ssn, 'T_wat', nlag = 50, maxlag = 400000)
```

Plot all distances together

```
plot(tor.wt$gam.unconnect[1:20]~tor.wt$distance.unconnect[1:20], options(scipen = 5),
     type='b', lty=1, pch=19, ylim=c(0,15), col='blue', ylab='Semivariance T_wat',
     xlab='Distance (m)', cex.lab=1, las=1)
```

```
lines(tor.wt$gam.connect[1:13]~tor.wt$distance.connect[1:13], type='b', col='purple',
      lty=3, pch=19)
lines(emp.var.wt$gamma[1:23]~emp.var.wt$distance[1:23],col='orange',  type='b',
      pch=19, lty=3 )
legend(100, 14, legend=c("Eucl", "F-con", 'F-unc'),
       col=c("orange", "purple", 'blue'), lty=c(1,1,1), lwd=2,  cex=0.7)
```



The above plot shows that, for a given distance, water T varies little over the watercourse dimension, and more over the Euclidean dimension, but only beyond 50 km distance.

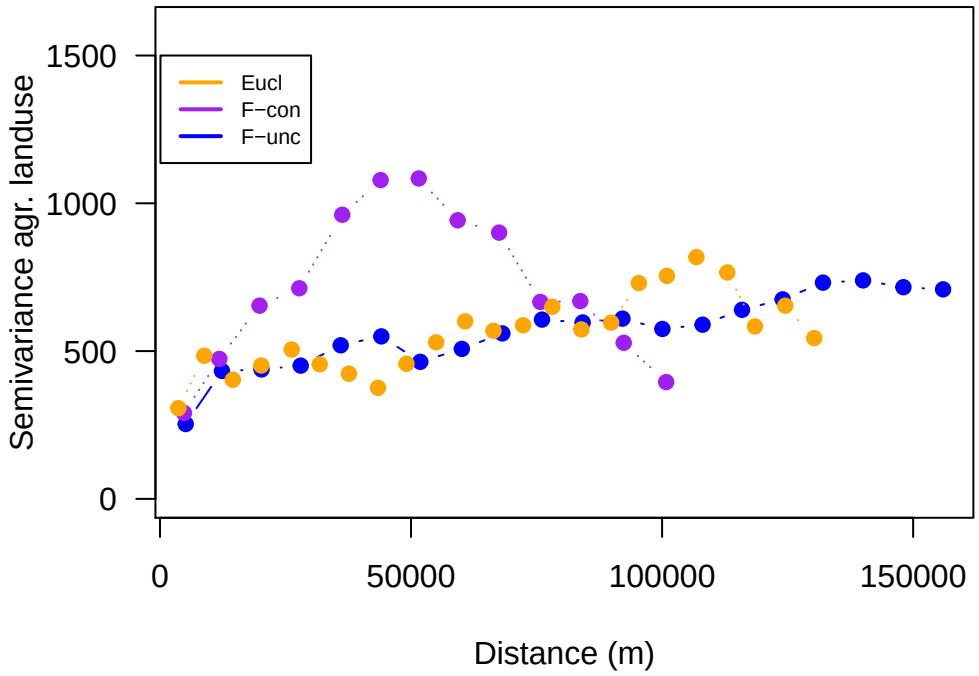
Now let's examine the variogram for local land-use

```
# first variogram along the Euclidean dimension
emp.var.agr=EmpiricalSemivariogram(spat.course.ssn, 'buf.agr.p', nlag = 30, maxlag = 200000)
# then the torgegram over flow-connected and unconnected distances
tor.agr=Torgegram(spat.course.ssn, 'buf.agr.p', nlag = 50, maxlag = 400000)
```

Plot it together

```
plot(tor.agr$gam.unconnect[1:20]~tor.agr$distance.unconnect[1:20], options(scipen = 5),
     type='b', lty=1, pch=19, ylim=c(0,1600 ), col='blue', ylab='Semivariance agr. landuse',
     xlab='Distance (m)', cex.lab=1, las=1)
```

```
lines(tor.agr$gam.connect[1:13]~tor.agr$distance.connect[1:13], type='b',
      col='purple', lty=3, pch=19)
lines(emp.var.agr$gamma[1:23]~emp.var.agr$distance[1:23],col='orange',
      type='b', pch=19, lty=3 )
legend(100, 1500, legend=c("Eucl", "F-con", 'F-unc'),
       col=c("orange", "purple", 'blue'), lty=c(1,1,1), lwd=2,  cex=0.7)
```




```
# Here we see that local landuse varies more rapidly along flow-connected locations
# reflecting the changes from headwaters to mainstems
```

The above variogram show that agricultural landuse changes rapidly along flow-connected locations, reflecting changes from up to downstream within ~50km.

As extreme case, we can explore the variogram for the variable *PCA1.long*. This is a synthetic variable refelecting the logitudinal continuum. As expected, the variance increases along flow-connected locations, but remains low over the other dimensions.

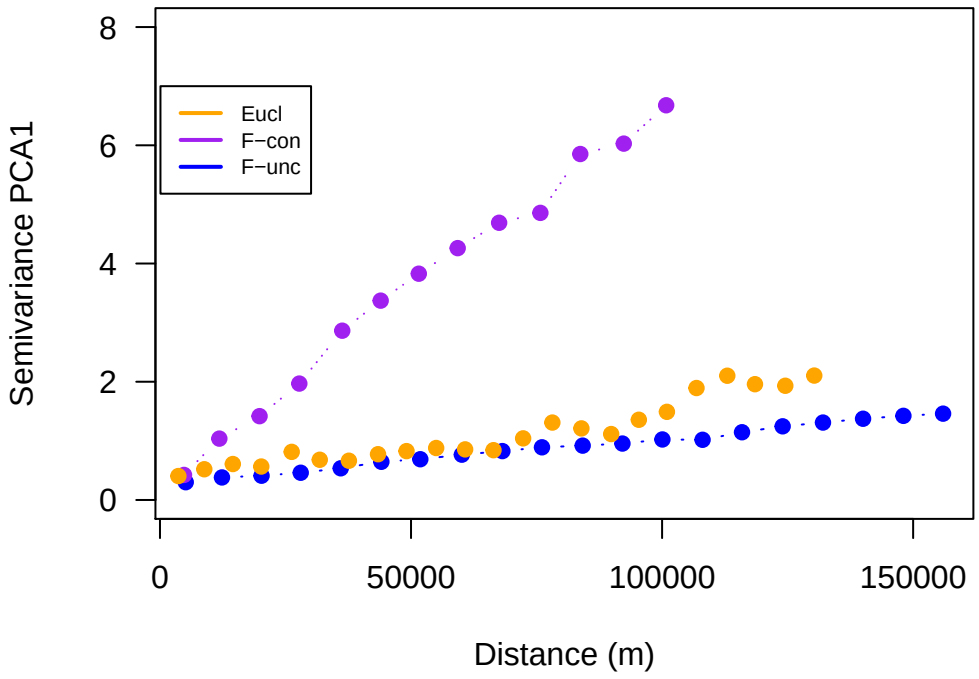
```
# first the variogram for Euclidean and then the Torgegram
emp.var.PCA1=EmpiricalSemivariogram(spat.course.ssn, 'PCA1.long', nlag = 30, maxlag = 200000)
tor.PCA1=Torgegram(spat.course.ssn, 'PCA1.long', nlag = 50, maxlag = 400000)
```

Plot it together as before

```
plot(tor.PCA1$gam.unconnect[1:20]~tor.PCA1$distance.unconnect[1:20], options(scipen = 5),
     type='b', lty=1, pch=19, ylim=c(0,8), col='blue', ylab='Semivariance PCA1',
     xlab='Distance (m)', cex.lab=1, las=1)

lines(tor.PCA1$gam.connect[1:13]~tor.PCA1$distance.connect[1:13], type='b', col='purple',
      lty=3, pch=19)
lines(emp.var.PCA1$gamma[1:23]~emp.var.PCA1$distance[1:23],col='orange',  type='b',
      pch=19, lty=3 )

legend(100, 7, legend=c("Eucl", "F-con", 'F-unc'),
       col=c("orange", "purple", 'blue'), lty=c(1,1,1), lwd=2,  cex=0.7)
```



Now let's run some models. Explore the influence of key environmental drivers on macroinvertebrate metrics.

First, have a look again at the variables in the data;

```
names(spat.course.ssn)
```

```
## $Obs
##  [1] "code"       "X"          "Y"          "richness"   "shannon"
##  [6] "simpson"    "density"    "Star_icmi"  "T_wat"      "pH"
## [11] "Ox_sat"     "Ox_dis"     "N_tot"      "NO3"        "NH4"
## [16] "P"          "T_air"      "upDist"     "h2oArea"    "h2oAgric"
## [21] "h2oWood"    "Z"          "buf_agric_" "buf_wood_a" "mean_slope"
## [26] "afvArea"    "NEAR_FID"   "NEAR_DIST"  "NEAR_X"     "NEAR_Y"
## [31] "NEAR_ANGLE" "rid"        "ratio"      "locID"      "netID"
## [36] "pid"        "PCA1.long"  "LIMeco"     "buf.agr.p"  "buf.wood.p"
## [41] "h2oAgric_p" "h2oWood_p"  "feed_gra"   "feed_xyl"   "feed_shr"
## [46] "feed_gat"   "feed_pff"   "feed_pre"   "feed_oth"
```

As example, we fit models for the porportion of shredders (*feed_shr*) in the community.

We will include the longitudinal gradient (*PCA1.long*), the % of agricultural landuse (*buf.agr.p*) and water quality (*LIMeco*), as predictor (covariates).

```
shr.0=glmssn(feed_shr~PCA1.long+buf.agr.p+LIMeco,spat.course.ssn,
             CorModels = NULL, use.nugget = TRUE,EstMeth = "ML")

summary(shr.0)
```

Start with a non-spatial model (CorModels=NULL). This is equivalent to a classic lm.

```
##
## Call:
## glmssn(formula = feed_shr ~ PCA1.long + buf.agr.p + LIMeco, ssn.object = spat.course.ssn,
##     CorModels = NULL, use.nugget = TRUE, EstMeth = "ML")
##
## Residuals:
##       Min        1Q    Median        3Q       Max
## -0.074099 -0.026835 -0.006961  0.017427  0.161439
##
## Coefficients:
##               Estimate Std. Error t value Pr(>|t|)
## (Intercept)  0.0014740  0.0277824   0.053    0.958
## PCA1.long   -0.0043976  0.0035455  -1.240    0.216
## buf.agr.p   -0.0007341  0.0001541  -4.763  < 2e-16 ***
## LIMeco       0.1322798  0.0322791   4.098  0.00006 ***
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
```

```
##
## Covariance Parameters:
##  Covariance.Model Parameter Estimate
##            Nugget   parsill  0.00162
##
## Residual standard error: 0.04026982
## Generalized R-squared: 0.3545288
```

We see that both landuse and water quality are important factors.

Now we can fit some spatial models. We start with the full autocovariance functions (Euclidean, Tail.up, Tail.down).

```
shr.1=glmssn(feed_shr~PCA1.long+buf.agr.p+LIMeco,spat.course.ssn,
             CorModels = c("Exponential.tailup", "Exponential.taildown",
   "Exponential.Euclid"), addfunccol = "afvArea", EstMeth = "ML")

summary(shr.1)
```

```
##
## Call:
## glmssn(formula = feed_shr ~ PCA1.long + buf.agr.p + LIMeco, ssn.object = spat.course.ssn,
##     CorModels = c("Exponential.tailup", "Exponential.taildown",
##         "Exponential.Euclid"), addfunccol = "afvArea", EstMeth = "ML")
##
## Residuals:
##       Min        1Q    Median        3Q       Max
## -0.073192 -0.023236 -0.003967  0.021409  0.166026
##
## Coefficients:
##               Estimate Std. Error t value Pr(>|t|)
## (Intercept)  0.0141687  0.0279533   0.507  0.61283
## PCA1.long   -0.0063257  0.0037939  -1.667  0.09709 .
## buf.agr.p   -0.0007112  0.0001586  -4.484  0.00001 ***
## LIMeco       0.1110628  0.0327433   3.392  0.00084 ***
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
##
## Covariance Parameters:
##      Covariance.Model Parameter        Estimate
##    Exponential.tailup   parsill       0.0003413
##    Exponential.tailup     range 1015608.7873397
##  Exponential.taildown   parsill       0.0000703
##  Exponential.taildown     range    8916.6028923
##    Exponential.Euclid   parsill       0.0002278
##    Exponential.Euclid     range    5548.2069642
##                Nugget   parsill       0.0009745
##
## Residual standard error: 0.04017313
## Generalized R-squared: 0.3256791
```

Here we see a different output. The variogram parameters for each autocovariance functions are also given. We also see that the model parameters (*Estimate, Std.Error*) are different from the non-spatial model. We also see that the Sill of the tail.down component is very small. We could eventually omit it from the model.

Model selection is a stepwise process. Once we are happy with the covariates (the fixed effect), we can work on the autocorrelation structures.

Here we fit a couple of additional models with different variogram functions.

```
shr.2=glmssn(feed_shr~PCA1.long+buf.agr.p+LIMeco,spat.course.ssn,
             CorModels = c( "LinearSill.tailup",
   "Exponential.Euclid"), addfunccol = "afvArea", EstMeth = "ML")

#summary(shr.2)
```

```
shr.3=glmssn(feed_shr~PCA1.long+buf.agr.p+LIMeco,spat.course.ssn,
             CorModels = c( "Exponential.tailup"), addfunccol = "afvArea", EstMeth = "ML")

#summary(shr.3)
```

```
shr.4=glmssn(feed_shr~PCA1.long+buf.agr.p+LIMeco,spat.course.ssn,
             CorModels = c( "Exponential.Euclid"), addfunccol = "afvArea", EstMeth = "ML")

#summary(shr.4)
```

We can then use the command *InfoCritCompare* to compare the different models for e.g. Root Mean Square Prediction Error (RMSPE) and AIC.

```
InfoCritCompare(list(shr.0, shr.1, shr.2, shr.3, shr.4))
```

```
##                                     formula EstMethod
## 1 feed_shr ~ PCA1.long + buf.agr.p + LIMeco        ML
## 2 feed_shr ~ PCA1.long + buf.agr.p + LIMeco        ML
## 3 feed_shr ~ PCA1.long + buf.agr.p + LIMeco        ML
## 4 feed_shr ~ PCA1.long + buf.agr.p + LIMeco        ML
## 5 feed_shr ~ PCA1.long + buf.agr.p + LIMeco        ML
##                                                    Variance_Components
## 1                                                                Nugget
## 2 Exponential.tailup + Exponential.taildown + Exponential.Euclid + Nugget
## 3                        LinearSill.tailup + Exponential.Euclid + Nugget
## 4                                            Exponential.tailup + Nugget
## 5                                            Exponential.Euclid + Nugget
##    neg2LogL       AIC           bias      std.bias      RMSPE        RAV
## 1 -699.3530 -689.3530 0.000009075508 0.00003360497 0.04101413 0.04069292
## 2 -708.8503 -686.8503 0.000309403257 0.00117571626 0.03891968 0.03920649
## 3 -709.6860 -691.6860 0.000321798906 0.00123339173 0.03893167 0.03884631
## 4 -707.2990 -693.2990 0.000293362168 0.00111114130 0.03926642 0.03932925
## 5 -703.7241 -689.7241 0.000031537393 0.00011793856 0.03979320 0.03956483
##    std.MSPE    cov.80    cov.90    cov.95
```

```
## 1 1.0184230 0.8205128 0.9076923 0.9487179
## 2 0.9955477 0.8153846 0.8923077 0.9435897
## 3 1.0098952 0.8102564 0.8974359 0.9435897
## 4 1.0078079 0.8153846 0.8871795 0.9435897
## 5 1.0138924 0.8307692 0.9128205 0.9384615
```

We can print specific values for clarity (e.g. Spatial components, AIC, RMSPE)

```
InfoCritCompare(list(shr.0, shr.1, shr.2, shr.3, shr.4))[,c(3,5,8,12)]
```

```
##                                                          Variance_Components
## 1                                                                     Nugget
## 2 Exponential.tailup + Exponential.taildown + Exponential.Euclid + Nugget
## 3                         LinearSill.tailup + Exponential.Euclid + Nugget
## 4                                             Exponential.tailup + Nugget
## 5                                             Exponential.Euclid + Nugget
##         AIC      RMSPE    cov.90
## 1 -689.3530 0.04101413 0.9076923
## 2 -686.8503 0.03891968 0.8923077
## 3 -691.6860 0.03893167 0.8974359
## 4 -693.2990 0.03926642 0.8871795
## 5 -689.7241 0.03979320 0.9128205
```

We see that spatial models including tail-up and/or tail-down (accounting for river topology) provide better predictions (lower RMSPE) than simple non-spatial model (shr.0), or models that only include Euclidean component (shr.4).

The *varcomp* function provide information on the variance components of the model (covariates + spatial components)

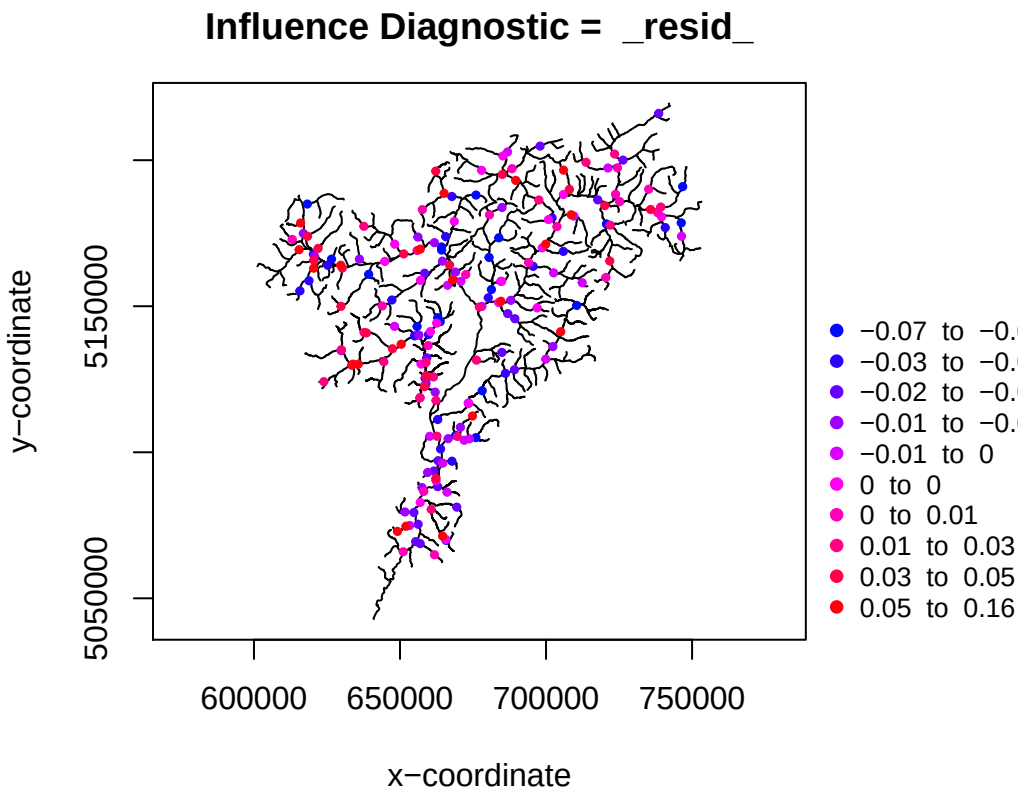
```
varcomp(shr.2)
```

```
##              VarComp Proportion
## 1  Covariates (R-sq) 0.33073666
## 2  LinearSill.tailup 0.15081926
## 3 Exponential.Euclid 0.43798818
## 4             Nugget 0.08045591
```

In the model *shr.2*, the included covariates (PCA1.long, Limeco, Buf.agr.p) explained 34% of variation. The tail-up autocovariance (reflecting correlation along flow-connected locations) accounted for 13% of variation, while the Euclidean covariance for 27%. The Nugget reflects the unexplained variance (with no spatial structure).

We can also plot the residuals of the model easily; this helps visualising spatial patterns in the residuals.

```
plot(resid(shr.2), asp=1, cex=0.5)
```



Excercise that you can try yourself:

- Plot additional variograms for other variables (e.g. feed_pre, Limeco, Shannon)
- Fit models for *Richness* using the same covariates used before.
- Try to fit both non-spatial and spatial models.
- Compare the models using *InfoCritCompare*. Which one gives better predictions (lower RMSPE)?

TIP

to plot the variogram over the three distances, use the example already provided. For *feed_pre* for instance:

```
emp.var.pre=EmpiricalSemivariogram(spat.course.ssn, 'feed_pre', nlag = 30, maxlag = 200000)
tor.pre=Torgegram(spat.course.ssn, 'feed_pre', nlag = 50, maxlag = 400000)
```

Then plot all together. Pay attention to the y-axis. For *feed_pre* the variance will be small (see: *tor.pre$gam.connect*). Set the ylim=c(0, 0.005) for visualization in this case.

TIP

Then you should try to fit a spatial and non-spatial model for *richness*. Follow the examples provided for shredders (*feed_shr*). Start with a non-spatial model (CorModels=NULL). Then fit a full spatial models with tail-up, tail-down and Euclidean components.