

Ancestral Graphs example with Stop-signal data

Sara Jahfari April 2017

Before running through the example bellow get an intuition for the method and stats reading Lourens Waldorp's 2011 NI paper [here](#).

1. Getting started

Ancestral Graphs relies on a number of packages such as `graphs`, `RBGL` and `ggm`. These packages are updated in a fast rate, and for now you will have to run an older version of R (version 3.0.2) in order to use the validated versions of these packages for AG. You can find the checked package versions in the folder `AG_codes/Rpackage_checked`.

For me it works really well to use `RSwch` to switch between the newest version of R and this older version for AG. After installing the older version of R, and using `RSwch` make sure that you are running R version 3.0.2 (2013-09-25).

```
# are you running the correct version of R?  
sessionInfo()
```

Now set the Base directory path to the `AG_stopexample` folder on your computer

```
# set datadir Base  
dir_base='/Users/sarajahfari/Github/AG_stopexample'  
  
#dir AG_codes, example_codes,  
dir_agcodes=paste(dir_base, '/AG_codes', sep='')  
dir_excodes=paste(dir_base, '/Example_codes', sep='')  
dir_data=paste(dir_base, '/Example_data', sep='')
```

and get/source the other required codes and packages

```
# source checked packages  
source("http://bioconductor.org/biocLite.R")  
biocLite("graph")  
source("http://bioconductor.org/biocLite.R")  
biocLite("RBGL")  
install.packages(paste(dir_agcodes, "/Rpackage_checked/ggm-1.995-3.tar.gz",  
  sep = ""), repos = NULL, type = "source")  
  
# source AG_codes  
file.sources = list.files(paste(dir_agcodes, "/rFunctions2",  
  sep = ""), pattern = "*.R", full.names = TRUE, recursive = T)  
sapply(file.sources, source, .GlobalEnv)
```

2. Get data, and define trials/conditions/regions

Read the single subjects data list with single trial estimates for a number of ROI's that will be used to infer connectivity. Next, I always create an index file that is easy to use with the AG codes.

```
# this reads the single subject data termed yDat, and creates  
# the condition indexes in a separate list  
source(paste(dir_excodes, "/index_yDatstop.R", sep = ""), chdir = F)  
head(yDat[[1]])
```

```
##           CaudateR40exc maxGPeR30exc maxGPiR30exc maxSTNR25exc      IFGR
## 01GoL_1      -0.595375      0.442298      0.066915      -0.031055 -0.329973
## 01GoL_10      0.105857      -0.026887      0.057072      -0.083707 -0.144638
## 01GoL_11      0.161698      0.380750      0.500733      -0.017357  0.291495
## 01GoL_12      -0.032499      0.463627      -0.033962      -0.052651  0.278092
## 01GoL_13      0.106706      0.105174      0.095832      0.159087  0.207860
## 01GoL_14      -0.500952      -0.032343      -0.253548      0.308119  0.607734
##           MotorCBA4aL PreSMARsmall ThalamusR40exc      type
## 01GoL_1      -0.398792      -0.369048      -0.183989  01GoL_1
## 01GoL_10      -0.194387      0.450988      0.012323  01GoL_10
## 01GoL_11      0.816016      0.066621      0.534921  01GoL_11
## 01GoL_12      0.268594      -0.064747      0.272632  01GoL_12
## 01GoL_13      0.298172      0.209098      0.401299  01GoL_13
## 01GoL_14      -0.012316      -0.080152      -0.199831  01GoL_14
```

Then, define the trial types of this task which you would like to model, and the nodes which should be in your model space

```
# these are the conditions that are evaluated separatly in
# FitmodelsStop.R (see below)
cond = list(ST, SR, Go, GoL, GoR)
names(cond) = c("ST", "SR", "Go", "GoL", "GoR")

# this is just a list with the row_indexes per subject for
# the succesfull stop trials
head(cond$ST)
```

```
## $`sub-001`
## [1] 50 51 52 53 54 55 56 57 58 59 60 61 124 125 126 127 128
## [18] 129 130 131 132 133 134 135
##
## $`sub-002`
## [1] 50 51 52 53 54 55 56 57 58 59 60 125 126 127 128 129 130
## [18] 131 132 133 134 135 136
##
## $`sub-003`
## [1] 51 52 53 54 55 56 57 58 59 60 61 126 127 128 129 130 131
## [18] 132 133 134 135 136 137 138 139 140
##
## $`sub-004`
## [1] 51 52 53 54 55 56 57 58 59 60 61 126 127 128 129 130 131
## [18] 132 133 134 135 136 137 138 139 140 141
##
## $`sub-005`
## [1] 49 50 51 52 53 54 55 56 57 58 122 123 124 125 126 127 128
## [18] 129 130 131 132 133 134
##
## $`sub-006`
## [1] 50 51 52 53 54 55 56 57 58 59 60 61 62 63 124 125 126
## [18] 127 128 129 130 131 132 133
```

```
# if responses are made with the left and right it can be
# difficult to fit the model with collapsed trials but also
# note that this wil reduce your number of trials by half
cond = list(STL, STR, SRL, SRR, GoL, GoR)
names(cond)=c('STL', 'STR', 'SRL', 'SRR', 'GoL', 'GoR')
```

```
# Define the nodes which should be in your model space
M0roi = c("CaudateR40exc", "PreSMARsmall", "IFGR", "maxSTNR25exc",
          "maxGPeR30exc", "maxGPiR30exc", "ThalamusR40exc")

C.Lab = M0roi # these are the regions that AG will use to evaluate connectivity between
```

3. Define the connectivity between nodes in different models

```
# source the models to use, these are the defined PFC-BG
# models to evaluate for connectivity/fits
source(paste(dir_excodes, "/StopModel.R", sep = ""), chdir = F)

# try [this is an interactive plot, you can change the layout
# of nodes and get out with esc]
drawGraph(Ag0) # see StopModel.R for definitions, but this should be the hyperdirect-Indirect model

# Now do the connectivity evaluation for each subject, each
# model/condition, to compute aic/bic and n-fits
source(paste(dir_excodes, "/FitmodelsStop.R", sep = ""), chdir = F)
```

Now evaluate fit and random effects AIC/BIC at group level

```
# this is the grouplevel AIC (see FitmodelsStop for code) for
# each model(cols)/condition(rows)
round(AMT, digits = 0)
```

	hindi	hyp	indir	dir	nfit-hindi	nfit-hyp	nfit-indir	nfit-dir
## ST	7161	8298	7509	7748	43	43	43	43
## SR	7456	8772	7955	8238	43	43	43	43
## Go	21763	25600	22884	23953	0	0	1	0
## GoL	11762	13772	12387	12902	11	5	16	13
## GoR	11397	13353	11998	12516	13	13	19	18

```
# this is the grouplevel BIC (see FitmodelsStop for code) for
# each model(cols)/condition(rows)
round(BMT, digits = 0)
```

	hindi	hyp	indir	dir	nfit-hindi	nfit-hyp	nfit-indir	nfit-dir
## ST	7241	8357	7574	7807	43	43	43	43
## SR	7536	8832	8020	8298	43	43	43	43
## Go	21864	25675	22965	24028	0	0	1	0
## GoL	11852	13840	12460	12969	11	5	16	13
## GoR	11486	13419	12070	12582	13	13	19	18

4. Select the winning model (hindi) to derive single subject connectivity estimates

```
# ag0 was the hindi model in StopModel.R
hindi = ag0

# conditions to get beta for [these are the conditions where
# the model fitted all ppn]
```

```

cond2 = list(ST, SR)
names(cond2) = c("ST", "SR")

# Make ST and SR lists using yDat
ST = list()
SR = list()

for (i in 1:length(yDat)) {
  ST[[i]] = yDat[[i]][cond2[[1]][[i]], C.Lab]
  SR[[i]] = yDat[[i]][cond2[[2]][[i]], C.Lab]
}

# compute covariance matrix
covList.ST = lapply(ST, cov)
covList.SR = lapply(SR, cov)

fitST = list()
fitSR = list()

for (i in 1:length(yDat)) {
  fitST[[i]] <- fitAncestralGraph(hindi, covList.ST[[i]], dim(ST[[i]])[1])
  fitSR[[i]] <- fitAncestralGraph(hindi, covList.SR[[i]], dim(SR[[i]])[1])
}

# compute the variance of beta per subject
var.g.ST <- ag.var.group(fitST, covList.ST, ST)
var.g.SR <- ag.var.group(fitSR, covList.SR, SR)

# save matrix for var beta and beta itself (zijn nog leeg)
varbeta.ST = matrix(, dim(var.g.ST)[3], dim(var.g.ST)[1])
varbeta.SR = matrix(, dim(var.g.SR)[3], dim(var.g.SR)[1])
beta.ST = matrix(, length(yDat), length(ag.theta(fitST[[1]])))
beta.SR = matrix(, length(yDat), length(ag.theta(fitSR[[1]])))

for (i in 1:length(yDat)) {
  varbeta.ST[i, ] = diag(var.g.ST[, , i])
  varbeta.SR[i, ] = diag(var.g.SR[, , i])
  beta.ST[i, ] = ag.theta(fitST[[i]])
  beta.SR[i, ] = ag.theta(fitSR[[i]])
}

# these are the standarized connections (to use for group
# comparisons)
sbeta.ST = round(beta.ST/varbeta.ST, dig = 8)
sbeta.SR = round(beta.SR/varbeta.SR, dig = 8)

```

Finally, select the defined directed and undirected connections and put this in a usable list which can be saved as tsv

```

# select the defined directed and undirected connections
beta.ST=beta.ST[,c(1:8,10)]
beta.SR=beta.SR[,c(1:8,10)]
sbeta.ST=sbeta.ST[,c(1:8,10)]

```

```

sbeta.SR=sbeta.SR[,c(1:8,10)]

colnames(beta.ST) =paste('ST-',c('caud->gpe','presma->caud','presma->stn','ifg->caud',
                                'ifg->stn','stn->gpi','gpe->gpi','gpi->thalamus',
                                'presma-ifg'),sep='')

colnames(beta.SR) =paste('SR-',c('caud->gpe','presma->caud','presma->stn','ifg->caud',
                                'ifg->stn','stn->gpi','gpe->gpi','gpi->thalamus',
                                'presma-ifg'),sep='')

colnames(sbeta.ST) =colnames(beta.ST)
colnames(sbeta.SR) =colnames(beta.SR)

Beta_output=list(Connectivity_ST=beta.ST, Connectivity_SR=beta.SR,standarized_con_ST=sbeta.ST,standarized_con_SR=sbeta.SR)

for (rn in 1:length(Beta_output)) {rownames(Beta_output[[rn]])=names(yDat)}
}

```

```

# arrow is direct in col.names, and - (presma-ifg) is undirected
head(Beta_output$Connectivity_ST)

```

```

##           ST-caud->gpe ST-presma->caud ST-presma->stn ST-ifg->caud
## sub-001  -0.32534493   -0.55749704   -0.007316717  0.266109294
## sub-002  -0.48860562   -0.33756271   -0.276528991  0.002147515
## sub-003   0.08619859   -0.40180361   -0.041358759  0.035535550
## sub-004  -0.24045212   -0.20431636    0.628892409 -0.358360363
## sub-005  -0.12537864   -0.38403947    0.126770183 -0.227053967
## sub-006  -0.44078481   -0.02563003    0.128984510 -0.443016775
##           ST-ifg->stn ST-stn->gpi ST-gpe->gpi ST-gpi->thalamus
## sub-001 -0.141143328  0.003738614  -0.4264254   -0.14515365
## sub-002  0.114201882  0.055687908  -0.7558637   -1.57800436
## sub-003  0.003940724  0.208368482  -0.8793710   -0.29854938
## sub-004 -0.816364543 -0.207181870  -0.2668323   -0.43127709
## sub-005 -0.396544915  0.061684750  -0.6557039   -0.05550985
## sub-006 -0.395269876  0.105049133  -0.5514878   -0.22893107
##           ST-presma-ifg
## sub-001    0.4615812
## sub-002    0.3413610
## sub-003    0.1925970
## sub-004    0.2600340
## sub-005    0.0893940
## sub-006    0.3113932

```

```

# arrow is direct in col.names, and - (presma-ifg) is undirected
head(Beta_output$standarized_con_ST)

```

```

##           ST-caud->gpe ST-presma->caud ST-presma->stn ST-ifg->caud
## sub-001  -0.00009765   -0.00005072   -0.00000064  0.00002781
## sub-002  -0.00000096   -0.00074737   -0.00002196  0.00001327
## sub-003   0.00402757   -0.70181803   -0.02425740  0.02596681
## sub-004  -0.00017681   -0.00009260    0.00002705 -0.00017788
## sub-005  -0.00122267   -0.00751744    0.00037188 -0.00204955
## sub-006  -0.00001853   -0.00018219    0.00050155 -0.00007106
##           ST-ifg->stn ST-stn->gpi ST-gpe->gpi ST-gpi->thalamus ST-presma-ifg

```

## sub-001	-0.00001255	0.00000026	-0.00000768	-0.00000097	0.00034208
## sub-002	0.00012644	0.00000100	-0.00000632	-0.00000051	0.00003346
## sub-003	0.01039742	0.02229524	-0.00324629	-0.00356488	0.01971200
## sub-004	-0.00007555	-0.00000733	-0.00001859	-0.00001560	0.00133518
## sub-005	-0.00057094	0.00007966	-0.00022248	-0.00005725	0.00468278
## sub-006	-0.00000868	0.00000170	-0.00000289	-0.00000834	0.00011922

All of these steps are also in the *EvaluateStop_example.R*. If you have questions let me know. Have fun!