

Applied SNA with R

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Chapter 1

About this book

This book will be build as part of a workshop on Applied Social Network Analysis with R. Its contents will be populated as the sessions take place, and for now there is particular program that we will follow, instead, we have the following workflow:

1. Participants will share their data and what they need to do with it.
2. Based on their data, I'll be preparing the sessions trying to show attendees how would I approach the problem, and at the same time, teach by example about the R language.
3. Materials will be published on this website and, hopefully, video recordings of the sessions.

At least in the first version, the book will be organized by session, this is, one chapter per session.

All the book materials can be downloaded from <https://github.com/>

[gvegayon/appliedsnar](https://gvegayon.com/appliedsnar)

In general, besides R itself, we will be using R studio and the following R packages: dplyr for data management, stringr for data cleaning, and of course igraph, netdiffuseR (a bit of a bias here), and statnet for our neat network analysis.¹

¹Some of you may be wondering “what about ggplot2 and friends? What about [tidyverse](#)”, well, my short answer is I jumped into R before all of that was that popular. When I started plots were all about [lattice](#), and after a couple of years on that, about base R graphics. What I’m saying is that so far I have not find a compelling reason to leave my “old-practices” and embrace all the tidyverse movement (religion?).

Chapter 2

Introduction

For this book we need the following

R Core Team ([2017b](#))

1. Install R from CRAN: <https://www.r-project.org/>
2. (optional) Install Rstudio: <https://rstudio.org>

While I find RStudio extremely useful, it is not necessary to use it with R.

Chapter 3

R Basics

3.1 What is R

A good reference book for both new and advanced user is [“The Art of R programming”](#) (Matloff 2011)¹

3.2 How to install packages

Nowadays there are two ways of installing R packages (that I’m aware of), either using `install.packages`, which is a function shipped with R, or use the `devtools` R package to install a package from some remote repository other than CRAN, here is a couple of examples:

```
# This will install the igraph package from CRAN  
> install.packages("netdiffuseR")
```

¹[Here](#) a free pdf version distributed by the author.

```
# This will install the bleeding-edge version from the project's github repo  
> devtools::install_github("USCCANA/netdiffuseR")
```

The first one, using `install.packages`, installs the CRAN version of `netdiffuseR`, whereas the second installs whatever version is published on <https://github.com/USCCANA/netdiffuseR>, which is usually called the development version.

In some cases users may want/need to install packages from command line as some packages need extra configuration to be installed. But we won't need to look at it now.

Chapter 4

Network Nomination Data

The data can be downloaded from [here](#).

The codebook for the data provided here is in [the appendix](#).

This chapter's goals are:

1. Read the data into R,
2. Create a network with it,
3. Compute descriptive statistics
4. Visualize the network

4.1 Data preprocessing

4.1.1 Reading the data into R

R has several ways of reading data in. Your data can be raw plain files like CSV, tab delimited or specified by column width, for which you can use the `readr` package (Wickham, Hester, and Francois 2017); or it can be binary files like dta (Stata), Octave, SPSS, for which `foreign` (R Core Team 2017a) can be used; or it could be excel files in which case you should be using `readxl` (Wickham and Bryan 2017). In our case, the data for this session is in Stata format:

```
library(foreign)

# Reading the data
dat <- foreign::read.dta("03-sns.dta")

# Taking a look at the data's first 5 columns and 5 rows
dat[1:5, 1:10]
```

```
##   photoid school hispanic female1 female2 female3 female4 grades1 grades2
## 1      1     111        1      NA      NA      0      0      NA      NA
## 2      2     111        1       0     NA     NA      0     3.0     NA
## 3      7     111        0       1       1       1       1     5.0     4.5
## 4     13     111        1       1       1       1       1     2.5     2.5
## 5     14     111        1       1       1       1     NA     3.0     3.5
##   grades3
## 1     3.5
## 2     NA
```

```
## 3      4.0
## 4      2.5
## 5      3.5
```

4.1.2 Creating a unique id for each participant

Now suppose that we want to create a unique id using the school and photo id. In this case, since both variables are numeric, a good way of doing it is to encode the id such that, for example, the last three x numbers are the photoid and the first ones are the school id. To do this we need to take into account the range of the variables. Here, photoid has the following range:

```
(photo_id_ran <- range(dat$photoid))
```

```
## [1]    1 2074
```

As the variable spans up to 2074, we need to set the last 4 units of the variable to store the photoid. We will use `dplyr` (Wickham et al. 2017) and `magrittr` (Bache and Wickham 2014)] (the pipe operator, `%>%`) to create this variable, and we will call it... `id` (mind blowing, right?):

```
library(dplyr)
```

```
##
```

```
## Attaching package: 'dplyr'
```

```
## The following objects are masked from 'package:stats':
```

```
##
```

```
##      filter, lag
```

```
## The following objects are masked from 'package:base':
##
## intersect, setdiff, setequal, union
```

```
library(magrittr)

(dat %<>% mutate(id = school*10000 + photoid)) %>%
  head %>%
  select(school, photoid, id)
```

```
##   school photoid    id
## 1     111      1 1110001
## 2     111      2 1110002
## 3     111      7 1110007
## 4     111     13 1110013
## 5     111     14 1110014
## 6     111     15 1110015
```

Wow, what happened in the last three lines of code! What is that %>%? Well, that's the [piping operator](#), and it is a very nice way of writing nested function calls. In this case, instead of having write something like

```
dat_filtered$id <- dat_filtered$school*10000 + dat_filtered$photoid
subset(head(dat_filtered), select = c(school, photoid, id))
```

4.2 Creating a network

- We want to build a social network. For that, we either use an adjacency matrix or an edgelist.
- Each individual of the SNS data nominated 19 friends from school. We will use those nominations to create the social network.
- In this case, we will create the network by coercing the dataset into an edgelist.

4.2.1 From survey to edgelist

Let's start by loading a couple of handy R packages for this task, `tidyr` (Wickham and Henry 2017), which we will use to reshape the data, and `stringr` (Wickham 2017), which we will use to process strings using *regular expressions*¹.

```
library(tidyr)
library(stringr)
```

Optionally, we can use the `tibble` type of object which is an alternative to the actual `data.frame`. This object is claimed to provide *more efficient methods for matrices and data frames*.

```
dat <- as_tibble(dat)
```

What I like from tibbles is that when you print them on the console these actually look nice:

¹Please refer to the help file `?'regular expression'` in R. The R package `rex` (Ushey, Hester, and Krzyzanowski 2017) is a very nice companion for writing regular expressions. There's also a neat (but experimental) RStudio addin that can be very helpful for understanding how regular expressions work, the `regexplain` addin.

```
dat
```

```
## # A tibble: 2,164 x 100
##   photoid school hispanic female1 female2 female3 female4 grades1 grades2
##   <int> <int>    <dbl>   <int>   <int>   <int>   <int>   <dbl> <dbl>
## 1      1    111      1    NA     NA      0      0    NA    NA
## 2      2    111      1      0    NA     NA      0      3    NA
## 3      7    111      0      1      1      1      1      5      4
## 4     13    111      1      1      1      1      1     2.5    2
## 5     14    111      1      1      1      1     NA      3      3
## 6     15    111      1      0      0      0      0     2.5    2
## 7     20    111      1      1      1      1      1     2.5    2
## 8     22    111      1    NA     NA      0      0    NA    NA
## 9     25    111      0      1      1     NA      1     4.5    3
## 10    27    111      1      0    NA      0      0     3.5    NA
## # ... with 2,154 more rows, and 91 more variables: grades3 <dbl>,
## #   grades4 <dbl>, everismk1 <int>, everismk2 <int>, everismk3 <int>,
## #   everismk4 <int>, everdrk1 <int>, everdrk2 <int>, everdrk3 <int>,
## #   everdrk4 <int>, home1 <int>, home2 <int>, home3 <int>, home4 <int>,
## #   sch_friend11 <int>, sch_friend12 <int>, sch_friend13 <int>,
## #   sch_friend14 <int>, sch_friend15 <int>, sch_friend16 <int>,
## #   sch_friend17 <int>, sch_friend18 <int>, sch_friend19 <int>,
## #   sch_friend110 <int>, sch_friend111 <int>, sch_friend112 <int>,
## #   sch_friend113 <int>, sch_friend114 <int>, sch_friend115 <int>,
## #   sch_friend116 <int>, sch_friend117 <int>, sch_friend118 <int>,
## #   sch_friend119 <int>, sch_friend21 <int>, sch_friend22 <int>,
## #   sch_friend23 <int>, sch_friend24 <int>, sch_friend25 <int>,
## #   sch_friend26 <int>, sch_friend27 <int>, sch_friend28 <int>,
```



```
## # sch_friend29 <int>, sch_friend210 <int>, sch_friend211 <int>,
## # sch_friend212 <int>, sch_friend213 <int>, sch_friend214 <int>,
## # sch_friend215 <int>, sch_friend216 <int>, sch_friend217 <int>,
## # sch_friend218 <int>, sch_friend219 <int>, sch_friend31 <int>,
## # sch_friend32 <int>, sch_friend33 <int>, sch_friend34 <int>,
## # sch_friend35 <int>, sch_friend36 <int>, sch_friend37 <int>,
## # sch_friend38 <int>, sch_friend39 <int>, sch_friend310 <int>,
## # sch_friend311 <int>, sch_friend312 <int>, sch_friend313 <int>,
## # sch_friend314 <int>, sch_friend315 <int>, sch_friend316 <int>,
## # sch_friend317 <int>, sch_friend318 <int>, sch_friend319 <int>,
## # sch_friend41 <int>, sch_friend42 <int>, sch_friend43 <int>,
## # sch_friend44 <int>, sch_friend45 <int>, sch_friend46 <int>,
## # sch_friend47 <int>, sch_friend48 <int>, sch_friend49 <int>,
## # sch_friend410 <int>, sch_friend411 <int>, sch_friend412 <int>,
## # sch_friend413 <int>, sch_friend414 <int>, sch_friend415 <int>,
## # sch_friend416 <int>, sch_friend417 <int>, sch_friend418 <int>,
## # sch_friend419 <int>, id <dbl>
```

Maybe too much piping... but its cool!

```
net <- dat %>%
  select(id, school, starts_with("sch_friend")) %>%
  gather(key = "varname", value = "content", -id, -school) %>%
  filter(!is.na(content)) %>%
  mutate(
    friendid = school*10000 + content,
    year      = as.integer(str_extract(varname, "(?<=[a-z])[0-9]")),
    nnom      = as.integer(str_extract(varname, "(?<=[a-z][0-9])[0-9]+"))
  )
```

Let's take a look at this step by step:

1. First, we subset the data: We want to keep `id`, `school`, `sch_friend*`. For the later we use the function `starts_with` (from the `tidyselect` package). This allows us to select all variables that starts with the word "sch_friend", which means that `sch_friend11`, `sch_friend12`, ... will all be selected.

```
dat %>%
```

```
  select(id, school, starts_with("sch_friend"))
```

```
## # A tibble: 2,164 x 78
```

```
##       id school sch_friend11 sch_friend12 sch_friend13 sch_friend14
```

```
##    <dbl> <int>      <int>      <int>      <int>      <int>
```

```
##  1 1.11e6   111         NA         NA         NA         NA
```

```
##  2 1.11e6   111        424        423        426        289
```

```
##  3 1.11e6   111        629        505         NA         NA
```

```
##  4 1.11e6   111        232        569         NA         NA
```

```
##  5 1.11e6   111        582        134         41        592
```

```
##  6 1.11e6   111         26        488         81        138
```

```
##  7 1.11e6   111        528         NA        492        395
```

```
##  8 1.11e6   111         NA         NA         NA         NA
```

```
##  9 1.11e6   111        135        185        553         84
```

```
## 10 1.11e6   111        346        168        559         5
```

```
## # ... with 2,154 more rows, and 72 more variables: sch_friend15 <int>
```

```
## #   sch_friend16 <int>, sch_friend17 <int>, sch_friend18 <int>,
```

```
## #   sch_friend19 <int>, sch_friend110 <int>, sch_friend111 <int>,
```

```
## #   sch_friend112 <int>, sch_friend113 <int>, sch_friend114 <int>,
```

```
## #   sch_friend115 <int>, sch_friend116 <int>, sch_friend117 <int>,
```

```
## # sch_friend118 <int>, sch_friend119 <int>, sch_friend21 <int>,
## # sch_friend22 <int>, sch_friend23 <int>, sch_friend24 <int>,
## # sch_friend25 <int>, sch_friend26 <int>, sch_friend27 <int>,
## # sch_friend28 <int>, sch_friend29 <int>, sch_friend210 <int>,
## # sch_friend211 <int>, sch_friend212 <int>, sch_friend213 <int>,
## # sch_friend214 <int>, sch_friend215 <int>, sch_friend216 <int>,
## # sch_friend217 <int>, sch_friend218 <int>, sch_friend219 <int>,
## # sch_friend31 <int>, sch_friend32 <int>, sch_friend33 <int>,
## # sch_friend34 <int>, sch_friend35 <int>, sch_friend36 <int>,
## # sch_friend37 <int>, sch_friend38 <int>, sch_friend39 <int>,
## # sch_friend310 <int>, sch_friend311 <int>, sch_friend312 <int>,
## # sch_friend313 <int>, sch_friend314 <int>, sch_friend315 <int>,
## # sch_friend316 <int>, sch_friend317 <int>, sch_friend318 <int>,
## # sch_friend319 <int>, sch_friend41 <int>, sch_friend42 <int>,
## # sch_friend43 <int>, sch_friend44 <int>, sch_friend45 <int>,
## # sch_friend46 <int>, sch_friend47 <int>, sch_friend48 <int>,
## # sch_friend49 <int>, sch_friend410 <int>, sch_friend411 <int>,
## # sch_friend412 <int>, sch_friend413 <int>, sch_friend414 <int>,
## # sch_friend415 <int>, sch_friend416 <int>, sch_friend417 <int>,
## # sch_friend418 <int>, sch_friend419 <int>
```

2. Then, we reshape it to *long* format: By transposing all the `sch_friend*` to long. We do this by means of the function `gather` (from the `tidyr` package). This is an alternative to the `reshape` function, and I personally find it easier to use. Let's see how it works:

```
dat %>%
  select(id, school, starts_with("sch_friend")) %>%
  gather(key = "varname", value = "content", -id, -school)
```

```
## # A tibble: 164,464 x 4
##       id school varname      content
##   <dbl> <int> <chr>      <int>
## 1 1110001    111 sch_friend11      NA
## 2 1110002    111 sch_friend11     424
## 3 1110007    111 sch_friend11     629
## 4 1110013    111 sch_friend11     232
## 5 1110014    111 sch_friend11     582
## 6 1110015    111 sch_friend11      26
## 7 1110020    111 sch_friend11     528
## 8 1110022    111 sch_friend11      NA
## 9 1110025    111 sch_friend11     135
## 10 1110027    111 sch_friend11     346
## # ... with 164,454 more rows
```

In this case the `key` parameter sets the name of the variable that will contain the name of the variable that was reshaped, while `value` is the name of the variable that will hold the content of the data (that's why I named those like that). The `-id, -school` bit tells the function to “drop” those variables before reshaping, in other words, “reshape everything but `id` and `school`”.

Also, notice that we passed from 2164 rows to 19 (nominations) * 2164 (subjects) * 4 (waves) = 164464 rows, as expected.

3. As the nomination data can be empty for some cells, we need to

take care of those cases, the NAs, so we filter the data:

```
dat %>%
  select(id, school, starts_with("sch_friend")) %>%
  gather(key = "varname", value = "content", -id, -school) %>%
  filter(!is.na(content))
```

```
## # A tibble: 39,561 x 4
##       id school varname      content
##   <dbl> <int> <chr>      <int>
## 1 1110002    111 sch_friend11    424
## 2 1110007    111 sch_friend11    629
## 3 1110013    111 sch_friend11    232
## 4 1110014    111 sch_friend11    582
## 5 1110015    111 sch_friend11     26
## 6 1110020    111 sch_friend11    528
## 7 1110025    111 sch_friend11    135
## 8 1110027    111 sch_friend11    346
## 9 1110029    111 sch_friend11    369
## 10 1110030    111 sch_friend11    462
## # ... with 39,551 more rows
```

4. And finally, we create three new variables from this dataset: friendid, year, and nom_num (nomination number). All this using regular expressions:

```
dat %>%
  select(id, school, starts_with("sch_friend")) %>%
  gather(key = "varname", value = "content", -id, -school) %>%
  filter(!is.na(content)) %>%
```

```
mutate(
  friendid = school*10000 + content,
  year      = as.integer(str_extract(varname, "(?<=[a-z])[0-9]")),
  nnom      = as.integer(str_extract(varname, "(?<=[a-z][0-9])[0-9]+"))
)
```

```
## # A tibble: 39,561 x 7
```

```
##       id school varname      content friendid  year  nnom
##    <dbl> <int> <chr>          <int>    <dbl> <int> <int>
##  1 1110002   111 sch_friend11    424  1110424     1     1
##  2 1110007   111 sch_friend11    629  1110629     1     1
##  3 1110013   111 sch_friend11    232  1110232     1     1
##  4 1110014   111 sch_friend11    582  1110582     1     1
##  5 1110015   111 sch_friend11     26  1110026     1     1
##  6 1110020   111 sch_friend11    528  1110528     1     1
##  7 1110025   111 sch_friend11    135  1110135     1     1
##  8 1110027   111 sch_friend11    346  1110346     1     1
##  9 1110029   111 sch_friend11    369  1110369     1     1
## 10 1110030   111 sch_friend11    462  1110462     1     1
## # ... with 39,551 more rows
```

The regular expression `(?<=[a-z])` matches a string that is preceeded by any letter from *a* to *z*, whereas the expression `[0-9]` matches a single number. Hence, from the string "sch_friend12", the regular expression will only match the 1, as it is the only number followed by a letter. On the other hand, the expression `(?<=[a-z][0-9])` matches a string that is preceeded by a letter from *a* to *z* and a number from 0 to 9; and

the expression `[0-9]+` matches a string of numbers—so it could be more than one. Hence, from the string `"sch_friend12"`, we will get 2. We can actually see this

```
str_extract("sch_friend12", "(?<=[a-z])[0-9]")
```

```
## [1] "1"
```

```
str_extract("sch_friend12", "(?<=[a-z][0-9])[0-9]+")
```

```
## [1] "2"
```

And finally, the `as.integer` function coerces the returning value from the `str_extract` function from character to integer. Now that we have this edgelist, we can create an `igraph` object

4.2.2 igraph network

For coercing the edgelist into an `igraph` object, we will be using the `graph_from_data_frame` function in `igraph` (Csardi and Nepusz 2006). This function receives a data frame where the two first columns are `source(ego)` and `target(alter)`, whether is it directed or not, and an optional data frame with vertices, in which's first column should contain the vertex ids.

Using the optional vertices argument is a good practice since by doing so you are telling the function what is the set of vertex ids that you are expecting to find. Using the original dataset, we will create a data frame name vertices:

```
vertex_attrs <- dat %>%  
  select(id, school, hispanic, female1, starts_with("eversmk"))
```

Now, let's now use the function `graph_from_data_frame` to create an `igraph` object:

```
library(igraph)

ig_year1 <- net %>%
  filter(year == "1") %>%
  select(id, friendid, nnom) %>%
  graph_from_data_frame(
    vertices = vertex_attrs
  )
```

```
## Error in graph_from_data_frame(., vertices = vertex_attrs): Some vertex
```

Ups! It seems that individuals are making nominations to other students that were not included on the survey. How to solve that? Well, it all depends on what you need to do! In this case, we will go for the *quietly-remove-em'-and-don't-tell* strategy:

```
ig_year1 <- net %>%
  filter(year == "1") %>%

  # Extra line, all nominations must be in ego too.
  filter(friendid %in% id) %>%

  select(id, friendid, nnom) %>%
  graph_from_data_frame(
    vertices = vertex_attrs
  )
```



```
ig_year1
```

```
## IGRAPH 23a67a2 DN-- 2164 9514 --
## + attr: name (v/c), school (v/n), hispanic (v/n), female1 (v/n),
## | everismk1 (v/n), everismk2 (v/n), everismk3 (v/n), everismk4 (v/n),
## | nnom (e/n)
## + edges from 23a67a2 (vertex names):
## [1] 1110007->1110629 1110013->1110232 1110014->1110582 1110015->1110026
## [5] 1110025->1110135 1110027->1110346 1110029->1110369 1110035->1110034
## [9] 1110040->1110390 1110041->1110557 1110044->1110027 1110046->1110030
## [13] 1110050->1110086 1110057->1110263 1110069->1110544 1110071->1110167
## [17] 1110072->1110289 1110073->1110014 1110075->1110352 1110084->1110305
## [21] 1110086->1110206 1110093->1110040 1110094->1110483 1110095->1110043
## + ... omitted several edges
```

So there we have, our network with 2164 nodes and 9514 edges. The next steps: get some descriptive stats and visualize our network.

4.3 Network descriptive stats

While we could do all networks at once, in this part we will focus on computing some network statistics for one of the schools only. We start by school 111. The first question that you should be asking your self now is, “how can I get that information from the igraph object?”. Well, vertex attributes and edges attributes can be accessed via the V and E functions respectively; moreover, we can list what vertex/edge attributes are available:

```
list.vertex.attributes(ig_year1)
```

```
## [1] "name"      "school"    "hispanic"  "female1"   "eversmk1"  "eversmk2"
## [7] "eversmk3"  "eversmk4"
```

```
list.edge.attributes(ig_year1)
```

```
## [1] "nnom"
```

Just like we would do with data frames, accessing vertex attributes is done via the dollar sign operator `$` together with the `V` function, for example, accessing the first 10 elements of the variable `hispanic` can be done as follows:

```
V(ig_year1)$hispanic[1:10]
```

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

Now that you know how to access vertex attributes, we can get the network corresponding to school 111 by identifying which vertices are part of it and pass that information to the `induced_subgraph` function:

```
# Which ids are from school 111?
school111ids <- which(V(ig_year1)$school == 111)

# Creating a subgraph
ig_year1_111 <- induced_subgraph(
  graph = ig_year1,
  vids  = school111ids
)
```

The `which` function in R returns a vector of indices indicating which elements are true. In our case it will return a vector of indices of the

vertices which have the attribute `school` equal to 111. Now that we have our subgraph, we can compute different centrality measures² for each vertex and store them in the `igraph` object itself:

```
# Computing centrality measures for each vertex
V(ig_year1_111)$indegree <- degree(ig_year1_111, mode = "in")
V(ig_year1_111)$outdegree <- degree(ig_year1_111, mode = "out")
V(ig_year1_111)$closeness <- closeness(ig_year1_111, mode = "total")

## Warning in closeness(ig_year1_111, mode = "total"): At centrality.c:
## 2784 :closeness centrality is not well-defined for disconnected graphs
V(ig_year1_111)$betweenness <- betweenness(ig_year1_111, normalized = TRUE)
```

From here, we can *go back* to our old habits and get the set of vertex attributes as a data frame so we can compute some summary statistics on the centrality measurements that we just got

```
# Extracting each vertex features as a data.frame
stats <- as_data_frame(ig_year1_111, what = "vertices")

# Computing quantiles for each variable
stats_degree <- with(stats, {
  cbind(
    indegree = quantile(indegree, c(.025, .5, .975)),
    outdegree = quantile(outdegree, c(.025, .5, .975)),
    closeness = quantile(closeness, c(.025, .5, .975)),
    betweenness = quantile(betweenness, c(.025, .5, .975))
  )
})
```

²For more information about the different centrality measurements, please take a look at the “Centrality” article on [Wikipedia](#).

```
})
```

```
stats_degree
```

```
##      indegree outdegree   closeness betweenness
## 2.5%         0         0 3.526640e-06 0.0000000000
## 50%          4         4 1.595431e-05 0.001879006
## 97.5%        16        16 1.601822e-05 0.016591048
```

The `with` function is somewhat similar to what `dplyr` allows us to do when we want to work with the dataset but without mentioning its name everytime that we ask for a variable. Without using the `with` function, the previous could have been done as follows:

```
stats_degree <-
```

```
  cbind(
    indegree  = quantile(stats$indegree, c(.025, .5, .975)),
    outdegree = quantile(stats$outdegree, c(.025, .5, .975)),
    closeness = quantile(stats$closeness, c(.025, .5, .975)),
    betweenness = quantile(stats$betweenness, c(.025, .5, .975))
  )
```

Now we will compute some statistics at the graph level:

```
cbind(
  size      = vcount(ig_year1_111),
  nedges    = ecountr(ig_year1_111),
  density   = edge_density(ig_year1_111),
  recip     = reciprocity(ig_year1_111),
  centr     = centr_betw(ig_year1_111)$centralization,
```

```
pathLen = mean_distance(ig_year1_111)
)
```

```
##      size nedges      density      recip      centr pathLen
## [1,]   533    2638 0.009303277 0.3731513 0.02179154 4.23678
```

Triadic census

```
triadic <- triad_census(ig_year1_111)
triadic
```

```
## [1] 24059676  724389  290849   3619   3383   4401   3219
## [8]    2997    407    33    836    235    163    137
## [15]    277    85
```

To get a nicer view of this, we can use a table that I retrieved from `?triad_census`. Moreover, instead of looking at the raw counts, we can normalize the triadic object by its sum so we get proportions instead³

```
knitr::kable(cbind(
  Pcent = triadic/sum(triadic)*100,
  read.csv("triadic_census.csv")
), digits = 2)
```

³During our workshop, Prof. De la Haye suggested using $\binom{n}{3}$ as a normalizing constant. It turns out that $\text{sum}(\text{triadic}) = \text{choose}(n, 3)!$ So either approach is correct.

Pcent	code	description
95.88	003	A,B,C, the empty graph.
2.89	012	A->B, C, the graph with a single directed edge.
1.16	102	A<->B, C, the graph with a mutual connection between two vertices.
0.01	021D	A<-B->C, the out-star.
0.01	021U	A->B<-C, the in-star.
0.02	021C	A->B->C, directed line.
0.01	111D	A<->B<-C.
0.01	111U	A<->B->C.
0.00	030T	A->B<-C, A->C.
0.00	030C	A<-B<-C, A->C.
0.00	201	A<->B<->C.
0.00	120D	A<-B->C, A<->C.
0.00	120U	A->B<-C, A<->C.
0.00	120C	A->B->C, A<->C.
0.00	210	A->B<->C, A<->C.
0.00	300	A<->B<->C, A<->C, the complete graph.

4.4 Plotting the network in igraph

4.4.1 Single plot

Let's take a look at how does our network looks like when we use the default parameters in the plot method of the igraph object:

```
plot(ig_year1)
```

Not very nice, right? A couple of things with this plot:

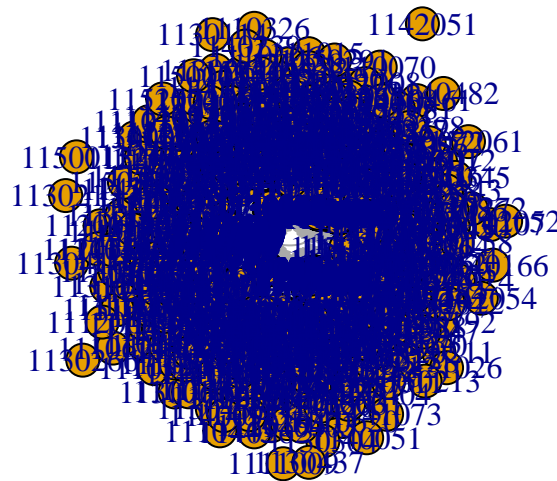


Figure 4.1: A not very nice network plot. This is what we get with the default parameters in igraph.

1. We are looking at all schools simultaneously, which does not make sense. So, instead of plotting `ig_year1`, we will focus on `ig_year1_111`.
2. All the vertices have the same size, and more over, are overlapping. So, instead of using the default size, we will size the vertices by indegree using the degree function, and passing the vector of degrees to `vertex.size`.⁴
3. Given the number of vertices in these networks, the labels are not useful here. So we will remove them by setting `vertex.label = NA`. Moreover, we will reduce the size of the arrows' tip by setting `edge.arrow.size = 0.25`.
4. And finally, we will set the color of each vertex to be a function

⁴Figuring out what is the optimal vertex size is a bit tricky. Without getting too technical, there's no other way of getting *nice* vertex size other than just playing with different values of it. A nice solution to this is using `netdiffuser::igraph_vertex_rescale` which rescales the vertices so that these keep their aspect ratio to a predefined proportion of the screen.

of whether the individual is hispanic or not. For this last bit we need to go a bit more of programming:

```
col_hispanic <- V(ig_year1_111)$hispanic + 1
col_hispanic <- coalesce(col_hispanic, 3)
col_hispanic <- c("steelblue", "tomato", "white")[col_hispanic]
```

Line by line, we did the following:

1. The first line added one to all no NA values, so that the 0s (non-hispanic) turned to 1s and the 1s (hispanic) turned to 2s.
2. The second line replaced all NAs with the number 3, so that our vector `col_hispanic` now ranges from 1 to 3 with no NAs in it.
3. In the last line we created a vector of colors. Essentially, what we are doing here is telling R to create a vector of length `length(col_hispanic)` by selecting elements by index from the vector `c("steelblue", "tomato", "white")`. This way, if, for example, the first element of the vector `col_hispanic` was a 3, our new vector of colors would have a "white" in it.

To make sure we know we are right, let's print the first 10 elements of our new vector of colors together with the original hispanic column:

```
cbind(
  original = V(ig_year1_111)$hispanic[1:10],
  colors    = col_hispanic[1:10]
)
```

```
##      original colors
## [1,] "1"         "tomato"
## [2,] "1"         "tomato"
```



```
## [3,] "0"      "steelblue"
## [4,] "1"      "tomato"
## [5,] "1"      "tomato"
## [6,] "1"      "tomato"
## [7,] "1"      "tomato"
## [8,] "1"      "tomato"
## [9,] "0"      "steelblue"
## [10,] "1"     "tomato"
```

With our nice vector of colors, now we can pass it to `plot.igraph` (which we call implicitly by just calling `plot`), via the `vertex.color` argument:

```
# Fancy graph
set.seed(1)
plot(
  ig_year1_111,
  vertex.size      = degree(ig_year1_111)/10 + 1,
  vertex.label     = NA,
  edge.arrow.size = .25,
  vertex.color     = col_hispanic
)
```

Nice! So it does look better. The only problem is that we have a lot of isolates. Let's try again by drawing the same plot without isolates. To do so we need to filter the graph, for which we will use the function `induced_subgraph`

```
# Which vertices are not isolates?
which_ids <- which(degree(ig_year1_111, mode = "total") > 0)
```

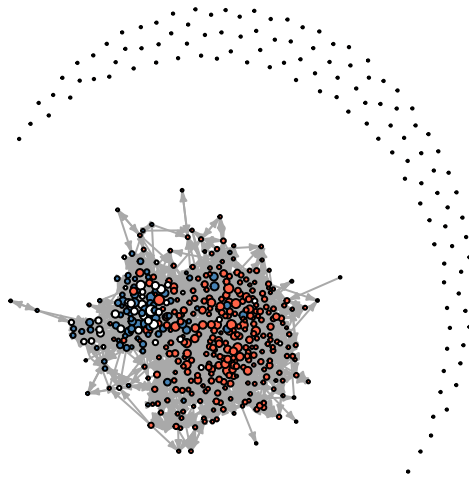


Figure 4.2: Friends network in time 1 for school 111.

```
# Getting the subgraph
ig_year1_111_sub <- induced_subgraph(ig_year1_111, which_ids)

# We need to get the same subset in col_hispanic
col_hispanic <- col_hispanic[which_ids]

# Fancy graph
set.seed(1)
plot(
  ig_year1_111_sub,
  vertex.size      = degree(ig_year1_111_sub)/5 + 1,
  vertex.label     = NA,
  edge.arrow.size  = .25,
  vertex.color     = col_hispanic
)
```

Now that's better! An interesting pattern that shows up is that individ-

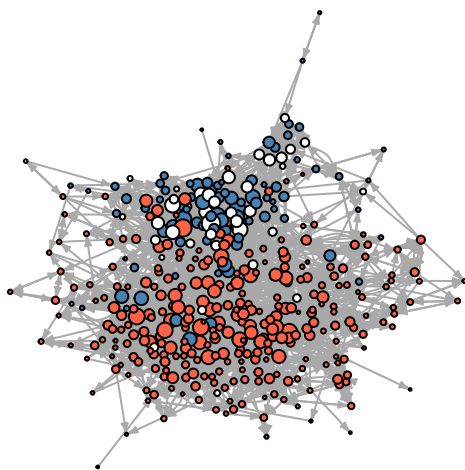


Figure 4.3: Friends network in time 1 for school 111. The graph excludes isolates.

uals seem to cluster by whether they are hispanic or not.

We can actually write this as a function so that, instead of us copying and pasting the code n times (supposing that we want to crate a plot similar to this n times). The next subsection does that.

4.4.2 Multiple plots

When you are repeating yourself over and over again, it is a good idea to write down a sequence of commands as a function. In this case, since we will be running the same type of plot for all schools/waves, we write a function in which the only things that changes are: (a) the school id, and (b) the color of the nodes.

```
myplot <- function(  
  net,  
  schoolid,
```

```
mindgr = 1,
vcol    = "tomato",
...) {

  # Creating a subgraph
  subnet <- induced_subgraph(
    net,
    which(degree(net, mode = "all") >= mindgr & V(net)$school == schoolid)
  )

  # Fancy graph
  set.seed(1)
  plot(
    subnet,
    vertex.size      = degree(subnet)/5,
    vertex.label     = NA,
    edge.arrow.size  = .25,
    vertex.color     = vcol,
    ...
  )
}
```

The function definition:

1. The `myplot <- function([arguments]) {[body of the function]}` tells R that we are going to create a function called `myplot`.
2. In the arguments part, we are declaring 4 specific arguments:

`net`, `schoolid`, `mindgr`, and `vcol`. These are an `igraph` object, the school id, the minimum degree that a vertex must have to be included in the plot, and the color of the vertices. Notice that, as a difference from other programming languages, in R we don't need to declare the types that these objects are.

3. The `ellipsis` object, `...`, is a special object in R that allows us passing other arguments without us specifying which. In our case, if you take a look at the `plot` bit of the body of the function, you will see that we also added `...`; this means that whatever other arguments (different from the ones that we explicitly defined) are passed to the function, these will be passed to the function `plot`, moreover, to the `plot.gexf` function (since the `subnet` object is actually an `igraph` object). In practice, this implies that we can, for example, set the argument `edge.arrow.size` when calling `myplot`, even though we did not include it in the function definition! (See `?dotsMethods` in R for more details).

In the following lines of code, using our new function, we will plot each schools' network in the same plotting device (window) with the help of the `par` function, and add legend with the `legend`:

```
# Plotting all together
oldpar <- par(no.readonly = TRUE)
par(mfrow = c(2, 3), mai = rep(0, 4), oma = c(1, 0, 0, 0))
myplot(ig_year1, 111, vcol = "tomato")
myplot(ig_year1, 112, vcol = "steelblue")
myplot(ig_year1, 113, vcol = "black")
myplot(ig_year1, 114, vcol = "gold")
myplot(ig_year1, 115, vcol = "white")
```

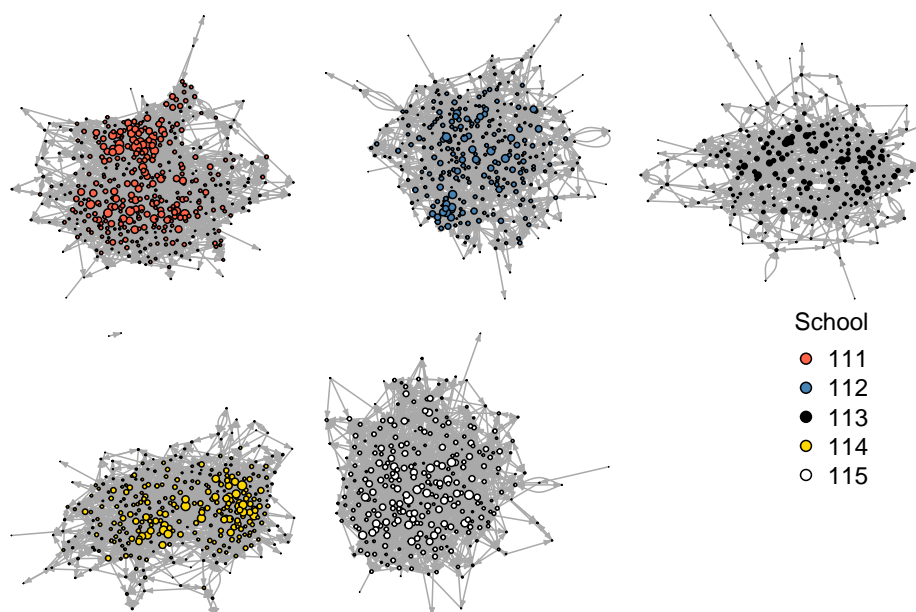


Figure 4.4: All 5 schools in time 1. Again, the graphs exclude isolates.

```
par(oldpar)

# A fancy legend
legend(
  "bottomright",
  legend = c(111, 112, 113, 114, 115),
  pt.bg = c("tomato", "steelblue", "black", "gold", "white"),
  pch    = 21,
  cex    = 1,
  bty    = "n",
  title  = "School"
)
```

So what happend here?

- `oldpar <- par(no.readonly = TRUE)` This line stores the current parameters for plotting. Since we are going to be changing them, we better make sure we are able to go back!.

- `par(mfrow = c(2, 3), mai = rep(0, 4), oma=rep(0, 4))`
Here we are setting various things at the same time. `mfrow` specifies how many *figures* will be drawn and in what order, in particular, we are asking the plotting device to allow for $2 \times 3 = 6$ plots organized in 2 rows and 3 columns, and these will be drawn by row.

`mai` specifies the size of the margins in inches. Setting all margins equal to zero (which is what we are doing now) gives more space to the network itself. The same is true for `oma`. See `?par` for more info.

- `myplot(ig_year1, ...)` This is simply calling our plotting function. The neat part of this is that, since we set `mfrow = c(2, 3)`, R takes care of *distributing* the plots in the device.
- `par(oldpar)` This line allows us to restore the plotting parameters.

4.5 Statistical tests

4.5.1 Is nomination number correlated with indegree?

Hypothesis: Individuals that on average are among the first nominations of their peers are more popular

```

# Getting all the data in long format
edgelist <- as_long_data_frame(ig_year1) %>%
  as_tibble

# Computing indegree (again) and average nomination number
# Include "On a scale from one to five how close do you feel"
# Also for egocentric friends (A. Friends)
indeg_nom_cor <- group_by(edgelist, to, to_name, to_school) %>%
  summarise(
    indeg    = length(nnom),
    nom_avg  = 1/mean(nnom)
  ) %>%
  rename(
    school = to_school
  )

indeg_nom_cor

```

```

## # A tibble: 1,561 x 5
## # Groups:   to, to_name [1,561]
##       to to_name school indeg nom_avg
##   <dbl> <chr>    <int> <int>   <dbl>
## 1     2 1110002    111    22   0.222
## 2     3 1110007    111     7   0.175
## 3     4 1110013    111     6   0.171
## 4     5 1110014    111    19   0.134
## 5     6 1110015    111     3   0.15
## 6     7 1110020    111     6   0.154

```



```
## 7      9 1110025    111      6  0.214
## 8     10 1110027    111     13  0.220
## 9     11 1110029    111     14  0.131
## 10    12 1110030    111      6  0.222
## # ... with 1,551 more rows
```

```
# Using pearson's correlation
```

```
with(indeg_nom_cor, cor.test(indeg, nom_avg))
```

```
##
```

```
## Pearson's product-moment correlation
```

```
##
```

```
## data:  indeg and nom_avg
```

```
## t = -12.254, df = 1559, p-value < 2.2e-16
```

```
## alternative hypothesis: true correlation is not equal to 0
```

```
## 95 percent confidence interval:
```

```
##  -0.3409964 -0.2504653
```

```
## sample estimates:
```

```
##          cor
```

```
## -0.2963965
```

```
save.image("03.rda")
```


Chapter 5

Exponential Random Graph Models

I strongly suggest reading the vignette included in the `ergm` R package

```
vignette("ergm", package="ergm")
```

So what are ERGMs anyway...

The purpose of ERGMs, in a nutshell, is to describe parsimoniously the local selection forces that shape the global structure of a network. To this end, a network dataset, like those depicted in Figure 1, may be considered like the response in a regression model, where the predictors are things like “propensity for individuals of the same sex to form partnerships” or “propensity for individuals to form triangles of partnerships”. In Figure 1(b), for example, it is evident that the individual nodes appear to cluster in groups

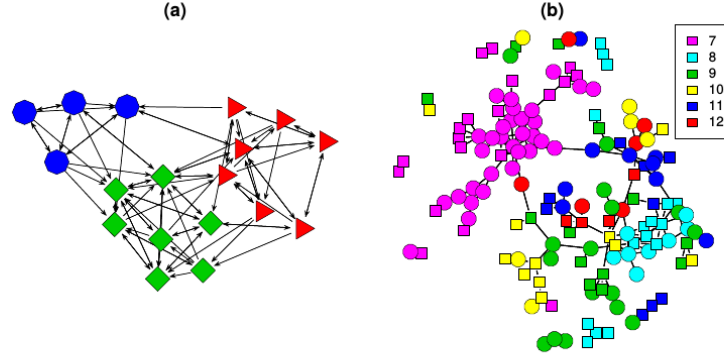


Figure 1: The (a) `samplike` and (b) `faux.mesa.high` networks described in Section 2. The values of nodal covariates may be indicated using various colors, shapes, and labels of nodes.

Figure 5.1: Source: Hunter et al. (2008)

of the same numerical labels (which turn out to be students' grades, 7 through 12); thus, an ERGM can help us quantify the strength of this intra-group effect.

— (David R. Hunter et al. 2008)

The distribution of \mathbf{Y} can be parameterized in the form

$$\Pr(\mathbf{Y} = \mathbf{y} | \theta, \mathcal{Y}) = \frac{\exp\{\theta^T \mathbf{g}(\mathbf{y})\}}{\kappa(\theta, \mathcal{Y})}, \quad \mathbf{y} \in \mathcal{Y}$$

Where $\theta \in \Omega \subset \mathbb{R}^q$ is the vector of model coefficients and $\mathbf{g}(\mathbf{y})$ is a q -vector of statistics based on the adjacency matrix \mathbf{y} .

Model (5) may be expanded by replacing $\mathbf{g}(\mathbf{y})$ with $\mathbf{g}(\mathbf{y}, \mathbf{X})$ to allow for additional covariate information \mathbf{X} about the network. The denominator,

$$\kappa(\theta, \mathcal{Y}) = \sum_{\mathbf{y} \in \mathcal{Y}} \exp\{\theta^T \mathbf{g}(\mathbf{y})\}$$

Is the normalizing factor that ensures that equation (5) is a legitimate probability distribution. Even after fixing \mathcal{Y} to be all the networks that have size n , the size of \mathcal{Y} makes this type of models hard to estimate as there are $N = 2^{n(n-1)}$ possible networks! (David R. Hunter et al. 2008)

Recent developments include new forms of dependency structures, to take into account more general neighborhood effects. These models relax the one-step Markovian dependence assumptions, allowing investigation of longer range configurations, such as longer paths in the network or larger cycles (Pattison and Robins 2002). Models for bipartite (Faust and Skvoretz 1999) and tripartite (Mische and Robins 2000) network structures have also been developed. (David R. Hunter et al. 2008, 9)

5.0.1 A naive example

In the simplest case, ergm is equivalent to a logistic regression

```
library(ergm)
```

```
## Loading required package: network

## network: Classes for Relational Data
## Version 1.15 created on 2019-04-01.
## copyright (c) 2005, Carter T. Butts, University of California-Irvine
##                               Mark S. Handcock, University of California -- Los Angeles
##                               David R. Hunter, Penn State University
##                               Martina Morris, University of Washington
##                               Skye Bender-deMoll, University of Washington
```

```
## For citation information, type citation("network").
## Type help("network-package") to get started.

##
## ergm: version 3.10.4-5075, created on 2019-06-30
## Copyright (c) 2019, Mark S. Handcock, University of California -- Los Angeles
##           David R. Hunter, Penn State University
##           Carter T. Butts, University of California -- Irvine
##           Steven M. Goodreau, University of Washington
##           Pavel N. Krivitsky, University of Wollongong
##           Martina Morris, University of Washington
##           with contributions from
##           Li Wang
##           Kirk Li, University of Washington
##           Skye Bender-deMoll, University of Washington
##           Chad Klumb
## Based on "statnet" project software (statnet.org).
## For license and citation information see statnet.org/attribution
## or type citation("ergm").

## NOTE: Versions before 3.6.1 had a bug in the implementation of the
## bd() constraint which distorted the sampled distribution somewhat.
## In addition, Sampson's Monks datasets had mislabeled vertices. See
## the NEWS and the documentation for more details.

## NOTE: Some common term arguments pertaining to vertex attribute
## and level selection have changed in 3.10.0. See terms help for
## more details. Use 'options(ergm.term=list(version="3.9.4"))' to
## use old behavior.
```

```
data("sampson")
```

```
samplike
```

```
## Network attributes:
```

```
## vertices = 18
```

```
## directed = TRUE
```

```
## hyper = FALSE
```

```
## loops = FALSE
```

```
## multiple = FALSE
```

```
## total edges= 88
```

```
## missing edges= 0
```

```
## non-missing edges= 88
```

```
##
```

```
## Vertex attribute names:
```

```
## cloisterville group vertex.names
```

```
##
```

```
## Edge attribute names:
```

```
## nominations
```

```
y <- sort(as.vector(as.matrix(samplike)))[-c(1:18)]
```

```
glm(y~1, family=binomial("logit"))
```

```
##
```

```
## Call: glm(formula = y ~ 1, family = binomial("logit"))
```

```
##
```

```
## Coefficients:
```

```
## (Intercept)
```

```
## -0.9072
```

```
##  
## Degrees of Freedom: 305 Total (i.e. Null); 305 Residual  
## Null Deviance: 367.2  
## Residual Deviance: 367.2 AIC: 369.2
```

```
ergm(samplike ~ edges)
```

```
## Starting maximum pseudolikelihood estimation (MPLE):
```

```
## Evaluating the predictor and response matrix.
```

```
## Maximizing the pseudolikelihood.
```

```
## Finished MPLE.
```

```
## Stopping at the initial estimate.
```

```
## Evaluating log-likelihood at the estimate.
```

```
##
```

```
## MLE Coefficients:
```

```
## edges
```

```
## -0.9072
```

```
pr <- mean(y)
```

```
log(pr) - log(1-pr) # Logit function
```

```
## [1] -0.9071582
```

```
qlogis(pr)
```

```
## [1] -0.9071582
```


5.1 Estimation of ERGMs

The ultimate goal is to be able to do statistical inference on the proposed model. In a *normal* setting, we would be able to use Maximum-Likelihood-Estimation (MLE) which basically consists on finding the model parameters θ that, given the observed data, maximizes the likelihood of the model. Such is usually done by applying [Newton's method](#) which requires been able to compute the log-likelihood of the model. This is a bit more complicated in ERGMs.

In the case of ERGMs, since part of the likelihood involves a normalizing constant that is a function of all possible networks, this is not as straight forward as it is in the regular setting. This is why we rely on simulations.

In statnet, the default estimation method is based on a method proposed by (Geyer and Thompson [1992](#)), Markov-Chain MLE, which uses Markov-Chain Monte Carlo for simulating networks and a modified version of the Newton-Raphson algorithm to do the parameter estimation part.

The idea of MC-MLE for this family of statistical models is the fact that the expectation of normalizing constant ratios can be approximated using the law of large numbers. In particular, the following:

$$\begin{aligned}
\frac{\kappa(\theta, \mathcal{Y})}{\kappa(\theta_0, \mathcal{Y})} &= \frac{\sum_{\mathbf{y} \in \mathcal{Y}} \exp\{\theta^T \mathbf{g}(\mathbf{y})\}}{\sum_{\mathbf{y} \in \mathcal{Y}} \exp\{\theta_0^T \mathbf{g}(\mathbf{y})\}} \\
&= \sum_{\mathbf{y} \in \mathcal{Y}} \left(\frac{1}{\sum_{\mathbf{y} \in \mathcal{Y}} \exp\{\theta_0^T \mathbf{g}(\mathbf{y})\}} \times \exp\{\theta^T \mathbf{g}(\mathbf{y})\} \right) \\
&= \sum_{\mathbf{y} \in \mathcal{Y}} \left(\frac{\exp\{\theta_0^T \mathbf{g}(\mathbf{y})\}}{\sum_{\mathbf{y} \in \mathcal{Y}} \exp\{\theta_0^T \mathbf{g}(\mathbf{y})\}} \times \exp\{(\theta - \theta_0)^T \mathbf{g}(\mathbf{y})\} \right) \\
&= \sum_{\mathbf{y} \in \mathcal{Y}} (\Pr(Y = \mathbf{y} | \mathcal{Y}, \theta_0) \times \exp\{(\theta - \theta_0)^T \mathbf{g}(\mathbf{y})\}) \\
&= E_{\theta_0}(\exp\{(\theta - \theta_0)^T \mathbf{g}(\mathbf{y})\})
\end{aligned}$$

The final line can be approximated by the law of large numbers. In particular, the MC-MLE algorithm uses this fact to maximize the ratio of log-likelihoods. The objective function can be approximated by simulating m networks from the distribution with parameter θ_0 :

$$l(\theta) - l(\theta_0) \approx (\theta - \theta_0)^T \mathbf{g}(\mathbf{y}_{obs}) - \log \left[\frac{1}{m} \sum_{i=1}^m \exp\{(\theta - \theta_0)^T \mathbf{g}(\mathbf{Y}_i)\} \right]$$

For more details see (David R. Hunter et al. [2008](#)). A sketch of the algorithm follows:

1. Initialize the algorithm with an initial guess of θ , call it $\theta^{(t)}$ (must be a rather OK guess)
2. While (no convergence) do:
 - a. Using $\theta^{(t)}$, simulate M networks by means of small changes in the \mathbf{Y}_{obs} (the observed network). This part is done by

using an importance-sampling method which weights each proposed network by it's likelihood conditional on $\theta^{(t)}$

- b. With the networks simulated, we can do the Newton step to update the parameter $\theta^{(t)}$ (this is the iteration part in the `ergm` package): $\theta^{(t)} \rightarrow \theta^{(t+1)}$.
- c. If convergence has been reach (which usually means that $\theta^{(t)}$ and $\theta^{(t+1)}$ are not very different), then stop, otherwise, go to step a.

For more details see (Lusher, Koskinen, and Robins 2012; Admiraal and Handcock 2006; Snijders 2002; Wang et al. 2009) provides details on the algorithm used by PNet (which is the same as the one used in RSiena). (Lusher, Koskinen, and Robins 2012) provides a short discussion on differences between `ergm` and PNet.

5.2 The `ergm` package

The `ergm` R package (Handcock et al. 2017)

From the previous section:¹

```
library(igraph)
library(magrittr)
library(dplyr)

load("03.rda")
```

In this section we will use the `ergm` package (from the `statnet` suit

¹You can download the 03.rda file from [this link](#).

of packages (Handcock et al. 2016)) suit, and the intergraph (Bojanowski 2015) package. The latter provides functions to go back and forth between igraph and network objects from the igraph and network packages respectively²

```
library(ergm)
library(intergraph)
```

As a rather important side note, the order in which R packages are loaded matters. Why is this important to mention now? Well, it turns out that at least a couple of functions in the network package have the same name of some functions in the igraph package. When the ergm package is loaded, since it depends on network, it will load the network package first, which will *mask* some functions in igraph. This becomes evident once you load ergm after loading igraph:

The following objects are masked from ‘package:igraph’:

```
add.edges, add.vertices, %c%, delete.edges, delete.vertices, get.edge.att
get.vertex.attribute, is.bipartite, is.directed, list.edge.attributes, li
set.edge.attribute, set.vertex.attribute
```

What are the implications of this? If you call the function `list.edge.attributes` for an object of class `igraph` R will return an error as the first function that matches that name comes from the network package! To avoid this you can use the double colon notation:

²Yes, the classes have the same name as the packages.

```
igraph::list.edge.attributes(my_igraph_object)
network::list.edge.attributes(my_network_object)
```

Anyway... Using the `asNetwork` function, we can coerce the `igraph` object into a `network` object so we can use it with the `ergm` function:

```
# Creating the new network
network_111 <- intergraph::asNetwork(ig_year1_111)

# Running a simple ergm (only fitting edge count)
ergm(network_111 ~ edges)
```

```
## [1] "Warning: This network contains loops"
## [1] "Warning: This network contains loops"

## Starting maximum pseudolikelihood estimation (MPLE):

## Evaluating the predictor and response matrix.

## Maximizing the pseudolikelihood.

## Finished MPLE.

## Stopping at the initial estimate.

## Evaluating log-likelihood at the estimate.

##
## MLE Coefficients:
## edges
## -4.734
```

So what happened here! We got a warning. It turns out that our network has loops (didn't thought about it before!). Let's take a look on that with the `which_loop` function

```
E(ig_year1_111)[which_loop(ig_year1_111)]
```

```
## + 1/2638 edge from 963da40 (vertex names):  
## [1] 1110111->1110111
```

We can get rid of these using the `igraph::-.igraph`. Moreover, just to illustrate how it can be done, let's get rid of the isolates using the same operator

```
# Creating the new network  
network_111 <- ig_year1_111  
  
# Removing loops  
network_111 <- network_111 - E(network_111)[which(which_loop(network_111))]  
  
# Removing isolates  
network_111 <- network_111 - which(degree(network_111, mode = "all") == 0)  
  
# Converting the network  
network_111 <- intergraph::asNetwork(network_111)
```

```
asNetwork(simplify(ig_year1_111)) ig_year1_111 %>% simplify  
%>% asNetwork
```

5.3 Running ERGMs

Proposed workflow:

1. Estimate the simplest model, adding one variable at a time.

2. After each estimation, run the `mcmc.diagnostics` function to see how good/bad behaved are the chains.
3. Run the `gof` function to see how good is the model at matching the network's structural statistics.

What to use:

1. `control.ergms`: Maximum number of iteration, seed for Pseudo-RNG, how many cores
2. `ergm.constraints`: Where to sample the network from. Gives stability and (in some cases) faster convergence as by constraining the model you are reducing the sample size.

Here is an example of a couple of models that we could compare³

```
ans0 <- ergm(  
  network_111 ~  
    edges +  
    nodematch("hispanic") +  
    nodematch("female1") +  
    nodematch("eversmk1") +  
    mutual  
  ,  
  constraints = ~bd(maxout = 19),  
  control = control.ergm(  
    seed = 1,  
    MCMLE.maxit = 10,  
    parallel = 4,
```

³Notice that this document may not include the usual messages that the `ergm` command generates during the estimation procedure. This is just to make it more printable-friendly.

```

    CD.maxit    = 10
  )
)

```

```

## Warning in nobs.ergm(object, ...): The number of observed dyads in this
## network is ill-defined due to complex constraints on the sample space.
## Disable this warning with 'options(ergm.loglik.warn_dyads=FALSE)'.

```

```

## Warning in nobs.ergm(object, ...): The number of observed dyads in this
## network is ill-defined due to complex constraints on the sample space.
## Disable this warning with 'options(ergm.loglik.warn_dyads=FALSE)'.

```

So what are we doing here:

1. The model is controlling for:
 - a. edges Number of edges in the network (as opposed to its density)
 - b. nodematch("some-variable-name-here") Includes a term that controls for homophily/heterophily
 - c. mutual Number of mutual connections between (i, j) , (j, i) . This can be related to, for example, triadic closure.

For more on control parameters, see (Morris, Handcock, and Hunter 2008).

```

ans1 <- ergm(
  network_111 ~
    edges +
    nodematch("hispanic") +
    nodematch("female1") +

```



```

    nodematch("eversmk1")
  ,
  constraints = ~bd(maxout = 19),
  control = control.ergm(
    seed      = 1,
    MCMLE.maxit = 10,
    parallel   = 4,
    CD.maxit   = 10
  )
)

```

```

## Warning in nobs.ergm(object, ...): The number of observed dyads in this
## network is ill-defined due to complex constraints on the sample space.
## Disable this warning with 'options(ergm.loglik.warn_dyads=FALSE)'.

```

```

## Warning in nobs.ergm(object, ...): The number of observed dyads in this
## network is ill-defined due to complex constraints on the sample space.
## Disable this warning with 'options(ergm.loglik.warn_dyads=FALSE)'.

```

This example takes longer to compute

```

ans2 <- ergm(
  network_111 ~
    edges +
    nodematch("hispanic") +
    nodematch("female1") +
    nodematch("eversmk1") +
    mutual +
    balance

```

```
,
constraints = ~bd(maxout = 19),
control = control.ergm(
  seed      = 1,
  MCMLE.maxit = 10,
  parallel   = 4,
  CD.maxit    = 10
)
)
```

```
## Warning in nobs.ergm(object, ...): The number of observed dyads in this
## network is ill-defined due to complex constraints on the sample space.
## Disable this warning with 'options(ergm.loglik.warn_dyads=FALSE)'.
```

```
## Warning in nobs.ergm(object, ...): The number of observed dyads in this
## network is ill-defined due to complex constraints on the sample space.
## Disable this warning with 'options(ergm.loglik.warn_dyads=FALSE)'.
```

Now, a nice trick to see all regressions in the same table, we can use the `texreg` package (Leifeld [2013](#)) which supports `ergm` outputs!

```
library(texreg)
```

```
## Version: 1.36.24
## Date: 2019-04-07
## Author: Philip Leifeld (University of Essex)
##
## Please cite the JSS article in your publications -- see citation("texreg")
##
## Attaching package: 'texreg'
```

```
## The following object is masked from 'package:magrittr':
```

```
##
```

```
##      extract
```

```
screenreg(list(ans0, ans1, ans2))
```

```
##
```

```
## =====
```

```
##           Model 1           Model 2           Model 3
```

```
## -----
```

```
## edges           -5.64 ***           -5.52 ***           -5.58 ***
```

```
##                (0.05)           (0.06)           (0.06)
```

```
## nodematch.hispanic    0.36 ***    0.50 ***    0.40 ***
```

```
##                (0.04)           (0.04)           (0.04)
```

```
## nodematch.female1    0.83 ***    1.10 ***    0.83 ***
```

```
##                (0.04)           (0.05)           (0.04)
```

```
## nodematch.eversmk1    0.35 ***    0.46 ***    0.36 ***
```

```
##                (0.04)           (0.05)           (0.04)
```

```
## mutual              4.09 ***              -3.55 ***
```

```
##                (0.07)              (0.25)
```

```
## balance              0.02 ***
```

```
##                (0.00)
```

```
## -----
```

```
## AIC                -32986.67        -31399.10        -33035.32
```

```
## BIC                -32936.32        -31358.82        -32974.91
```

```
## Log Likelihood      16498.33         15703.55         16523.66
```

```
## =====
```

```
## *** p < 0.001; ** p < 0.01; * p < 0.05
```

	Model 1	Model 2	Model 3
edges	−5.64*** (0.05)	−5.52*** (0.06)	−5.58*** (0.06)
nodematch.hispanic	0.36*** (0.04)	0.50*** (0.04)	0.40*** (0.04)
nodematch.female1	0.83*** (0.04)	1.10*** (0.05)	0.83*** (0.04)
nodematch.eversmk1	0.35*** (0.04)	0.46*** (0.05)	0.36*** (0.04)
mutual	4.09*** (0.07)		−3.55*** (0.25)
balance			0.02*** (0.00)
AIC	−32986.67	−31399.10	−33035.32
BIC	−32936.32	−31358.82	−32974.91
Log Likelihood	16498.33	15703.55	16523.66

*** $p < 0.001$; ** $p < 0.01$; * $p < 0.05$

Table 5.1: Statistical models

Or, if you are using `rmarkdown`, you can export the results using LaTeX or html, let's try the latter to see how it looks like here:

```
library(texreg)
texreg(list(ans0, ans1, ans2))
```

5.4 Model Goodness-of-Fit

In raw terms, once each chain has reach stationary distribution, we can say that there are no problems with autocorrelation and that each sample point is iid. This implies that, since we are running the model with more than 1 chain, we can use all the samples (chains) as a single dataset.

Recent changes in the `ergm` estimation algorithm mean that these plots can no longer be used to ensure that the mean

statistics from the model match the observed network statistics. For that functionality, please use the GOF command: `gof(object, GOF=~model)`.

—?ergm::mcmc.diagnostics

Since `ans0` is the one model which did best, let's take a look at its GOF statistics. First, let's see how the MCMC did. For this we can use the `mcmc.diagnostics` function included in the package. This function is actually a wrapper of a couple of functions from the `coda` package (Plummer et al. 2006) which is called upon the `$sample` object which holds the *centered* statistics from the sampled networks. This last point is important to consider since at first look it can be confusing to look at the `$sample` object since it neither matches the observed statistics, nor the coefficients.

When calling the function `mcmc.diagnostics(ans0, centered = FALSE)`, you will see a lot of output including a couple of plots showing the trace and posterior distribution of the *uncentered* statistics (`centered = FALSE`). In the next code chunks we will reproduce the output from the `mcmc.diagnostics` function step by step using the `coda` package. First we need to *uncenter* the sample object:

```
# Getting the centered sample
sample_centered <- ans0$sample

# Getting the observed statistics and turning it into a matrix so we can add it
# to the samples
observed <- summary(ans0$formula)
observed <- matrix(
```

```

observed,
nrow = nrow(sample_centered[[1]]),
ncol = length(observed),
byrow = TRUE
)

# Now we uncenter the sample
sample_uncentered <- lapply(sample_centered, function(x) {
  x + observed
})

# We have to make it an mcmc.list object
sample_uncentered <- coda::mcmc.list(sample_uncentered)

```

This is what is called under the hood:

1. *Empirical means and sd, and quantiles:*

```

summary(sample_uncentered)

##
## Iterations = 16384:1063936
## Thinning interval = 1024
## Number of chains = 4
## Sample size per chain = 1024
##
## 1. Empirical mean and standard deviation for each variable,
##    plus standard error of the mean:
##
##              Mean      SD Naive SE Time-series SE

```

```
## edges          2474.3 55.40    0.8656      4.129
## nodematch.hispanic 1619.5 43.56    0.6806      3.836
## nodematch.female1 1802.3 49.50    0.7735      4.900
## nodematch.eversmk1 1738.0 45.32    0.7081      2.926
## mutual          485.1 20.07    0.3136      3.544
```

```
##
```

```
## 2. Quantiles for each variable:
```

```
##
```

```
##          2.5%  25%  50%  75% 97.5%
## edges          2365 2438 2475 2511 2580
## nodematch.hispanic 1530 1590 1621 1650 1701
## nodematch.female1 1713 1768 1801 1833 1910
## nodematch.eversmk1 1647 1709 1738 1767 1824
## mutual          446  472  485  498  527
```

2. Cross correlation:

```
coda::crosscorr(sample_uncentered)
```

```
##          edges nodematch.hispanic nodematch.female1
## edges          1.0000000          0.8099803          0.8419023
## nodematch.hispanic 0.8099803          1.0000000          0.6845240
## nodematch.female1 0.8419023          0.6845240          1.0000000
## nodematch.eversmk1 0.8127786          0.6668579          0.6946880
## mutual          0.7144121          0.6064003          0.6720229
##          nodematch.eversmk1  mutual
## edges          0.8127786 0.7144121
## nodematch.hispanic          0.6668579 0.6064003
## nodematch.female1          0.6946880 0.6720229
```

```
## nodematch.eversmk1          1.0000000 0.5909593
## mutual                      0.5909593 1.0000000
```

3. *Autocorrelation*: Just for now, we will only take a look at autocorrelation for chain 1 only. Autocorrelation should be rather low (in a general MCMC setting). If autocorrelation is high, then it means that your sample is not iid (no markov property). A way out to solve this is *thinning* the sample.

```
coda::autocorr(sample_uncentered)[[1]]
```

```
## , , edges
##
##          edges nodematch.hispanic nodematch.female1
## Lag 0      1.0000000          0.8139761          0.7795009
## Lag 1024    0.8868373          0.7222805          0.6971419
## Lag 5120    0.5948994          0.5251881          0.4922158
## Lag 10240   0.4600845          0.4504976          0.3755953
## Lag 51200   0.1982049          0.2079237          0.3221285
##          nodematch.eversmk1    mutual
## Lag 0          0.7837272 0.6565207
## Lag 1024        0.7006181 0.6511008
## Lag 5120        0.4847903 0.6123226
## Lag 10240       0.3949433 0.5450916
## Lag 51200       0.3131978 0.3781621
##
## , , nodematch.hispanic
##
##          edges nodematch.hispanic nodematch.female1
```


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```
## Lag 0      0.8139761      1.0000000      0.6678498
## Lag 1024   0.7368708      0.8947521      0.6118379
## Lag 5120   0.5294057      0.6364242      0.4658087
## Lag 10240  0.4054664      0.4877295      0.3715878
## Lag 51200  0.2058656      0.1750285      0.3230496
##           nodematch.eversmk1      mutual
## Lag 0      0.5997413 0.6338096
## Lag 1024    0.5398809 0.6235126
## Lag 5120    0.3828159 0.5759901
## Lag 10240   0.2940047 0.5148339
## Lag 51200   0.2682960 0.3923427
##
## , , nodematch.female1
##
##           edges nodematch.hispanic nodematch.female1
## Lag 0      0.7795009      0.6678498      1.0000000
## Lag 1024    0.6998063      0.6046370      0.9102620
## Lag 5120    0.4930271      0.4699355      0.6838324
## Lag 10240   0.3680917      0.3863329      0.5241266
## Lag 51200   0.1291978      0.1212720      0.3078540
##           nodematch.eversmk1      mutual
## Lag 0      0.5886437 0.6480628
## Lag 1024    0.5273102 0.6419102
## Lag 5120    0.3701848 0.6093541
## Lag 10240   0.2933634 0.5327467
## Lag 51200   0.1884934 0.3444436
##
```

```

## , , nodematch.eversmk1
##
##          edges nodematch.hispanic nodematch.female1
## Lag 0      0.7837272      0.5997413      0.5886437
## Lag 1024    0.6948882      0.5391618      0.5277555
## Lag 5120    0.4488066      0.4103141      0.3543596
## Lag 10240   0.3440736      0.3622540      0.2786189
## Lag 51200   0.1413846      0.1251185      0.3037022
##          nodematch.eversmk1    mutual
## Lag 0      1.0000000 0.5189905
## Lag 1024    0.9024858 0.5109281
## Lag 5120    0.6426104 0.4754632
## Lag 10240   0.5235972 0.4043018
## Lag 51200   0.3427353 0.2511635
##
## , , mutual
##
##          edges nodematch.hispanic nodematch.female1
## Lag 0      0.6565207      0.6338096      0.6480628
## Lag 1024    0.6473638      0.6296240      0.6400673
## Lag 5120    0.6106484      0.6120531      0.6093092
## Lag 10240   0.5779115      0.6078153      0.5675734
## Lag 51200   0.3343059      0.3086253      0.4037995
##          nodematch.eversmk1    mutual
## Lag 0      0.5189905 1.0000000
## Lag 1024    0.5133709 0.9825012
## Lag 5120    0.4949412 0.9123847

```

```
## Lag 10240          0.4953194 0.8212019
## Lag 51200          0.4237535 0.4968927
```

4. *Geweke Diagnostic*: From the function's help file:

"If the samples are drawn from the stationary distribution of the chain, the two means are equal and Geweke's statistic has an asymptotically standard normal distribution. [...] The Z-score is calculated under the assumption that the two parts of the chain are asymptotically independent, which requires that the sum of frac1 and frac2 be strictly less than 1."

—?coda::geweke.diag

Let's take a look at a single chain:

```
coda::geweke.diag(sample_uncentered)[[1]]
```

```
##
## Fraction in 1st window = 0.1
## Fraction in 2nd window = 0.5
##
##          edges nodematch.hispanic  nodematch.female1
##          0.5295          0.4904          1.6354
## nodematch.eversmk1          mutual
##          0.6644          1.1170
```

5. *(not included) Gelman Diagnostic*: From the function's help file:

Gelman and Rubin (1992) propose a general approach to monitoring convergence of MCMC output in which $m > 1$ parallel chains are run with starting values that

are overdispersed relative to the posterior distribution. Convergence is diagnosed when the chains have ‘forgotten’ their initial values, and the output from all chains is indistinguishable. The `gelman.diag` diagnostic is applied to a single variable from the chain. It is based a comparison of within-chain and between-chain variances, and is similar to a classical analysis of variance.

—?coda::gelman.diag

As a difference from the previous diagnostic statistic, this uses all chains simulatenously:

```
coda::gelman.diag(sample_uncentered)
```

```
## Potential scale reduction factors:
##
##               Point est. Upper C.I.
## edges                1.16      1.42
## nodematch.hispanic    1.10      1.28
## nodematch.female1     1.28      1.68
## nodematch.eversmk1    1.34      1.81
## mutual                1.32      1.79
##
## Multivariate psrf
##
## 1.44
```

As a rule of thumb, values that are in the $[.9, 1.1]$ are good.

One nice feature of the `mcmc.diagnostics` function is the nice trace and posterior distribution plots that it generates. If you have the R

package `latticeExtra` (Sarkar and Andrews 2016), the function will override the default plots used by `coda::plot.mcmc` and use `lattice` instead, creating a nicer looking plots. The next code chunk calls the `mcmc.diagnostic` function, but we suppress the rest of the output (see figure ??).

```
mcmc.diagnostics(ans0, center = FALSE) # Suppressing all the output
```

If we called the function `mcmc.diagnostics` this message appears at the end:

MCMC diagnostics shown here are from the last round of simulation, prior to computation of final parameter estimates. Because the final estimates are refinements of those used for this simulation run, these diagnostics may understate model performance. To directly assess the performance of the final model on in-model statistics, please use the GOF command: `gof(ergmFitObject, GOF=~model)`.

```
—mcmc.diagnostics(ans0)
```

Not that bad (although the mutual term could do better)!⁴ First, observe that in the plot we see 4 different lines, why is that? Well, since we were running in parallel using 4 cores the algorithm actually ran 4 different chains of the MCMC algorithm. An eyeball test is to see if all the chains moved at about the same place, if we have that we can start thinking about model convergence from the mcmc perspective.

Once we are sure to have reach convergence on the MCMC algorithm, we can start thinking about how well does our model predicts the

⁴The statnet wiki website as a very nice example of (very) bad and good mcmc diagnostics plots [here](#).

Sample statistics

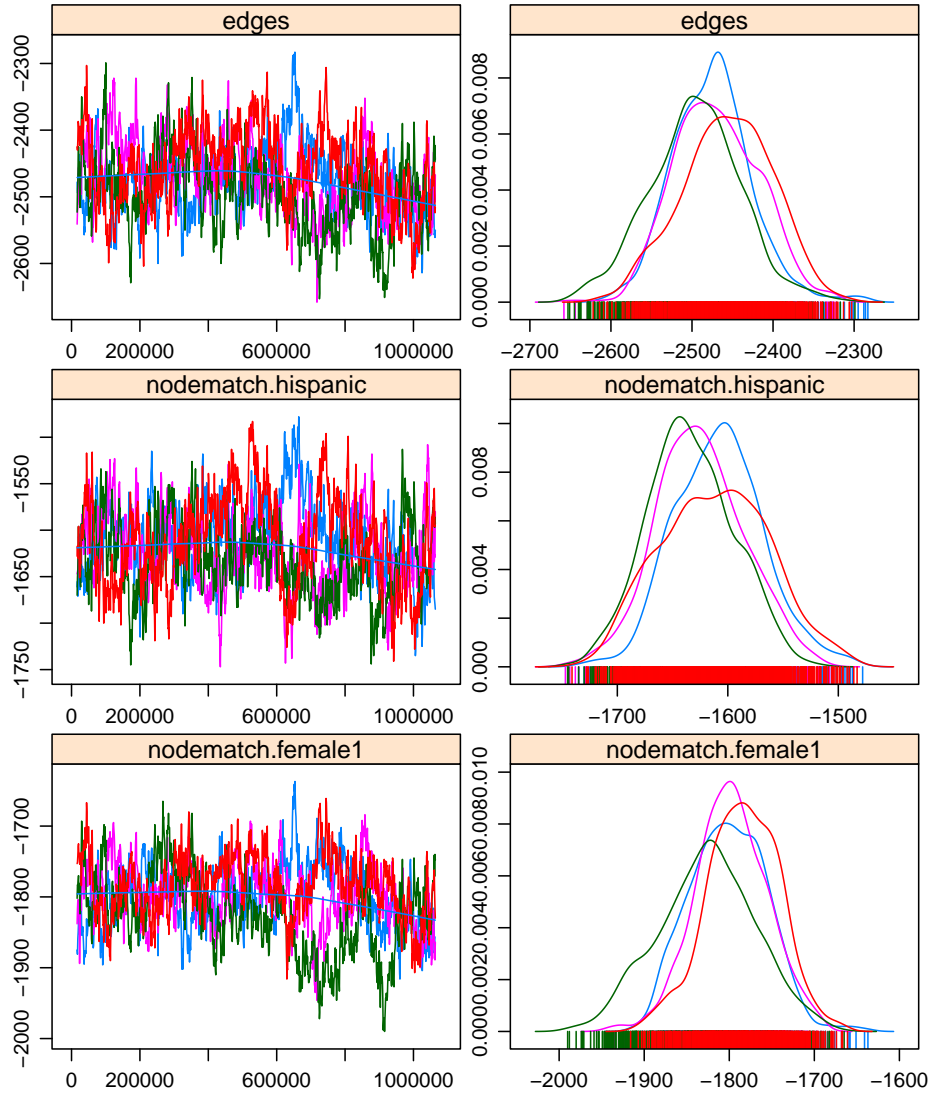


Figure 5.2: Trace and posterior distribution of sampled network statistics.

observed network's properties. Besides of the statistics that define our ERGM, the `gof` function's default behavior show GOF for:

- a. In degree distribution,

Sample statistics

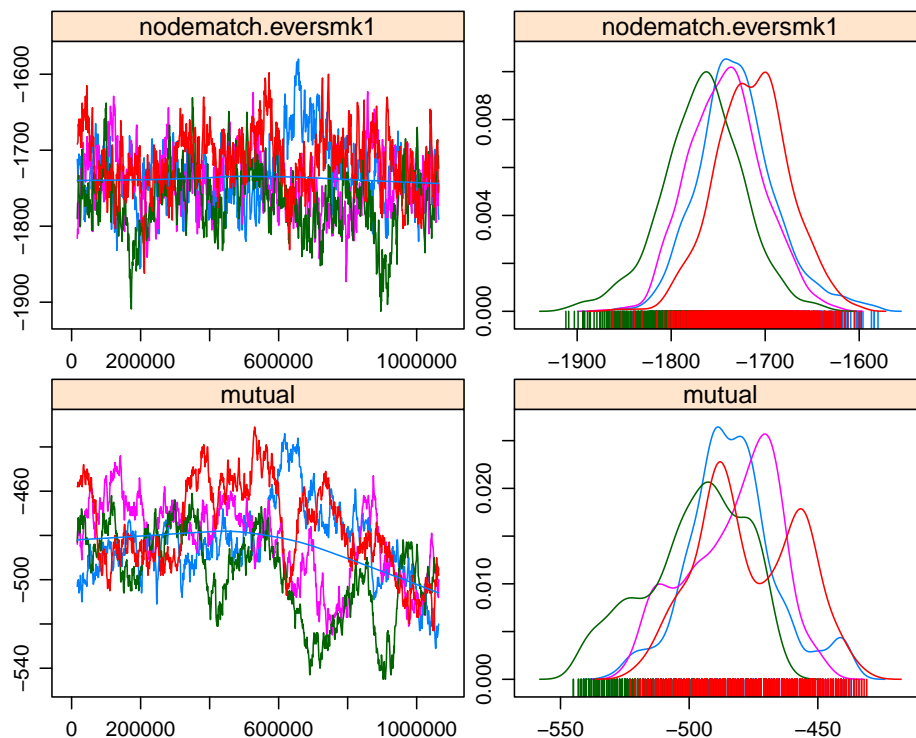


Figure 5.3: Trace and posterior distribution of sampled network statistics (cont'd).

- b. Out degree distribution,
- c. Edge-wise shared partners, and
- d. Geodesics

Let's take a look at it

```
# Computing and printing GOF estatistics
```

```
ans_gof <- gof(ans0)
```

```
ans_gof
```

```
##
```

```
## Goodness-of-fit for in-degree
```

##

##		obs	min	mean	max	MC	p-value
##	0	13	0	1.89	8		0.00
##	1	34	3	9.04	18		0.00
##	2	37	11	23.63	33		0.00
##	3	48	28	41.83	59		0.44
##	4	37	41	56.87	75		0.00
##	5	47	44	64.71	84		0.04
##	6	42	39	63.33	85		0.02
##	7	39	42	53.78	74		0.00
##	8	35	25	40.58	60		0.50
##	9	21	14	26.19	43		0.38
##	10	12	9	17.37	26		0.16
##	11	19	2	9.53	17		0.00
##	12	4	0	4.93	11		0.90
##	13	7	0	2.35	7		0.04
##	14	6	0	1.27	5		0.00
##	15	3	0	0.44	3		0.02
##	16	4	0	0.21	2		0.00
##	17	3	0	0.05	1		0.00
##	18	3	0	0.00	0		0.00
##	19	2	0	0.00	0		0.00
##	20	1	0	0.00	0		0.00
##	22	1	0	0.00	0		0.00

##

Goodness-of-fit for out-degree

##


```

##      obs min   mean max MC p-value
## 0      4   0  1.85   5      0.20
## 1     28   3  8.99  15      0.00
## 2     45  12 23.25  35      0.00
## 3     50  24 40.87  52      0.06
## 4     54  42 57.89  76      0.68
## 5     62  49 66.04  85      0.70
## 6     40  41 62.23  79      0.00
## 7     28  37 54.08  70      0.00
## 8     13  29 40.05  52      0.00
## 9     16  17 27.65  41      0.00
## 10    20   8 16.72  30      0.46
## 11     8   2  9.30  19      0.76
## 12    11   1  4.98  11      0.04
## 13    13   0  2.38   7      0.00
## 14     6   0  0.97   4      0.00
## 15     6   0  0.50   3      0.00
## 16     7   0  0.17   1      0.00
## 17     4   0  0.06   1      0.00
## 18     3   0  0.01   1      0.00
## 19     0   0  0.01   1      1.00
##
## Goodness-of-fit for edgewise shared partner
##
##      obs   min    mean  max MC p-value
## esp0 1032 2012 2210.11 2303      0
## esp1  755  156  222.10  441      0

```

```
## esp2 352 4 13.42 93 0
## esp3 202 0 0.77 19 0
## esp4 79 0 0.04 3 0
## esp5 36 0 0.00 0 0
## esp6 14 0 0.00 0 0
## esp7 4 0 0.00 0 0
## esp8 1 0 0.00 0 0
```

```
##
```

```
## Goodness-of-fit for minimum geodesic distance
```

```
##
```

```
##      obs   min    mean   max MC p-value
## 1    2475 2301 2446.44 2568    0.56
## 2   10672 12062 13688.54 14617    0.00
## 3   31134 48722 55636.04 60092    0.00
## 4   50673 77284 79447.41 81661    0.00
## 5   42563 14452 20165.40 26886    0.00
## 6   18719  325 1274.88 2453    0.00
## 7    4808   1  51.78 361    0.00
## 8     822   0   2.13 102    0.00
## 9     100   0   0.06 4    0.00
## 10      7   0   0.01 1    0.00
## Inf 12333   0 1593.31 4558    0.00
```

```
##
```

```
## Goodness-of-fit for model statistics
```

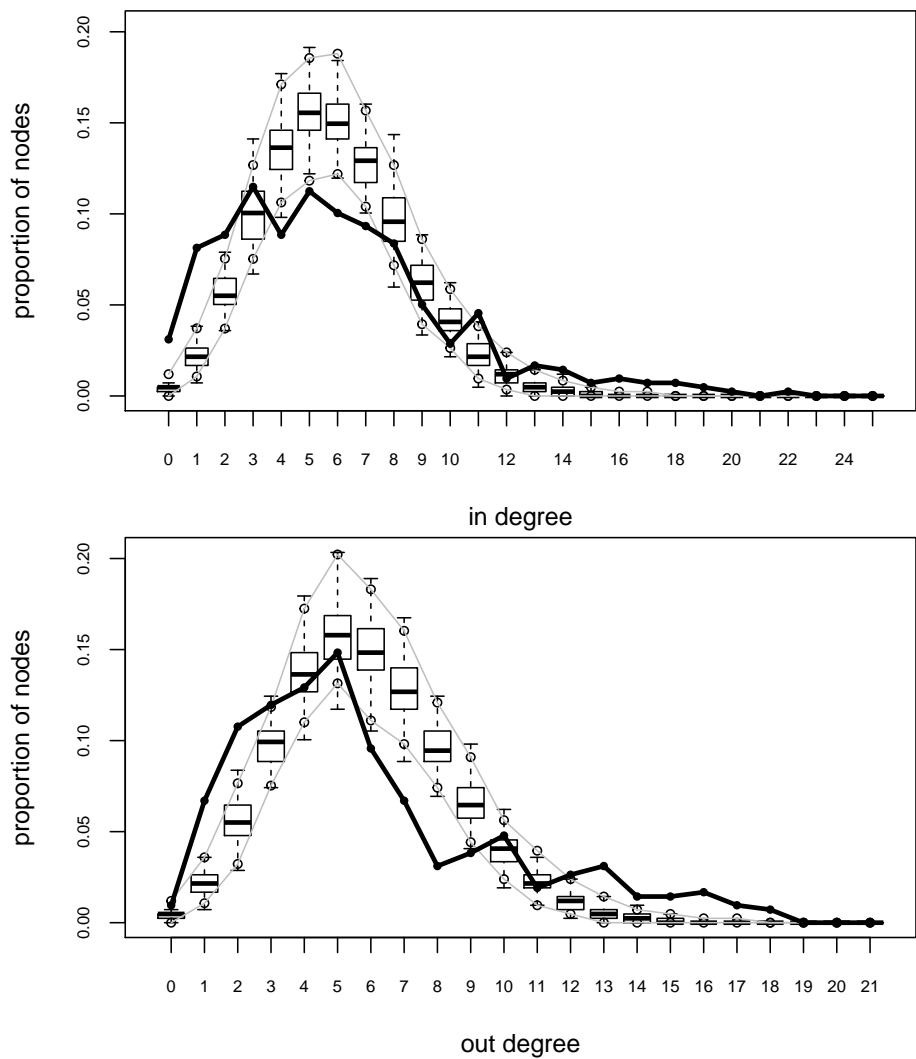
```
##
```

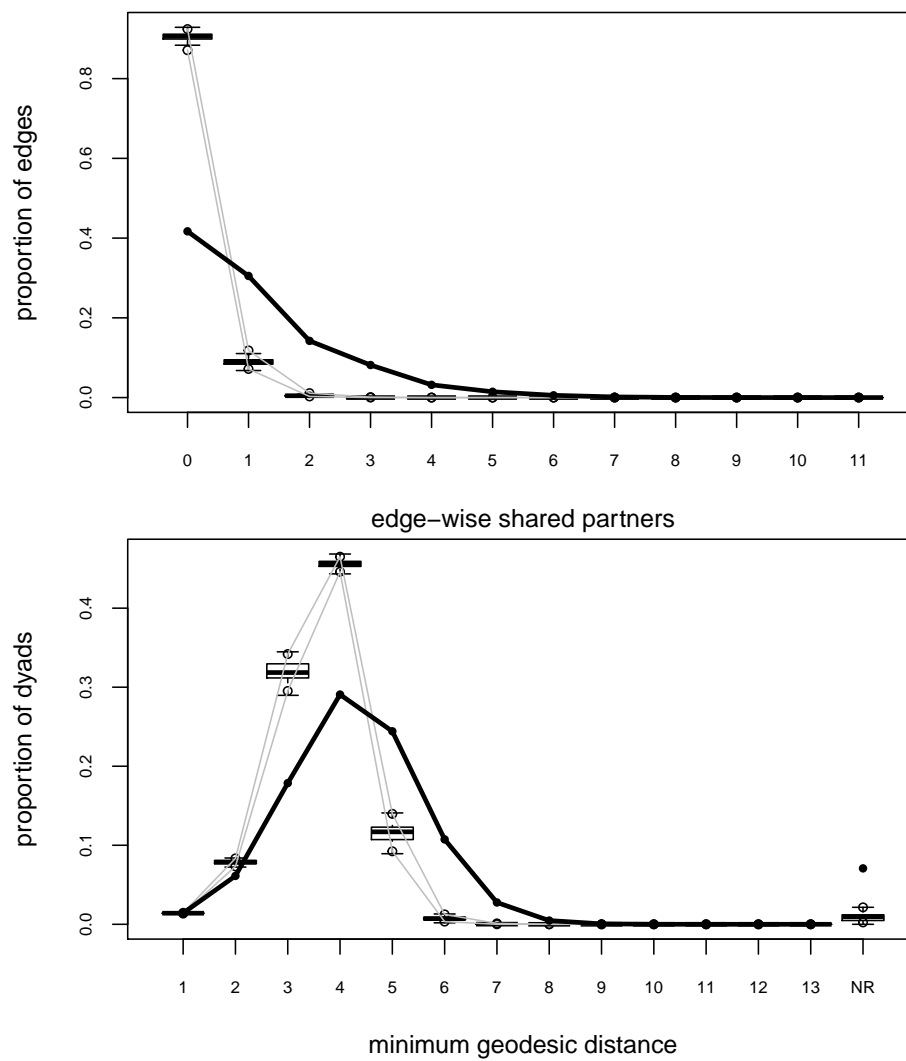
```
##              obs   min    mean   max MC p-value
## edges          2475 2301 2446.44 2568    0.56
```

##	nodematch.hispanic	1615	1499	1578.58	1662	0.32
##	nodematch.female1	1814	1690	1791.16	1883	0.54
##	nodematch.eversmk1	1738	1595	1716.19	1834	0.56
##	mutual	486	436	475.48	504	0.50

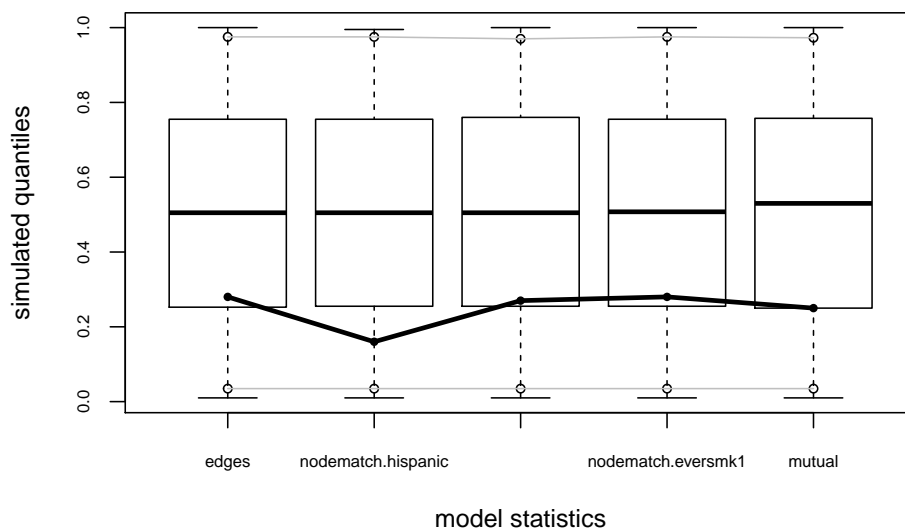
Plotting GOF statistics

plot(ans_gof)





Goodness-of-fit diagnostics



Try the following configuration instead

```
ans0_bis <- ergm(
  network_111 ~
    edges +
    nodematch("hispanic") +
    nodematch("female1") +
    mutual +
    esp(0:3) +
    idegree(0:10)
  ,
  constraints = ~bd(maxout = 19),
  control = control.ergm(
    seed      = 1,
    MCMLE.maxit = 15,
    parallel   = 4,
```

```
CD.maxit      = 15,  
MCMC.samplesize = 2048*4,  
MCMC.burnin = 30000,  
MCMC.interval = 2048*4  
)  
)
```

Increase the sample size so the curves are more smooth, longer intervals (thinning) so we reduce the autocorrelation, larger burnin. All this together to improve the Gelman test statistic. We also added idegree from 0 to 10, and esp from 0 to 3 to explicitly match those statistics in our model.

```
knitr::include_graphics("awful-chains.png")
```

5.5 More on MCMC convergence

For more on this issue, I recommend reviewing [chapter 1](#) and [chapter 6](#) from the Handbook of MCMC (Brooks et al. 2011). Both chapters are free to download from the [book's website](#).

For GOF take a look at section 6 of [ERGM 2016 Sunbelt tutorial](#), and for a more technical review you can take a look at (David R Hunter, Goodreau, and Handcock 2008).

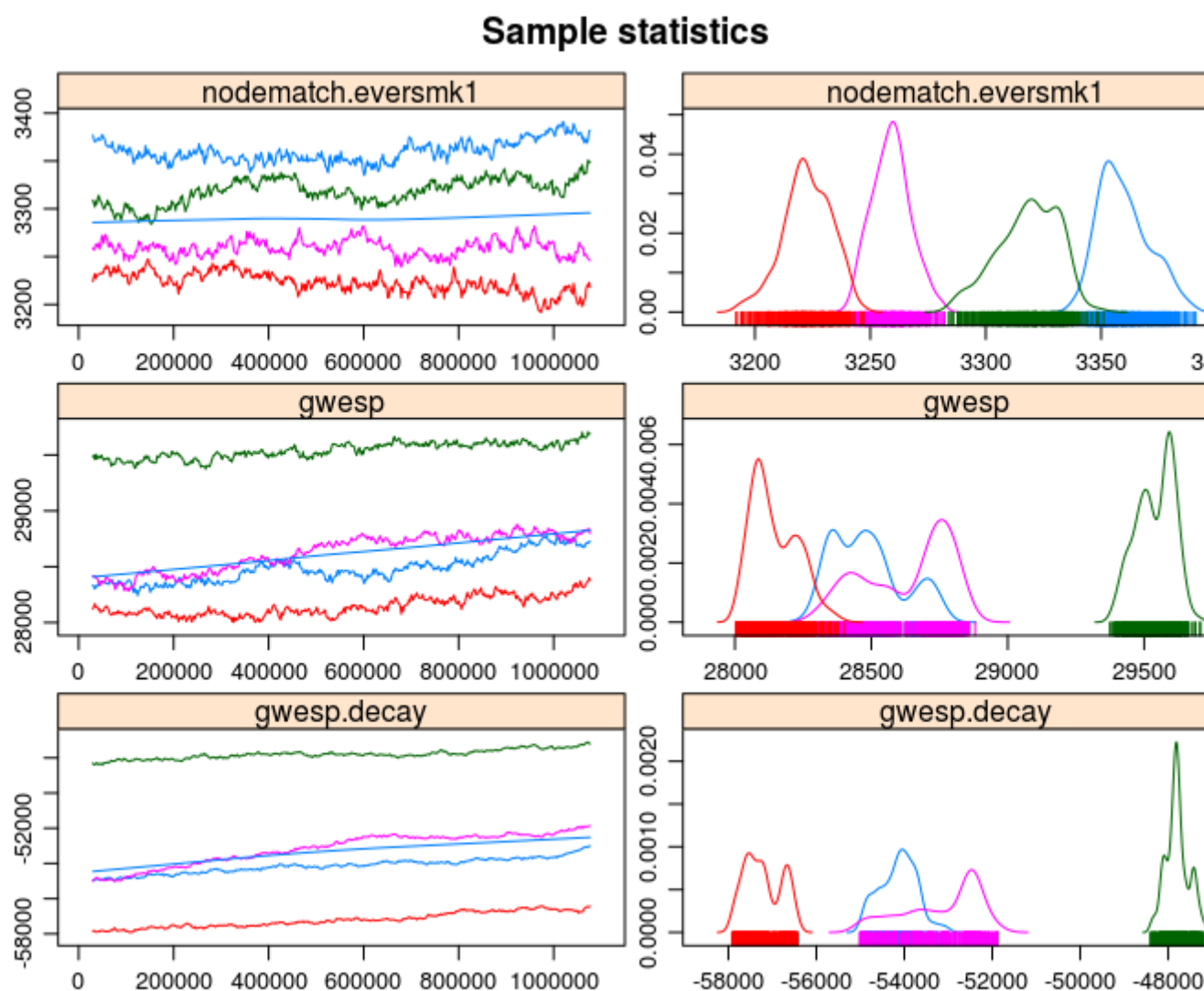


Figure 5.4: An example of a terrible ERGM (no convergence at all). Also, a good example of why running multiple chains can be useful

Chapter 6

(Separable) Temporal Exponential Family Random Graph Models

This tutorial is great! https://statnet.org/trac/raw-attachment/wiki/Sunbelt2016/tergm_tutorial.pdf

Chapter 7

Stochastic Actor Oriented Models

Stochastic Actor Oriented Models (SOAM), also known as Siena models were introduced by CITATION NEEDED.

As a difference from ERGMs, Siena models look at the data generating process from the individuals' point of view. Based on McFadden's ideas of probabilistic choice, the model is founded in the following equation

$$U_i(x) - U_i(x') \sim \text{Extreame Value Distribution}$$

In other words, individuals choose between states x and x' in a probabilistic way (with some noise),

$$\frac{\exp \{f_i^Z(\beta^Z, x, z)\}}{\sum_{Z' \in \mathcal{C}} \exp \{f_i^Z(\beta, x, z')\}}$$

snijders_(sociological methodology 2001)

(Snijders, Bunt, and Steglich [2010](#), @lazega2015, @Ripley2011)

Appendix A

Datasets

A.1 SNS data

A.1.1 About the data

- This data is part of the NIH Challenge grant # RC1AA019239 “Social Networks and Networking That Puts Adolescents at High Risk”.
- In general terms, the SNS’s goal was(is) “Understand the network effects on risk behaviors such as smoking initiation and substance use”.

A.1.2 Variables

The data has a *wide* structure, which means that there is one row per individual, and that dynamic attributes are represented as one column

per time.

- photoid Photo id at the school level (can be repeated across schools).
- school School id.
- hispanic Indicator variable that equals 1 if the individual ever reported himself as hispanic.
- female1, ..., female4 Indicator variable that equals 1 if the individual reported to be female at the particular wave.
- grades1, ..., grades4 Academic grades by wave. Values from 1 to 5, with 5 been the best.
- everismk1, ..., everismk4 Indicator variable of ever smoking by wave. A one indicated that the individual had smoked at the time of the survey.
- everdrk1, ..., everdrk4 Indicator variable of ever drinking by wave. A one indicated that the individual had drink at the time of the survey.
- home1, ..., home4 Factor variable for home status by wave. A one indicates home ownership, a 2 rent, and a 3 a "I don't know".

During the survey, participants were asked to name up to 19 of their school friends:

- sch_friend11, ..., sch_friend119 School friends nominations (19 in total) for wave 1. The codes are mapped to the variable photoid.
- sch_friend21, ..., sch_friend219 School friends nominations

(19 in total) for wave 2. The codes are mapped to the variable photoid.

- sch_friend31, ..., sch_friend319 School friends nominations (19 in total) for wave 3. The codes are mapped to the variable photoid.
- sch_friend41, ..., sch_friend419 School friends nominations (19 in total) for wave 4. The codes are mapped to the variable photoid.

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