In this session:

- You are going to learn about the igraph package
- You are going to compute several descriptive measures of networks and nodes and reproduce a graph seen in class
- You are going to run community detection algorithms and explore their results

1 Introduction

In this session we will introduce the igraph software package for network analysis. This guide uses R as the platform to using igraph, but there exist python bindings for igraph as well in case you prefer to use that. RStudio is an excellent IDE for R.

There are igraph bindings for Python and C++; it should be easy to translate the code in this guide into these other languages.

R is "a language and environment for statistical computing and graphics"[1] with a very active community of contributors. Available from http://www.r-project.org/.

RStudio is "a free and open source integrated development environment for R"[2]. It makes working with R more pleasant. Available from http://www.rstudio.com/.

igraph is "a free software package for creating and manipulating undirected and directed graphs"[3]. Available from http://igraph.sourceforge.net/.

The computers in the PC Lab should have these three components installed. If igraph is not installed, then you can do so through RStudio's install manager or directly through the command line with the install.packages instruction. Then, to load the library so that you can use its functionality you should introduce the following command into the console:

```
> library(igraph)
```

2 Basics

This section will cover the basic commands for creating, manipulating and visualizing graphs using igraph. It should also help as an introduction to the main R commands. If you are unfamiliar with R, there are many online tutorials. However, for this session there is very little programming involved so you are not required to learn a new programming language from scratch.

2.1 Creating graphs

The objects we study in this course are *graphs* (or *networks*). They consist of a set of *nodes* and a set of *edges*. As an example, if you type into the RStudio console the following command

```
g <- graph( c(1,2, 1,3, 2,3, 3,5), n=5 )
```

In this command, we are assigning to the variable g a graph that has nodes $V = \{1, 2, 3, 4, 5\}$ and has edges $E = \{(1, 2), (1, 3), (2, 3), (3, 5)\}$

The commands V(g) and E(g) print the list of nodes and edges of the graph g:

[1] From http://www.r-project.org/about.html
[2] From http://www.rstudio.com/ide/
[3] From http://igraph.sourceforge.net/introduction.html

```
> V(g)
Vertex sequence:
[1] 1 2 3 4 5
> E(g)
Edge sequence:

[1] 1 -> 2
[2] 1 -> 3
[3] 2 -> 3
[4] 3 -> 5
```

You can add nodes and edges to an already existing graph, e.g.:

```
> g <- graph.empty() + vertices(letters[1:10], color="red")
> g <- g + vertices(letters[11:20], color="blue")
> g <- g + edges(sample(V(g), 30, replace=TRUE), color="green")
> V(g)
Vertex sequence:
 [1] "a" "b" "c" "d" "e" "f" "g" "h" "i" "j" "k" "l" "m" "n" "o" "p" "q" "r" "s" "t"
> E(g)
Edge sequence:

[1]  q -> q
[2]  n -> a
[3]  j -> p
[4]  s -> h
[5]  f -> c
[6]  h -> f
[7]  g -> r
[8]  t -> t
[9]  j -> o
[10] c -> f
[11] i -> a
[12] o -> q
[13] c -> j
[14] r -> i
[15] a -> b
```

These lines create a graph g with 20 nodes and 15 random edges. Notice that nodes and edges can also have attributes, e.g. in this example we are assigning different colors to nodes. The command `sample` returns a vector containing a sample of 30 random vertices from g.

2.1.1 Loading graphs

We have seen how to create graphs from scratch, but most often we will be loading them from a file containing the graph in some sort of format. `igraph` handles many graph formats already. The simplest one is a file containing the edge list. For example, suppose that we have a file `list.txt` containing the following three edges:

```
0 1
1 2
2 3
```

We can create a graph using the command

```
> g <- read.graph("graph.txt", format="edgelist")
> V(g)
Vertex sequence:
[1] 1 2 3 4
> E(g)
Edge sequence:

[1] 1 -> 2
```

```
[2] 2 -> 3
[3] 3 -> 4
```

Notice that the node ids within `igraph` start with 1, but the input file expects the first id to be 0. We believe this is a bug in the implementation of `igraph`, but you should keep this in mind.

We can also access online graphs, e.g. the following command loads a *Pajek* graph from an online site

```
karate <- read.graph("http://cneurocvs.rmki.kfki.hu/igraph/karate.net", format="pajek")
```

2.1.2 Graph generators

`igraph` implements also many useful graph generators. We have already seen a few models in class, in particular: the Edös-Rényi model (ER), the Barabasi-Albert model (BA), and the Watts-Strogratz model (WS). The following commands generate graphs using these models:

```
er_graph <- erdos.renyi.game(100, 2/100)
ws_graph <- watts.strogatz.game(1, 100, 4, 0.05)
ba_graph <- barabasi.game(100)
```

2.2 Manipulating attributes in graphs

We can add attributes to nodes and edges of the graphs. These are useful for selecting certain types of nodes, and for visualization purposes.

```
> g <- erdos.renyi.game(10, 0.5)
> V(g)$color <- sample( c("red", "black"), vcount(g), rep=TRUE)
> E(g)$color <- "grey"
> red <- V(g)[ color == "red" ]
> bl <- V(g)[ color == "black" ]
> E(g)[ red %--% red ]$color <- "red"
> E(g)[ bl %--% bl ]$color <- "black"
```

What these commands do is to generate a random graph with 10 nodes, assigns random colors to the nodes, colors edges joining red nodes in red, and edges joining black nodes in black. All remaining edges are colored grey.

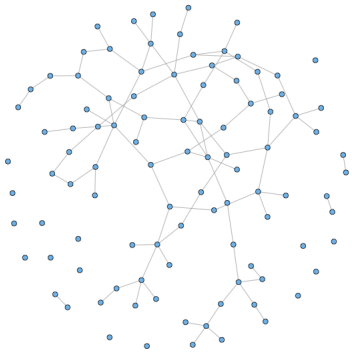
The next example assigns random weights to a lattice graph and then colors the ones having weight over 0.9 red, and the rest grey.

```
> g <- graph.lattice( c(10,10) )
> E(g)$weight <- runif(ecount(g))
> E(g)$color <- "grey"
> E(g)[ weight > 0.9 ]$color <- "red"
```

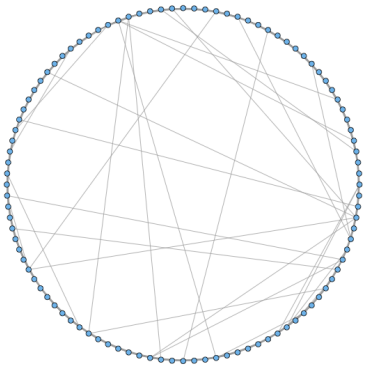
2.3 Visualizing graphs

A very important part in the analysis of networks is being able to *visualize* them. As an example the following commands render the three graphs depicted in the figure below.

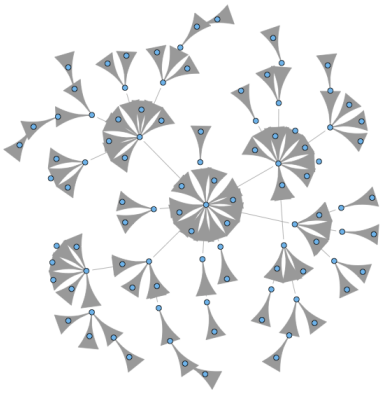
```
> er_graph <- erdos.renyi.game(100, 2/100)
> plot(er_graph, vertex.label=NA, vertex.size=3)
> ws_graph <- watts.strogatz.game(1, 100, 4, 0.05)
> plot(ws_graph, layout=layout.circle, vertex.label=NA, vertex.size=3)
> ba_graph <- barabasi.game(100)
> plot(ba_graph, vertex.label=NA, vertex.size=3)
```



Erdös-Rényi



Watts-Strogatz



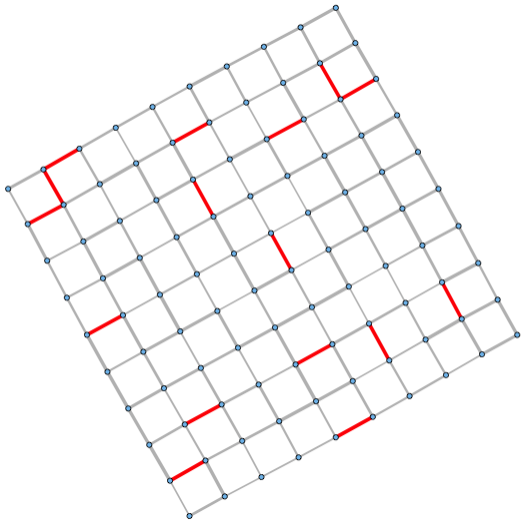
Barabási-Albert

The plot command is very flexible and has many parameters that control the behavior of the visualization. You can already see a few in the example above. For example, `vertex.label` controls the label written in the nodes, if set to `NA` then no text label is written. You can access all the parameters and their possible values through the help system by typing

```
> help(igraph.plotting)
```

As another example, consider adding attributes to edges for a nicer visualization:

```
> g <- graph.lattice( c(10,10) )
> E(g)$weight <- runif(ecount(g))
> E(g)$color <- "grey"
> E(g)[ weight > 0.9 ]$color <- "red"
> plot(g, vertex.size=2, vertex.label=NA, layout=layout.kamada.kawai,
edge.width=2+3*E(g)$weight)
```



2.4 Measuring graphs

There are many measures that help us understand and characterize networks. We have seen three in class already: diameter (and average path length), clustering coefficient (or transitivity), and degree distribution. `igraph` provides functions that compute these measures for you. The functions are: `diameter`, `transitivity`, `average.path.length`, `degree`, and `degree.distribution`. The examples below illustrate the usage of these functions.

For `diameter` and `average.path.length`

```
> g <- graph.lattice( length=100, dim=1, nei=4 )
> average.path.length(g)
[1] 8.79798
> diameter(g)
```

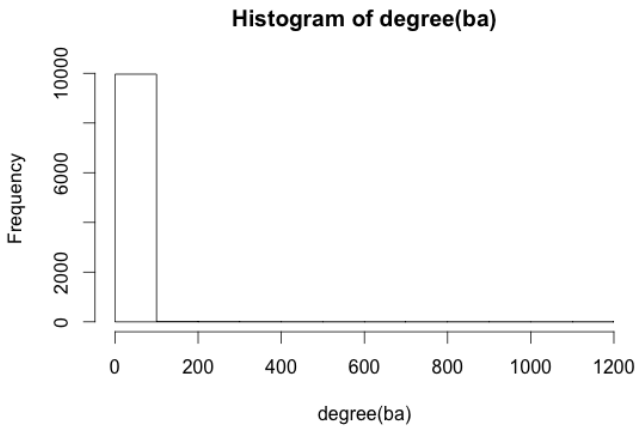
```
[1] 25
> g <- rewire.edges( g, prob=0.05 )
> average.path.length(g)
[1] 3.132323
> diameter(g)
[1] 6
```

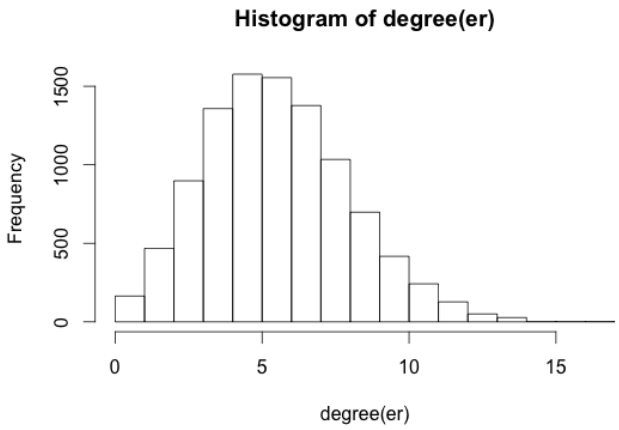
For `transitivity`

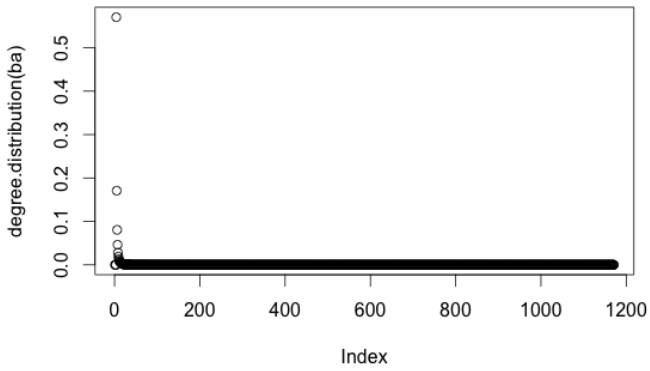
```
> ws <- watts.strogatz.game(1, 100, 4, 0.05)
> transitivity(ws)
[1] 0.5466147
> p_hat <- ecount(ws)/(vcount(ws)*(vcount(ws))/2)
> p_hat
[1] 0.08
> er <- erdos.renyi.game(100, p_hat)
> transitivity(er)
[1] 0.08411215
```

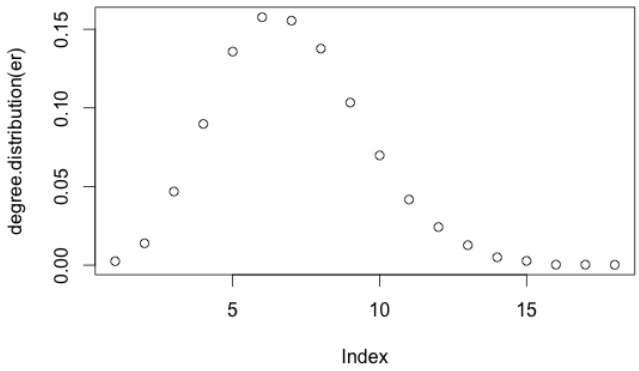
For `degree` and `degree.distribution`

```
> g <- graph.ring(10)
> plot(g)
> degree(g)
 [1] 2 2 2 2 2 2 2 2 2 2

> ba <- barabasi.game(10000, m=3)
> p_hat <- ecount(ba)/ ((vcount(ba)-1)*vcount(ba)/2)
> er <- erdos.renyi.game(10000, p_hat)
> degree.distribution(er)
 [1] 0.0025 0.0139 0.0468 0.0898 0.1358 0.1577 0.1555 0.1377 0.1034 0.0698 0.0417 0.0242
[13] 0.0127 0.0050 0.0027 0.0003 0.0003 0.0002

> hist(degree(er))
> hist(degree(ba))
> plot(degree.distribution(er))
> plot(degree.distribution(ba))
```









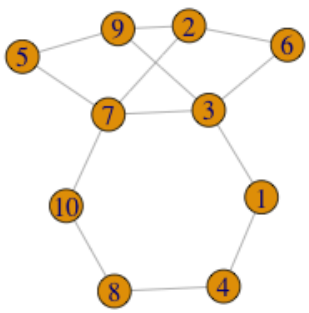
Barabási-Albert

Erdös-Rényi

3 Node centrality

There are commands for degree, closeness and betweenness centrality, as well as other measures such as pagerank and related. Here you can find an example:

```
> set.seed(1)
> g <- sample_gnp(10, 3/10)
> plot(g, vertex.size=25, layout=layout.kamada.kawai)
```



```
> betweenness(g)
 [1]  6.0000000  3.2500000 13.2500000  2.5833333  0.9166667
 [6] 0.9166667 13.2500000  2.5833333  3.2500000
[10]  6.0000000

> edge_betweenness(g)
 [1] 12.500000  8.500000  4.250000  6.583333  7.166667
 [6] 9.250000  6.583333  5.666667  4.083333  7.166667
[11]  4.250000 12.500000  8.500000

> degree(g)
 [1] 2 3 4 2 2 2 4 2 3 2

> closeness(g)
 [1] 0.05263158 0.05263158 0.06666667 0.04347826 0.04761905
 [6] 0.04761905 0.06666667 0.04347826 0.05263158 0.05263158

> page.rank(g)$vector
 [1] 0.08274197 0.10913228 0.14429762 0.08724407 0.07658406
 [6] 0.07658406 0.14429762 0.08724407 0.10913228 0.08274197
```

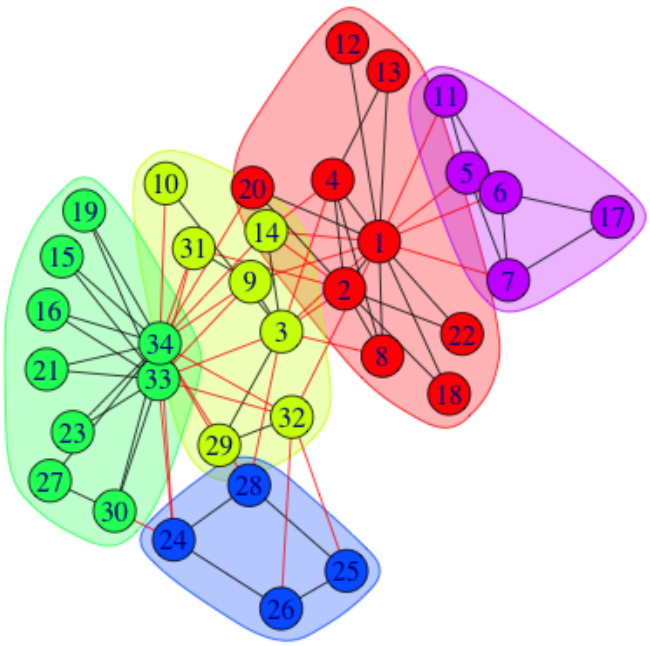
4 Community detection with `igraph`

In this session you will run and compare different community finding algorithms. In the `igraph` package there are a few already implemented, including some we have seen in theory class:

- `edge.betweenness.community` [Newman and Girvan, 2004]
- `fastgreedy.community` [Clauset et al., 2004] (modularity optimization method)
- `label.propagation.community` [Raghavan et al., 2007]
- `leading.eigenvector.community` [Newman, 2006]
- `multilevel.community` [Blondel et al., 2008] (the Louvain method)
- `optimal.community` [Brandes et al., 2008]
- `spinglass.community` [Reichardt and Bornholdt, 2006]
- `walktrap.community` [Pons and Latapy, 2005]
- `infomap.community` [Rosvall and Bergstrom, 2008]

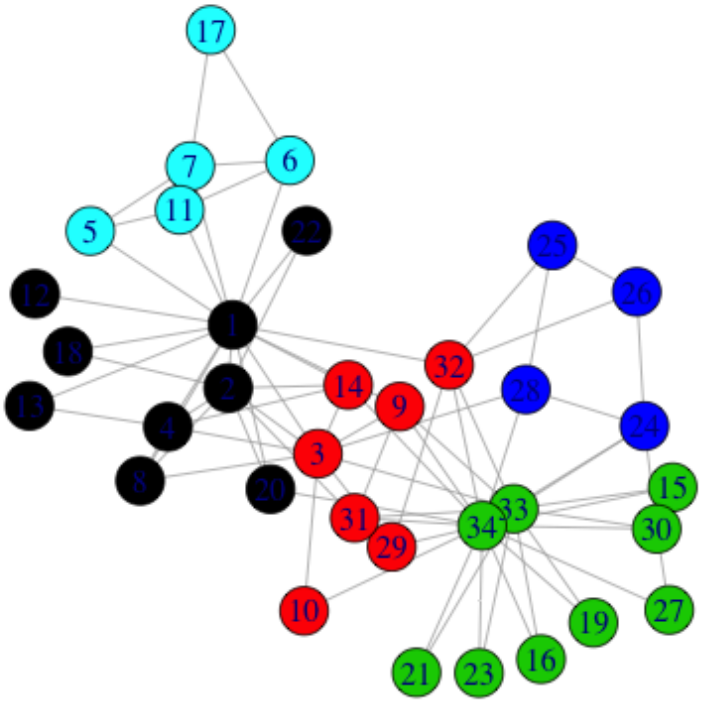
All of these methods return a `commmunities` object, which you can then use to explore, plot, and compute metrics on. As an example, consider the following snippet of code:

```
> karate <- graph.famous("Zachary")
> wc <- walktrap.community(karate)
> modularity(wc)
[1] 0.3532216
> membership(wc)
 [1] 1 1 2 1 5 5 5 1 2 2 5 1 1 2 3 3 5 1 3 1 3 1 3 4 4 4 3 4 2 3 2 2 3 3
> plot(wc, karate)
```



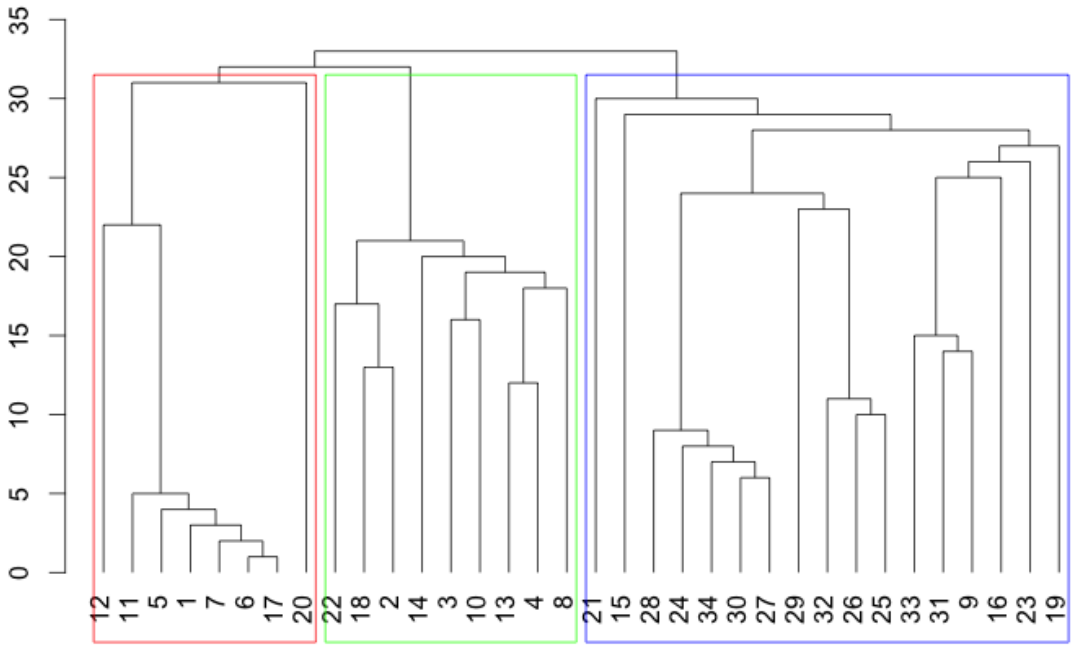
An alternative way of plotting communities without the shaded regions is:

```
> plot(karate, vertex.color=membership(wc))
```



For those algorithms that output communities with hierarchical structure, this information can be visualized using the `dendPlot` function, which displays the corresponding dendogram:

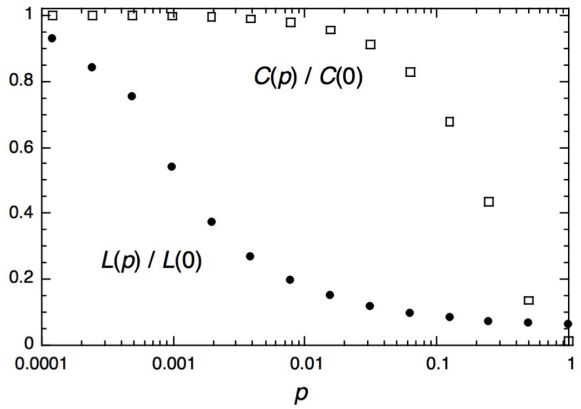
```
> karate <- graph.famous("Zachary")
> fc <- fastgreedy.community(karate)
> dendPlot(fc)
```



5 Your tasks

Before proceeding, make sure you understand the code and examples provided in this guide. Be prepared to consult `igraph`'s help and documentation[4] to carry out the following tasks.

Task 1. Reproduce the following graph seen in class, that is, plot the clustering coefficient and the average shortest-path as a function of the parameter p of the Watts-Strogatz model.



Notice that in order to include both values — average shortest path and clustering coefficient — in the same figure, the clustering coefficient and the average shortest-path values are normalized to be within the range $[0, 1]$. This is achieved by dividing the values by the value obtained at the left-most point, that is, when $p = 0$. Note the logarithmic scale of the "x" axis.

Task 2. Load the network from `edges.txt` provided with this session's files. Make sure you read it as an undirected graph.

[4] http://igraph.sourceforge.net/documentation.html

1. Describe the network a little. How many edges and nodes does it have? What is its diameter? And transitivity? And degree distribution? Does it look like a random network? Visualize the network with node sizes proportional to their pagerank.

2. Now, use a community detection algorithm of your choice from the list provided. How many nodes does the largest community found contain? Plot the histogram of community sizes. Plot the graph with its communities.

6 Deliverables

To deliver: You must deliver a brief report describing your results. The formats accepted for the report are, in principle, pdf, Word, OpenOffice, and Postscript. You also have to hand in the script or scripts you used to solve the tasks.

Procedure: Submit your work through the raco platform as a single zipped file.

Deadline: Work must be delivered within 3 weeks from the lab session you attend. Late submissions risk being penalized or not accepted at all. If you anticipate problems with the deadline, tell me as soon as possible.

References

[Blondel et al., 2008] Blondel, V. D., Guillaume, J.-l., Lambiotte, R., and Lefebvre, E. (2008). Fast unfolding of community hierarchies in large networks. *Networks*, pages 1–6.

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[Clauset et al., 2004] Clauset, A., Newman, M. E. J., and Moore, C. (2004). Finding community structure in very large networks. *Physical Review E*.

[Newman, 2006] Newman, M. E. J. (2006). Finding community structure in networks using the eigenvectors of matrices. *Physical review. E, Statistical, nonlinear, and soft matter physics*, 74:036104.

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[Pons and Latapy, 2005] Pons, P. and Latapy, M. (2005). Computing communities in large networks using random walks. *Journal of Graph Algorithms and Applications*, 10:191–218.

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[Reichardt and Bornholdt, 2006] Reichardt, J. and Bornholdt, S. (2006). Statistical mechanics of community detection. *Physical Review E*, 74.

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