R software for network analysis

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Joint with Mark and Carter and many others

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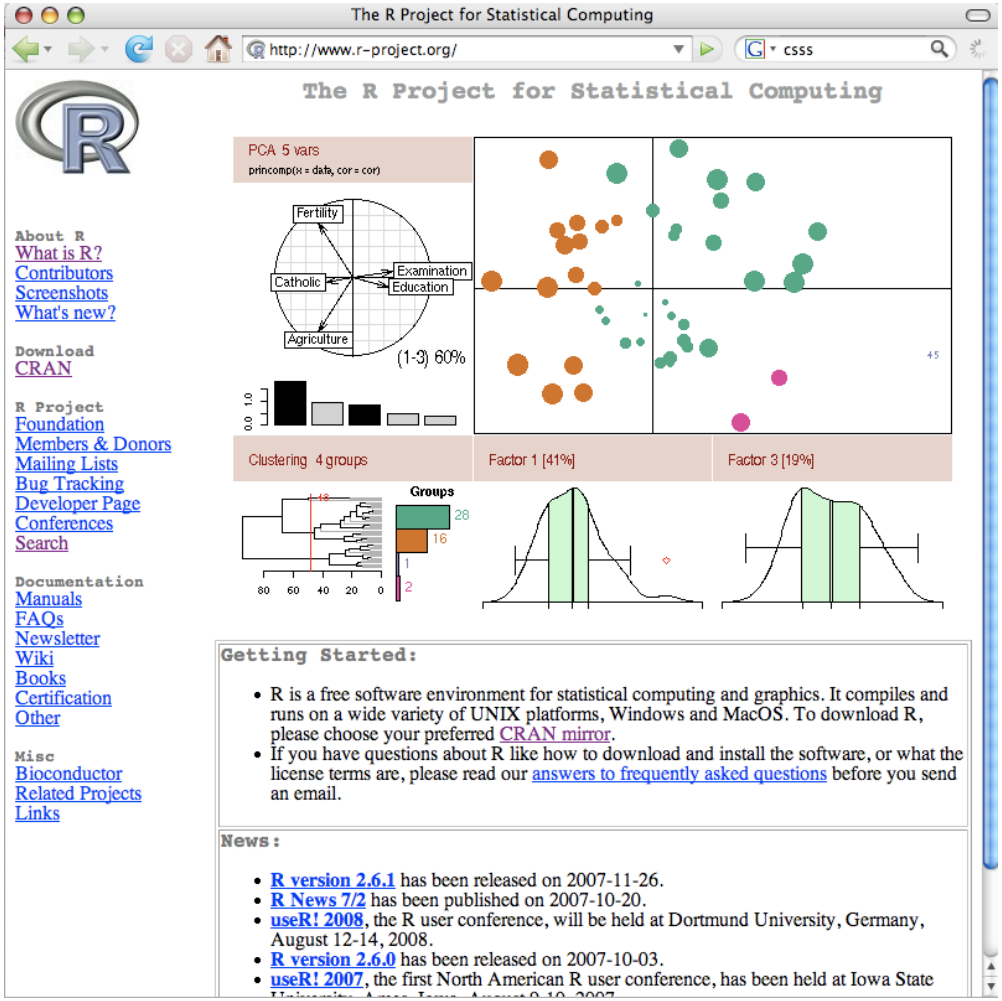
The R project and statnet

`www.r-project.org`



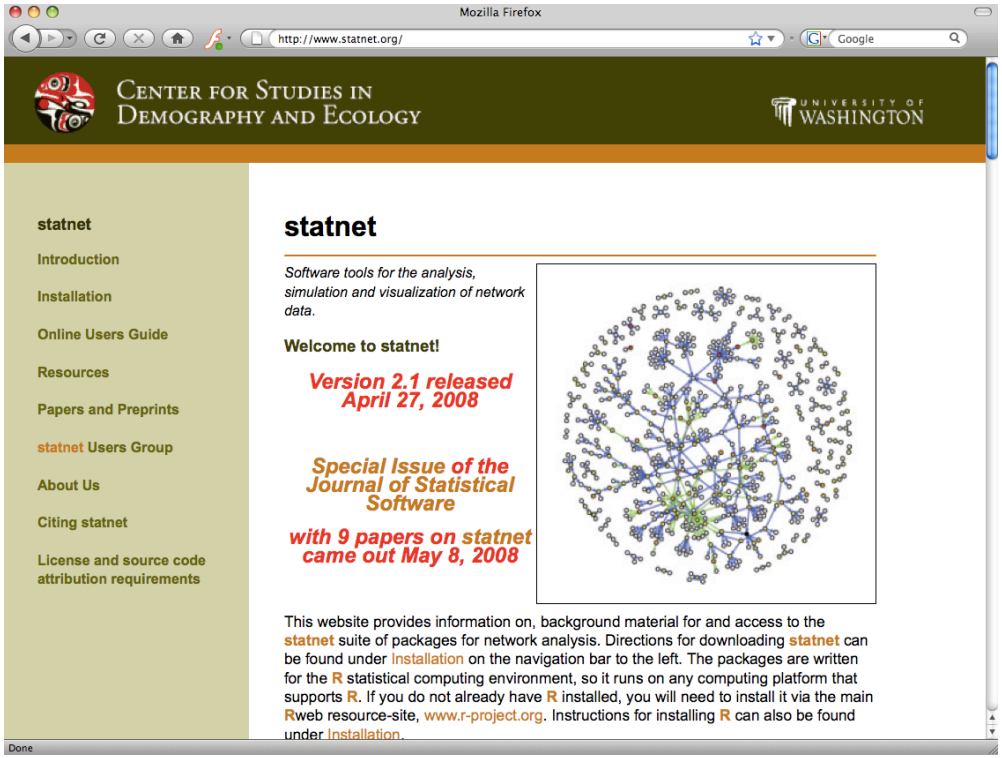
R: A statistical environment

- Open-source
- Extendible; ∼1500 user-created packages exist
- Mostly written in C
- Well-maintained (if not always well-documented) by a core group of the world's top computational statisticians

statnet

`www.statnet.org`

Thanks Carter!



statnet: A suite of R packages for network analysis

Includes packages:

- sna
- network
- ergm
- latentnet
- degreenet
- ...

Special issue (v 24) of *J. Stat. Soft.* devoted to statnet

A simple R package exploiting the R/C interface

```
% ls -RF1 pakij/
DESCRIPTION*
R/
src/

pakij//R:
my_runif.R
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pakij/R/my_runif.R

```
my_runif <- function(n) {
  .C("hey_diddle_diddle",
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     foo=double(n)
     )$foo
}
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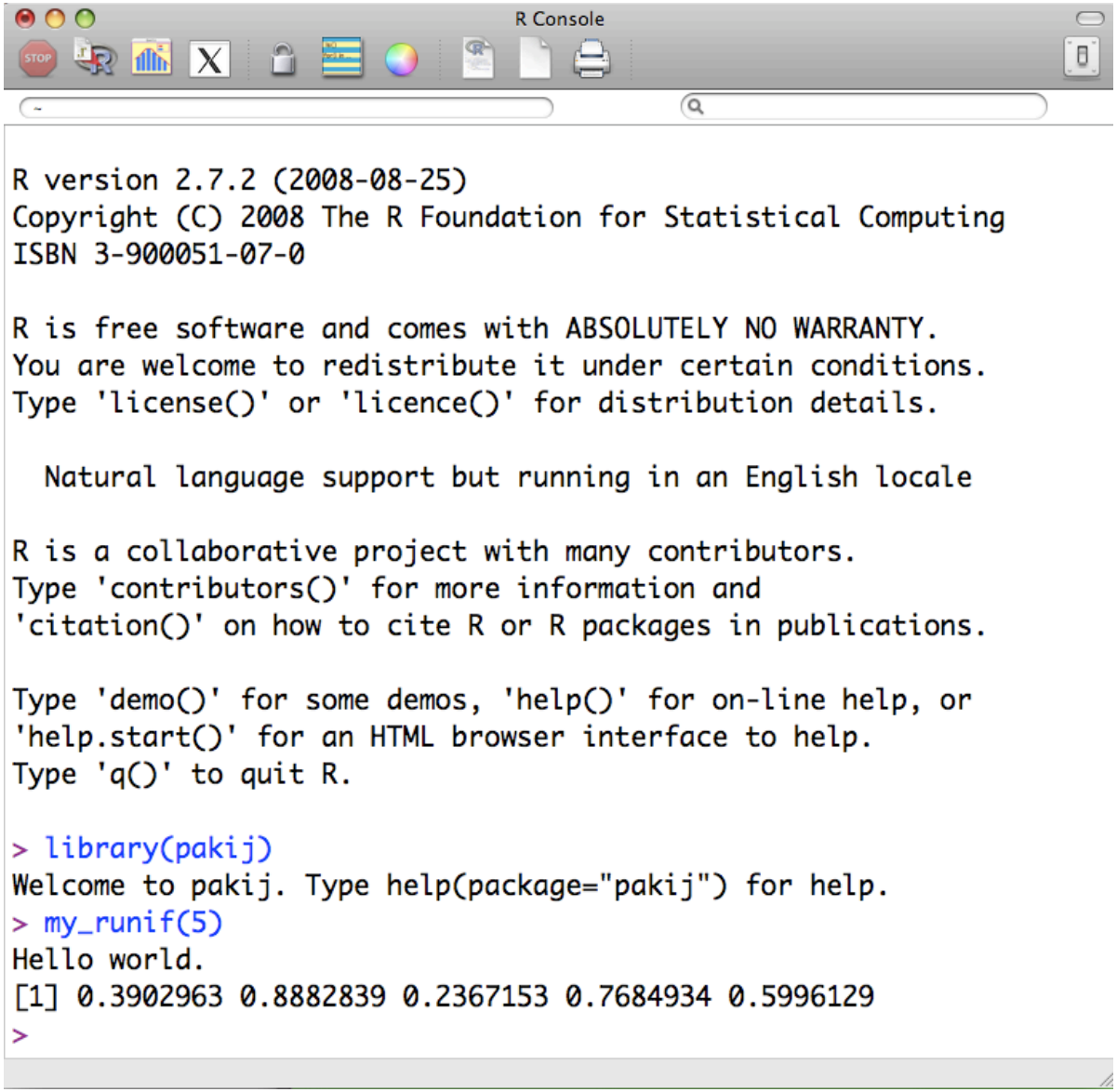
pakij/src/my_runif.c

```
#include <R.h>

void hey_diddle_diddle (int *n, double *answer) {
  Rprintf("Hello world.\n");
  GetRNGstate();  /* R: enable uniform RNG */
  for (int i=0; i<*n; i++)
    answer[i] = unif_rand();
  PutRNGstate();  /* Disable RNG before return */
}
```

Using the pakij package



The R API

- Entry points in the R executable callable from C code
- Example: Carter exploits this in the `network` package.

In network/R:

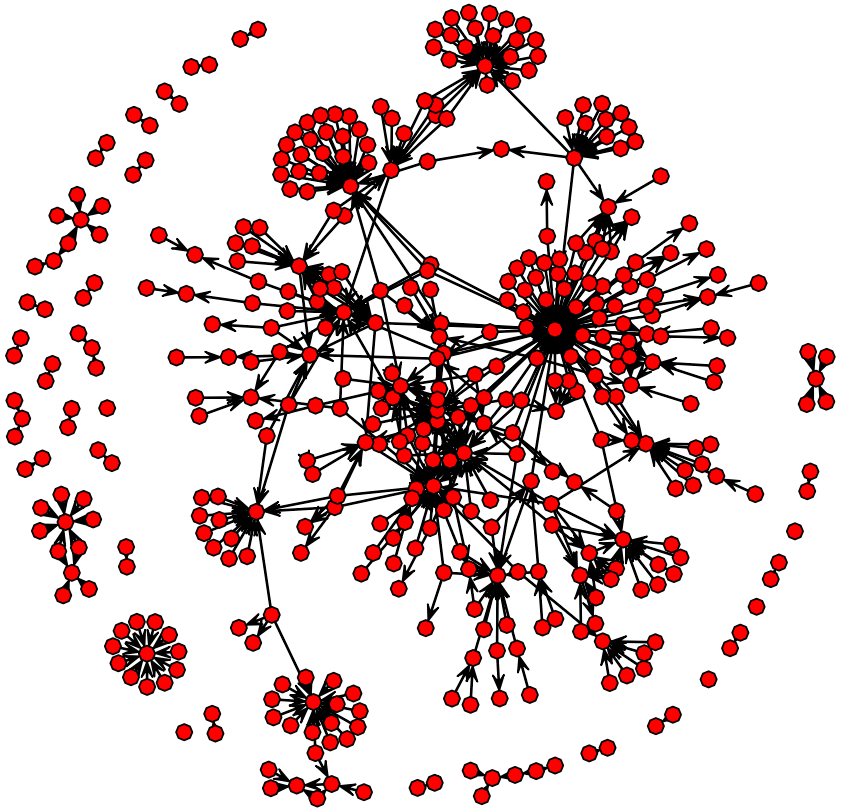
```
add.edge<-function(x, tail, head, names.eval=NULL,
                   vals.eval=NULL, edge.check=FALSE, ...){
  #Check to be sure we were called with a network
  if(!is.network(x))
    stop("add.edge requires an argument of class network.")
  #Do the deed
  invisible(.Call("addEdge_R",x,tail,head,names.eval,vals.eval,
                  edge.check, PACKAGE="network"))
}
```

In network/src:

```
SEXP addEdge_R(SEXP x, SEXP tail, SEXP head, SEXP namesEval,
               SEXP valsEval, SEXP edgeCheck) {
   ...
```

An E. Coli network (Salgado et al., 2001) in R

```
> plot(ecoli1)
```



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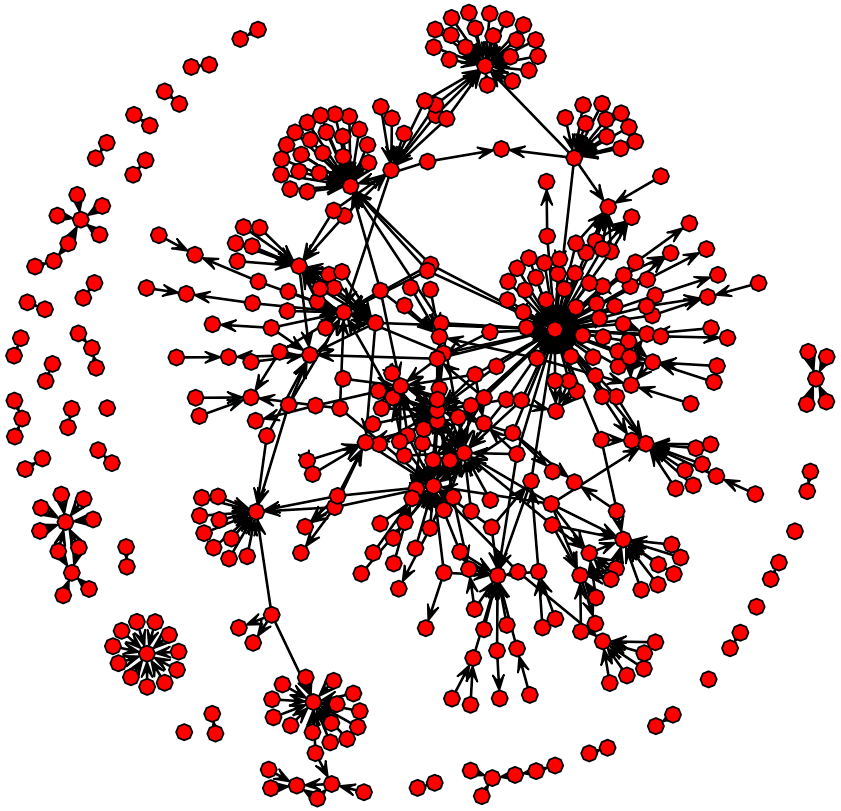

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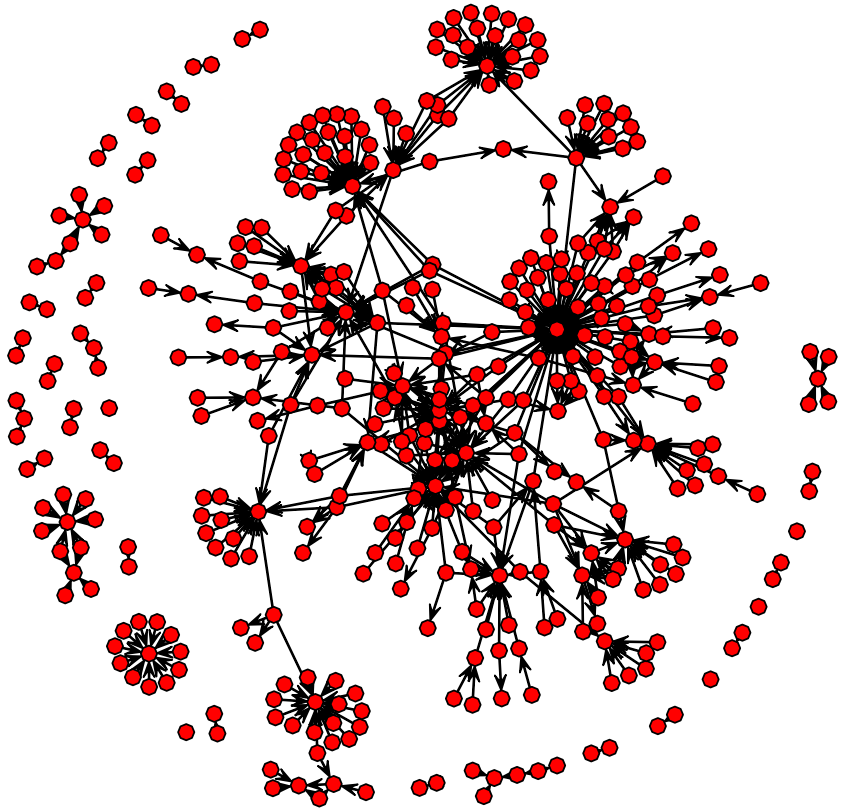
> class(ecoli1)
[1] "network"
> summary(ecoli1)
Network attributes:
  vertices: 423
   directed : TRUE
   hyper : FALSE
   loops : FALSE
   multiple : FALSE
   bipartite : FALSE
   total edges= 519
   density = 0.002907465

 Vertex attributes:

self:
FALSE  TRUE
  364    59
```



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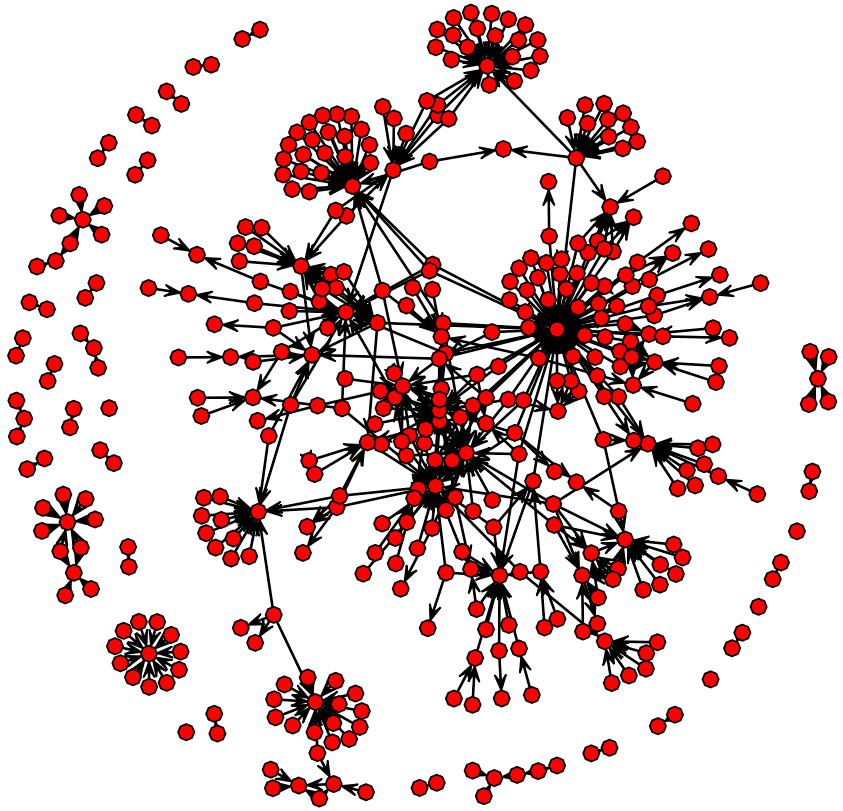
> summary(ecoli1 ~ edges + odegree(0:5))
   edges odegree0 odegree1 odegree2 odegree3 odegree4 odegree5
     519       81      229       71       25       13        3
```



A simple ERGM using the ergm package in R

The `ecoli1` network has 519 edges, 423 nodes (thus 423×422 possible directed edges). Take $g(y) = \#$ edges in y:

$$\begin{aligned} P(Y = y) &\propto \exp\{\theta \times \#\text{ edges in } y\} \\ &= \left(\frac{p}{1-p}\right)^{(\#\text{ edges in } y)} \end{aligned}$$

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```
> model1 <- ergm(ecoli1 ~ edges)
> model1$coef
    edges
-5.837562
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This means the MLE is $\hat{\theta} = -5.84$. It is exact because $g(y)$ in this example ensures independent Y_{ij}, so MPLE=MLE!

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Observe:

```
> log(519 / (423 * 422 - 519))
[1] -5.837562
```

Another simple ERGM

Let's consider an edge to have one of four categories, depending on whether or not each of its endpoints is self-regulating:

```
> model2 <- ergm(ecoli1 ~ nodemix("self"))
> summary(model2)
Pseudolikelihood Results:
                      Estimate Std. Error MCMC s.e. p-value
mix.self.FALSE.FALSE -6.61974    0.07543         NA  <1e-04
mix.self.TRUE.FALSE  -7.48923    0.28874         NA  <1e-04
mix.self.FALSE.TRUE  -4.22686    0.05730         NA  <1e-04
mix.self.TRUE.TRUE   -5.04049    0.21389         NA  <1e-04
```

This choice of $g(y)$ also ensures independent Y_{ij}, so the MLE and the MPLE are the same. Thus, the MLE is found analytically and there is no MCMC standard error.