INA - INAscene - scenario analyses for projects

Experiment 2 from Garrett (2021). Evaluating the likelihood of management success in a region, including uncertainty quantification

INAscene function in the INA package

This package implements impact network analysis (INA), an analysis of the effects of information and other technologies on regional outcomes such as the establishment of an invasive pathogen, through linked socioeconomic networks and biophysical networks.

```
# use the following three commented commands if you do not yet have
# INA or need to update the version

#install.packages("devtools") # use this command if you do not yet have devtools
#installed

#library(devtools)

#devtools::install_github("GarrettLab/INA")

library(INA)

library(igraph)
```

```
##
## Attaching package: 'igraph'

## The following objects are masked from 'package:stats':
##
##     decompose, spectrum

## The following object is masked from 'package:base':
##
##     union
```

```
library(plot3D)
```

```
## Warning in system2("/usr/bin/otool", c("-L", shQuote(DSO)), stdout = TRUE):
## running command ''/usr/bin/otool' -L '/Library/Frameworks/R.framework/Resources/
## library/tcltk/libs//tcltk.so'' had status 69
```

```
library(ggplot2)
```

This vignette is designed to illustrate how the function INAscene in the INA package can be used to evaluate likely project success and how changing the project strategy may increase the likelihood of success.

First, consider a luxurious scenario where there is a lot of information available about the system in which a management technology is to be distributed for invasive species management. In this scenario, the parameters chosen are known with confidence to be reasonable for the impact network analysis.

(In this scenario, the 'science of science' component is not used - that is, the threshold for communication is 0, because the scenario is based on evaluating outcomes assuming the project goes forward.)

The impact network analysis proceeds to evaluate the outcomes by which success of an intervention project will be judged, such as share of region invaded, health, productivity, and profit, given the starting conditions, network structures, and other parameters. Here we give examples for evaluating the proportion of the system that has been invaded as a priority.

Experiment 2A

In experiment 2A, the analysis is performed at the planning stage of a project, to determine the probability distribution of outcomes after 5 time steps.

For this example, the 100 nodes are randomly distributed across a 50 x 50 unit area. An invasive enters the northern part of the region (along the upper edge of the map) in 5% of nodes, and 5% of nodes (randomly distributed) have information about the management technology.

For convenience, a small number of realizations are considered here.

```
sens.exp2a <-
  INAscene(
  nreals = 10,
  ntimesteps = 5,
  doplot = F,
  readgeocoords = F,
  geocoords = NA,
  numnodes = 50,
  xrange = c(0, 50),
  yrange = c(0, 50),
  randgeo = T,
  readinitinfo = F,
  initinfo = NA,
  initinfo.norp = 'prop',
  initinfo.n = NA,
  initinfo.p = 0.05,
  initinfo.dist = 'random',
  readinitbio = F,
  initbio = NA,
  initbio.norp = 'prop',
  initbio.n = NA,
  initbio.p = 0.05,
  initbio.dist = 'upedge',
  readseam = F,
  seam = NA,
  seamdist = 'powerlaw',
  seamrandp = NA,
  seampla = 1,
  seamplb = 1.5,
  readbpam = F,
```

```
  bpam = NA,
  bpamdist = 'powerlaw',
  bpamrandp = NA,
  bpampla = 1,
  bpamplb = 1,
  readprobadoptvec = F,
  probadoptvec = NA,
  probadoptmean = 0.5,
  probadoptsd = 0.2,
  readprobestabvec = F,
  probestabvec = NA,
  probestabmean = 0.5,
  probestabsd = 0.1,
  maneffdir = 'decrease_estab',
  maneffmean = 0.5,
  maneffsd = 0.1,
  usethreshman = F,
  maneffthresh = NA,
  sampeffort = NA
  )
```

```
## [1] "ending parameter combination 1"
```

```
jt2 <- sens.exp2a$multdetails

# Check the distribution of the invasive establishment proportions (set o'
# estab)

jt2[[1]]$setoestab
```
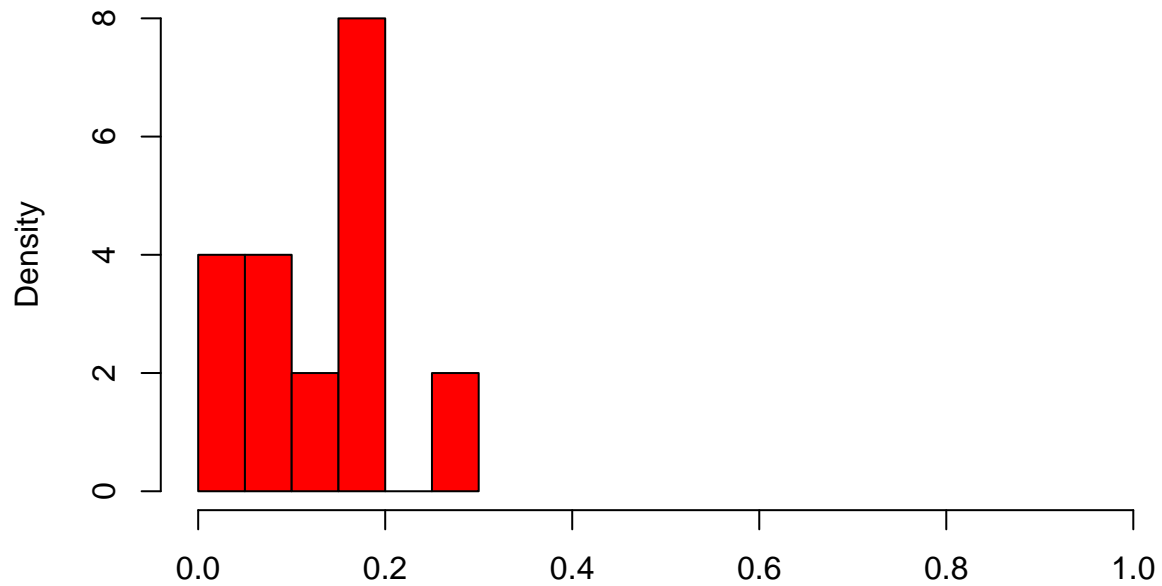
```
##  [1] 0.16 0.04 0.26 0.16 0.06 0.20 0.00 0.16 0.08 0.14
```

```
hist(
  jt2[[1]]$setoestab,
  main = 'Proportion nodes with invasive established',
  xlim = c(0, 1),
  xlab = '',
  col = 'red',
  freq = F
  )
```

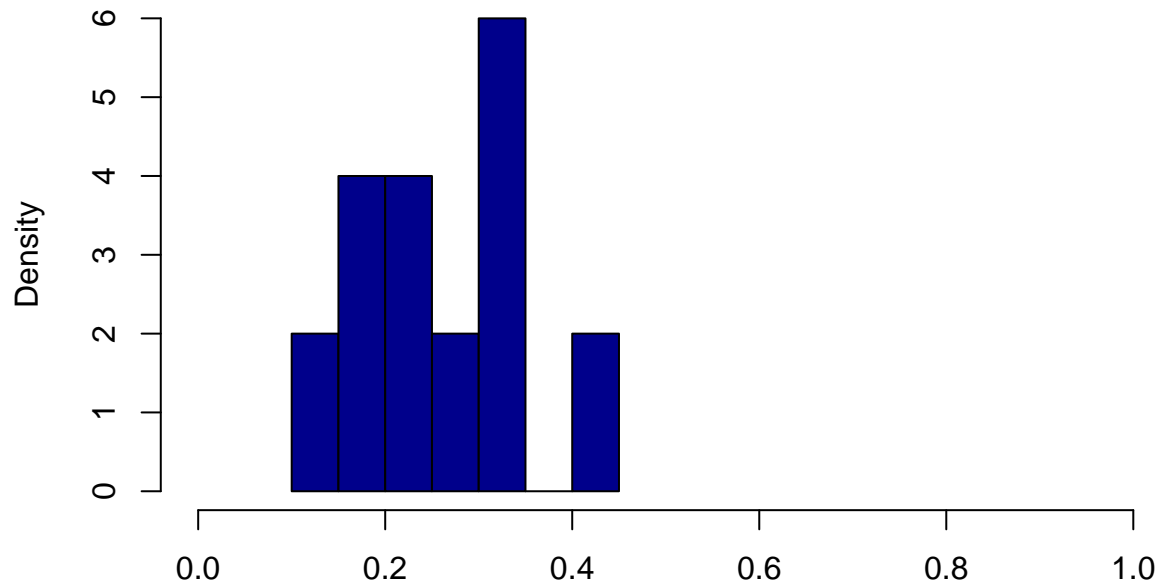**Proportion nodes with invasive established**


```
# Check the distribution of the proportion nodes deciding to adopt the
# technology (set o' dec)

jt2[[1]]$setodec
```

```
##  [1] 0.24 0.28 0.18 0.32 0.22 0.34 0.42 0.16 0.34 0.10
```

```
hist(
  jt2[[1]]$setodec,
  main = 'Proportion nodes with decision to adopt technology',
  xlim = c(0, 1),
  xlab = '',
  col = 'darkblue',
  freq = F
  )
```

Proportion nodes with decision to adopt technology


```
# Check the distribution of the proportion nodes that received communication
# about the technology (set o' com)

jt2[[1]]$setocom
```
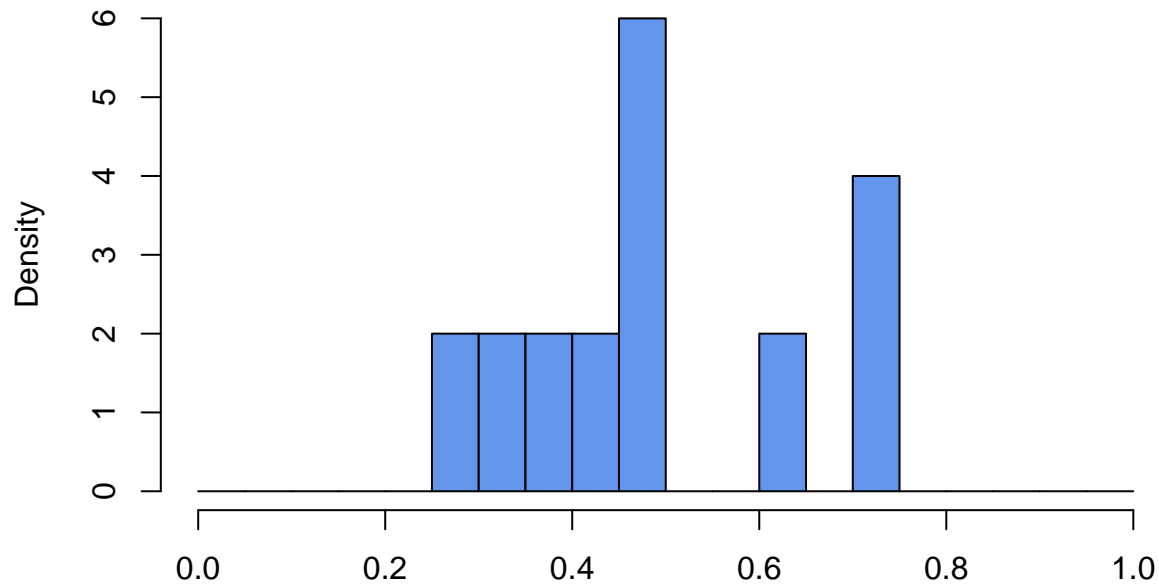
```
##  [1] 0.42 0.48 0.50 0.38 0.46 0.64 0.74 0.34 0.74 0.30
```

```
hist(
  jt2[[1]]$setocom,
  main = 'Proportion nodes receiving communication about technology',
  xlim = c(0, 1),
  xlab = '',
  col = 'cornflowerblue',
  breaks = seq(0, 1, 0.05),
  freq = F
  )
```

Proportion nodes receiving communication about technology

As the system is understood now, over the course of 5 time steps the species would become established in around 1/3 of the locations. Communication would reach around 2/3 of the locations, but only around 1/3 of locations would have the management technology applied.

Example 2B

In experiment 2B, project planners ask how the results are likely to change if the management effect size can be increased, so outcomes are evaluated for a range of values of the mean management effect size.

```r
sens.exp2b <-
  INAscene(
  nreals = 20,
  ntimesteps = 5,
  doplot = F,
  readgeocoords = F,
  geocoords = NA,
  numnodes = 50,
  xrange = c(0, 50),
  yrange = c(0, 50),
  randgeo = T,
  readinitinfo = F,
  initinfo = NA,
  initinfo.norp = 'prop',
  initinfo.n = NA,
  initinfo.p = 0.05,
  initinfo.dist = 'random',
  readinitbio = F,
  initbio = NA,
  initbio.norp = 'prop',
  initbio.n = NA,
  initbio.p = 0.05,
```

```
  initbio.dist = 'upedge',
  readseam = F,
  seam = NA,
  seamdist = 'powerlaw',
  seamrandp = NA,
  seampla = 1,
  seamplb = 0.5,
  readbpam = F,
  bpam = NA,
  bpamdist = 'powerlaw',
  bpamrandp = NA,
  bpampla = 1,
  bpamplb = 0.5,
  readprobadoptvec = F,
  probadoptvec = NA,
  probadoptmean = 0.9,
  probadoptsd = 0.1,
  readprobestabvec = F,
  probestabvec = NA,
  probestabmean = 0.5,
  probestabsd = 0.2,
  maneffdir = 'decrease_estab',
  maneffmean = seq(0, 1, 0.1),
  maneffsd = 0.2,
  usethreshman = F,
  maneffthresh = NA,
  sampeffort = NA
  )
```

```
## [1] "ending parameter combination 1"
## [1] "ending parameter combination 2"
## [1] "ending parameter combination 3"
## [1] "ending parameter combination 4"
## [1] "ending parameter combination 5"
## [1] "ending parameter combination 6"
## [1] "ending parameter combination 7"
## [1] "ending parameter combination 8"
## [1] "ending parameter combination 9"
## [1] "ending parameter combination 10"
## [1] "ending parameter combination 11"
```

```
jt2 <- sens.exp2b$multout

# Plot how the mean establishment proportion is a function of the mean
# management effect

plot(
  jt2$maneffmean,
  jt2$mestab,
  xlab = 'Mean management effect size',
  ylab = 'Proportion nodes with invasive established',
  ylim = c(0, 1),
  col = 'red',
```
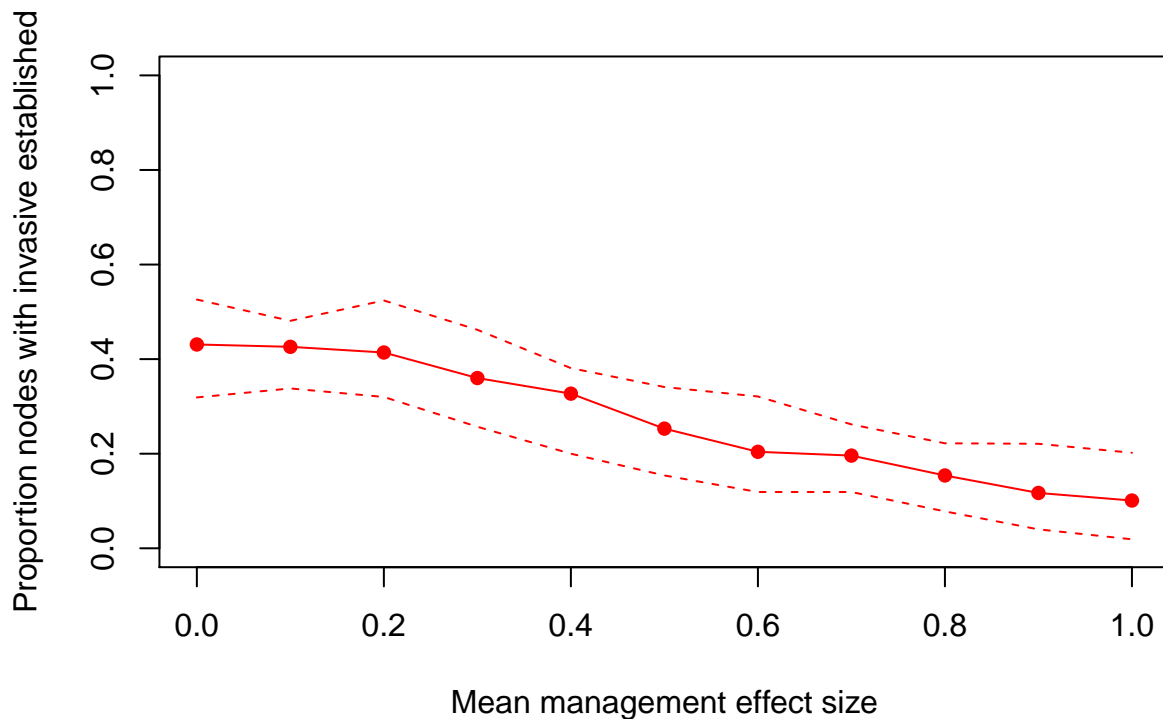
```
    pch = 16
    )
lines(jt2$maneffmean, jt2$mestab, col = 'red')

# also indicate the 95th percentile

lines(jt2$maneffmean, jt2$estab95, col='red', lty=2)

# also indicate the 5th percentile

lines(jt2$maneffmean, jt2$estab5, col='red', lty=2)
```


In this scenario, changing the mean management effect size from 0 to 1 can reduce the proportion of sites with bioentity establishment from around 0.4 to around 0.1. Other limiting factors, such as limits to communication, keep the proportion establishment from reaching 0.

Evaluating the influence of management effect size for four network types

To see this analysis for some common network types, let's try it again with the socioeconomic networks based on the same types of networks illustrated in Experiment 1. (Note that in real systems, links are probably somewhat more likely across shorter distances, while these example networks are not based on distance between the associated land nodes.)

The following examples are also different from the example just before in that only one node starts with the information present. A single starting node was used here to make clearer how the different network types would vary in their influence on the regional effects of changing the management effect size. A single starting node could be realistic for scenarios where there is a single innovator from whom others learn.

First, here is the analysis of how bioentity establishment responds to management effect size, for a socioeconomic network that is a random network.

```r
# Create a random network for use as a socioeconomic network

random.eq <- sample_gnp(n=50, p=0.05, directed=T, loops=F)
layout.random <- layout_with_kk(random.eq)
plot(
  random.eq,
  edge.arrow.size = 0.3,
  vertex.size = 10,
  vertex.label.cex = 0.5,
  layout = layout.random,
  vertex.color = 'orange'
  )
```
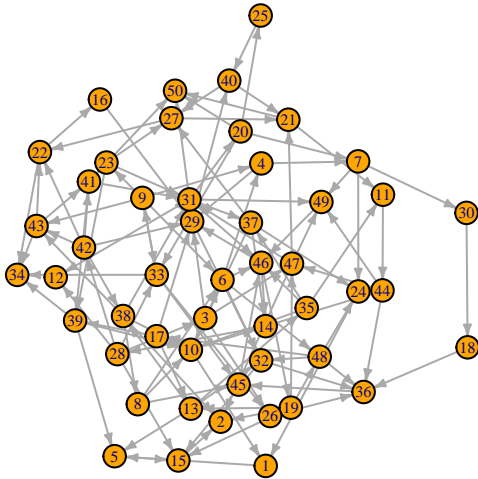


```r
# Convert igraph formatted adjacency matrix to simple matrix

random.eqni <- as_adjacency_matrix(random.eq, sparse=F)

sens.exp2br <-
  INAscene(
  nreals = 100,
  ntimesteps = 5,
  doplot = F,
  readgeocoords = F,
  geocoords = NA,
  numnodes = 50,
  xrange = c(0, 50),
  yrange = c(0, 50),
  randgeo = T,
  readinitinfo = F,
  initinfo = NA,
  initinfo.norp = 'num',
  initinfo.n = 1,
  initinfo.p = NA,
  initinfo.dist = 'random',
  readinitbio = F,
  initbio = NA,
  initbio.norp = 'prop',
```

```
    initbio.n = NA,
    initbio.p = 0.05,
    initbio.dist = 'upedge',
    readseam = T,
    seam = random.eqni,
    seamdist = NA,
    seamrandp = NA,
    seampla = NA,
    seamplb = NA,
    readbpam = F,
    bpam = NA,
    bpamdist = 'powerlaw',
    bpamrandp = NA,
    bpampla = 1,
    bpamplb = 0.5,
    readprobadoptvec = F,
    probadoptvec = NA,
    probadoptmean = 0.9,
    probadoptsd = 0.1,
    readprobestabvec = F,
    probestabvec = NA,
    probestabmean = 0.5,
    probestabsd = 0.2,
    maneffdir = 'decrease_estab',
    maneffmean = seq(0, 1, 0.1),
    maneffsd = 0.2,
    usethreshman = F,
    maneffthresh = NA,
    sampeffort = NA
    )
```

```
## [1] "ending parameter combination 1"
## [1] "ending parameter combination 2"
## [1] "ending parameter combination 3"
## [1] "ending parameter combination 4"
## [1] "ending parameter combination 5"
## [1] "ending parameter combination 6"
## [1] "ending parameter combination 7"
## [1] "ending parameter combination 8"
## [1] "ending parameter combination 9"
## [1] "ending parameter combination 10"
## [1] "ending parameter combination 11"
```

```
jt2 <- sens.exp2br$multout

# Plot the mean establishment proportion as a function of the mean management
# effect

plot(
  jt2$maneffmean,
  jt2$mestab,
  xlab = 'Mean management effect size',
  ylab = 'Proportion nodes with invasive established',
```

```
    ylim = c(0, 1),
    col = 'orange',
    pch = 16
    )
lines(jt2$maneffmean, jt2$mestab, col='orange')
title(main='Random network')
```

Random network


```
# For plotting the three scenarios later
mestab.rand <- jt2$mestab
```

Next, for a socioeconomic network that is a small world network.

```
# Create a small world network for use as a socioeconomic network

small.eq <- sample_smallworld(dim=1, size=50, nei=2, p=0.05, loops=F)
layout.small <- layout_with_kk(small.eq)
plot(
  small.eq,
  edge.arrow.size = 0.3,
  vertex.size = 10,
  vertex.label.cex = 0.5,
  layout = layout.small,
  vertex.color = 'darkblue'
  )
```
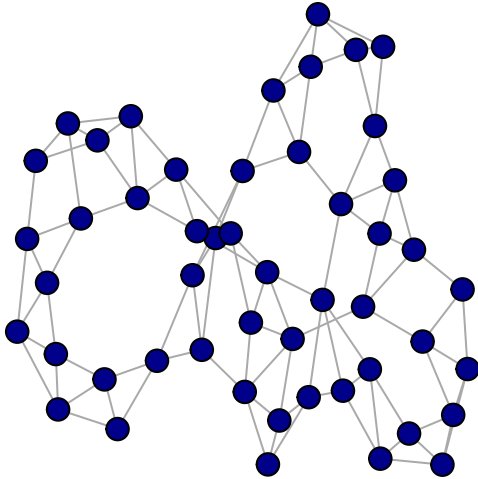
```r
# Convert igraph formatted adjacency matrix to simple matrix

small.eqni <- as_adjacency_matrix(small.eq, sparse=F)

sens.exp2bsw <-
  INAscene(
  nreals = 100,
  ntimesteps = 5,
  doplot = F,
  readgeocoords = F,
  geocoords = NA,
  numnodes = 50,
  xrange = c(0, 50),
  yrange = c(0, 50),
  randgeo = T,
  readinitinfo = F,
  initinfo = NA,
  initinfo.norp = 'num',
  initinfo.n = 1,
  initinfo.p = NA,
  initinfo.dist = 'random',
  readinitbio = F,
  initbio = NA,
  initbio.norp = 'prop',
  initbio.n = NA,
  initbio.p = 0.05,
  initbio.dist = 'upedge',
  readseam = T,
  seam = small.eqni,
  seamdist = NA,
  seamrandp = NA,
  seampla = NA,
  seamplb = NA,
  readbpam = F,
  bpam = NA,
  bpamdist = 'powerlaw',
  bpamrandp = NA,
  bpampla = 1,
```

```
  bpamplb = 0.5,
  readprobadoptvec = F,
  probadoptvec = NA,
  probadoptmean = 0.9,
  probadoptsd = 0.1,
  readprobestabvec = F,
  probestabvec = NA,
  probestabmean = 0.5,
  probestabsd = 0.2,
  maneffdir = 'decrease_estab',
  maneffmean = seq(0, 1, 0.1),
  maneffsd = 0.2,
  usethreshman = F,
  maneffthresh = NA,
  sampeffort = NA
  )
```

```
## [1] "ending parameter combination 1"
## [1] "ending parameter combination 2"
## [1] "ending parameter combination 3"
## [1] "ending parameter combination 4"
## [1] "ending parameter combination 5"
## [1] "ending parameter combination 6"
## [1] "ending parameter combination 7"
## [1] "ending parameter combination 8"
## [1] "ending parameter combination 9"
## [1] "ending parameter combination 10"
## [1] "ending parameter combination 11"
```

```
jt2 <- sens.exp2bsw$multout

# Plot the mean establishment proportion as a function of the mean management effect

plot(
  jt2$maneffmean,
  jt2$mestab,
  xlab = 'Mean management effect size',
  ylab = 'Proportion nodes with invasive established',
  ylim = c(0, 1),
  col = 'darkblue',
  pch = 16
  )
lines(jt2$maneffmean, jt2$mestab, col='darkblue')
title(main='Small world network')
```
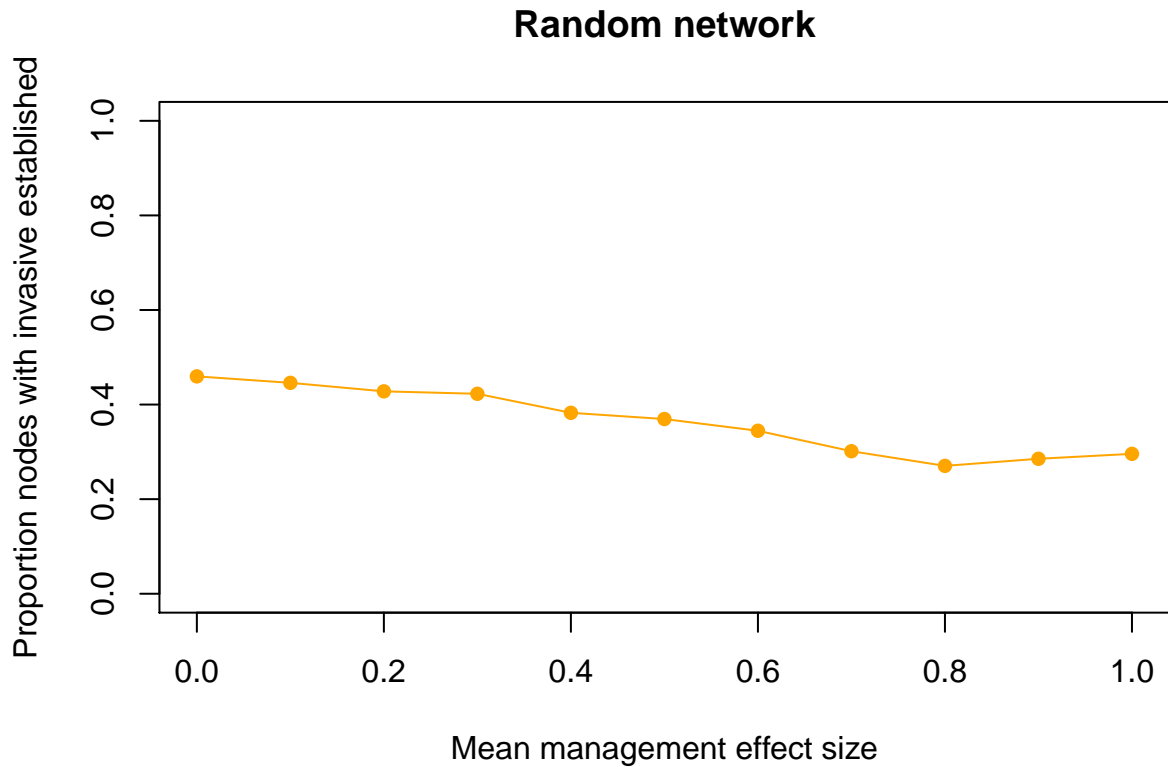
Small world network


```
# For plotting the three scenarios later
mestab.sw <- jt2$mestab
```

And, for comparison, a socioeconomic network that is technically generated as a small world network, but with a very low probability of rewiring - that is, a very low probability of links that reach across the system.

```
# Create a small world network for use as a socioeconomic network

smalllow.eq <- sample_smallworld(dim=1, size=50, nei=2, p=0.0001, loops=F)
layout.smalllow <- layout_with_kk(smalllow.eq)
plot(
  smalllow.eq,
  edge.arrow.size = 0.3,
  vertex.size = 10,
  vertex.label.cex = 0.5,
  layout = layout.smalllow,
  vertex.color = 'lightblue'
  )
```
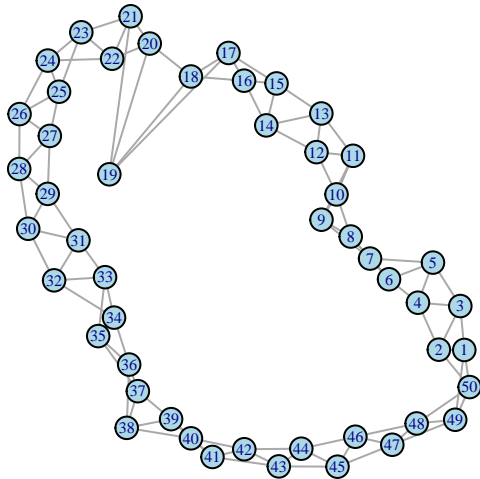
```r
# Convert igraph formatted adjacency matrix to simple matrix

smalllow.eqni <- as_adjacency_matrix(smalllow.eq, sparse=F)

sens.exp2bswlow <-
  INAscene(
  nreals = 100,
  ntimesteps = 5,
  doplot = F,
  readgeocoords = F,
  geocoords = NA,
  numnodes = 50,
  xrange = c(0, 50),
  yrange = c(0, 50),
  randgeo = T,
  readinitinfo = F,
  initinfo = NA,
  initinfo.norp = 'num',
  initinfo.n = 1,
  initinfo.p = NA,
  initinfo.dist = 'random',
  readinitbio = F,
  initbio = NA,
  initbio.norp = 'prop',
  initbio.n = NA,
  initbio.p = 0.05,
  initbio.dist = 'upedge',
  readseam = T,
  seam = smalllow.eqni,
  seamdist = NA,
  seamrandp = NA,
  seampla = NA,
  seamplb = NA,
  readbpam = F,
  bpam = NA,
  bpamdist = 'powerlaw',
  bpamrandp = NA,
  bpampla = 1,
```

```r
  bpamplb = 0.5,
  readprobadoptvec = F,
  probadoptvec = NA,
  probadoptmean = 0.9,
  probadoptsd = 0.1,
  readprobestabvec = F,
  probestabvec = NA,
  probestabmean = 0.5,
  probestabsd = 0.2,
  maneffdir = 'decrease_estab',
  maneffmean = seq(0, 1, 0.1),
  maneffsd = 0.2,
  usethreshman = F,
  maneffthresh = NA,
  sampeffort = NA
  )
```

```
## [1] "ending parameter combination 1"
## [1] "ending parameter combination 2"
## [1] "ending parameter combination 3"
## [1] "ending parameter combination 4"
## [1] "ending parameter combination 5"
## [1] "ending parameter combination 6"
## [1] "ending parameter combination 7"
## [1] "ending parameter combination 8"
## [1] "ending parameter combination 9"
## [1] "ending parameter combination 10"
## [1] "ending parameter combination 11"
```

```r
jt2 <- sens.exp2bswlow$multout

# Plot the mean establishment proportion as a function of the mean management
# effect

plot(
  jt2$maneffmean,
  jt2$mestab,
  xlab = 'Mean management effect size',
  ylab = 'Proportion nodes with invasive established',
  ylim = c(0, 1),
  col = 'lightblue',
  pch = 16
  )
lines(jt2$maneffmean, jt2$mestab, col='lightblue')
title(main='Small world network')
```
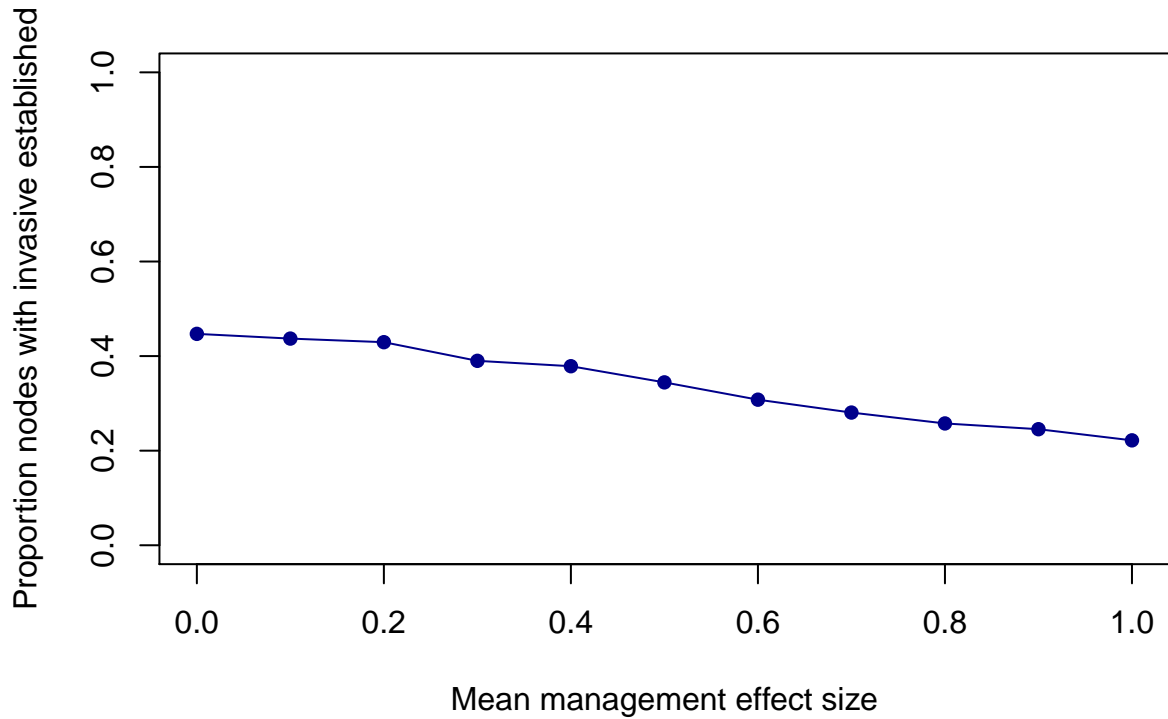
Small world network


```
# For plotting the three scenarios later
mestab.swlow <- jt2$mestab
```

And finally, for a socioeconomic network that is a scale-free network. Also, let's compare the the effect of changing the mean mangaement effect size for the three types of networks.

```
# Create a scale-free network for use as a socioeconomic network

scalefree.eq <- sample_pa(n=50, power=1, m=1, directed=F)
layout.scalefree <- layout_with_kk(scalefree.eq)
plot(
  scalefree.eq,
  edge.arrow.size = 0.3,
  vertex.size = 10,
  vertex.label.cex = 0.5,
  layout = layout.scalefree,
  vertex.color = 'red'
  )
```
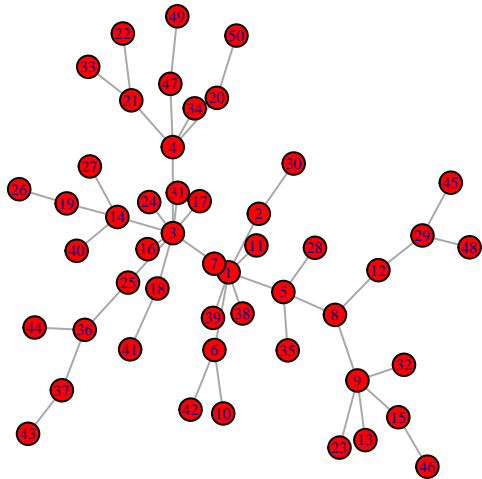
```r
# Convert igraph formatted adjacency matrix to simple matrix

scalefree.eqni <- as_adjacency_matrix(scalefree.eq, sparse=F)

sens.exp2bsf <-
  INAscene(
  nreals = 100,
  ntimesteps = 5,
  doplot = F,
  readgeocoords = F,
  geocoords = NA,
  numnodes = 50,
  xrange = c(0, 50),
  yrange = c(0, 50),
  randgeo = T,
  readinitinfo = F,
  initinfo = NA,
  initinfo.norp = 'num',
  initinfo.n = 1,
  initinfo.p = NA,
  initinfo.dist = 'random',
  readinitbio = F,
  initbio = NA,
  initbio.norp = 'prop',
  initbio.n = NA,
  initbio.p = 0.05,
  initbio.dist = 'upedge',
  readseam = T,
  seam = scalefree.eqni,
  seamdist = NA,
  seamrandp = NA,
  seampla = NA,
  seamplb = NA,
  readbpam = F,
  bpam = NA,
  bpamdist = 'powerlaw',
  bpamrandp = NA,
  bpampla = 1,
```

```
  bpamplb = 0.5,
  readprobadoptvec = F,
  probadoptvec = NA,
  probadoptmean = 0.9,
  probadoptsd = 0.1,
  readprobestabvec = F,
  probestabvec = NA,
  probestabmean = 0.5,
  probestabsd = 0.2,
  maneffdir = 'decrease_estab',
  maneffmean = seq(0, 1, 0.1),
  maneffsd = 0.2,
  usethreshman = F,
  maneffthresh = NA,
  sampeffort = NA
  )
```

```
## [1] "ending parameter combination 1"
## [1] "ending parameter combination 2"
## [1] "ending parameter combination 3"
## [1] "ending parameter combination 4"
## [1] "ending parameter combination 5"
## [1] "ending parameter combination 6"
## [1] "ending parameter combination 7"
## [1] "ending parameter combination 8"
## [1] "ending parameter combination 9"
## [1] "ending parameter combination 10"
## [1] "ending parameter combination 11"
```

```
jt2 <- sens.exp2bsf$multout

# Plot the mean establishment proportion as a function of the mean management effect

plot(
  jt2$maneffmean,
  jt2$mestab,
  xlab = 'Mean management effect size',
  ylab = 'Proportion nodes with invasive established',
  ylim = c(0, 1),
  col = 'red',
  pch = 16
  )
lines(jt2$maneffmean, jt2$mestab, col='red')
title(main='Scale-free network')
```
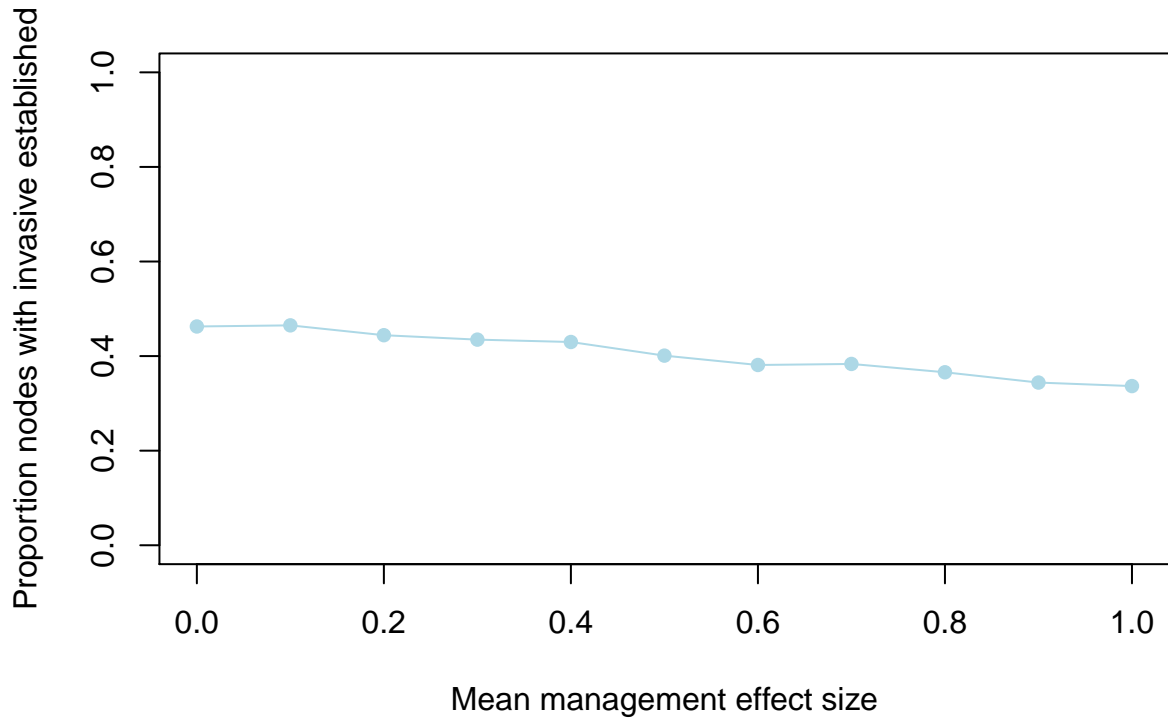
Scale–free network
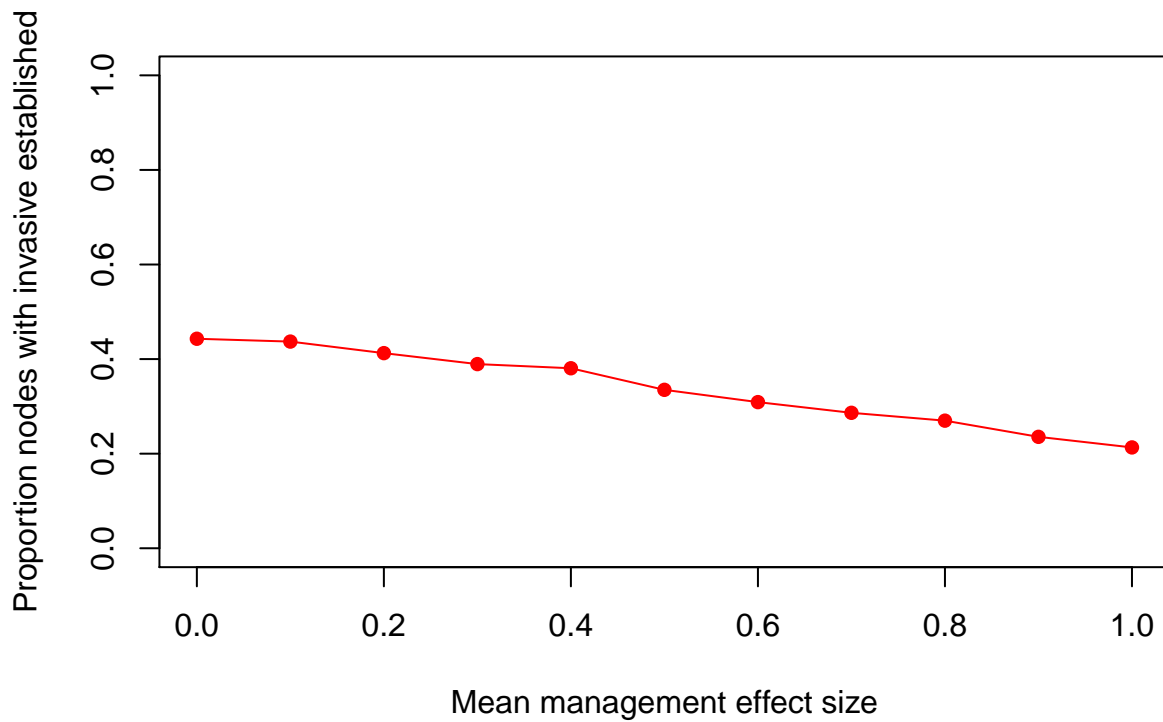

```r
# For plotting the three scenarios
mestab.sf <- jt2$mestab

# Looking at the results for the three networks together

plot(
  jt2$maneffmean,
  mestab.sf,
  xlab = 'Mean management effect size',
  ylab = 'Proportion nodes with invasive established',
  ylim = c(0, 1),
  col = 'red',
  type = 'l'
  )
lines(jt2$maneffmean, mestab.sw, col='darkblue', lty=1)
lines(jt2$maneffmean, mestab.swlow, col='lightblue', lty=1)
lines(jt2$maneffmean, mestab.rand, col='orange', lty=1)

text(
  x = 0.2,
  y = 0.9,
  labels = 'Ring (small world with low probability of rewiring)',
  col = 'lightblue',
  pos = 4
  )
text(x=0.2,y=0.7,labels='Random',col='orange', pos=4)
text(x=0.2,y=0.8,labels='Scale-free',col='red', pos=4)
text(x=0.2,y=0.6,labels='Small world',col='darkblue', pos=4)
```
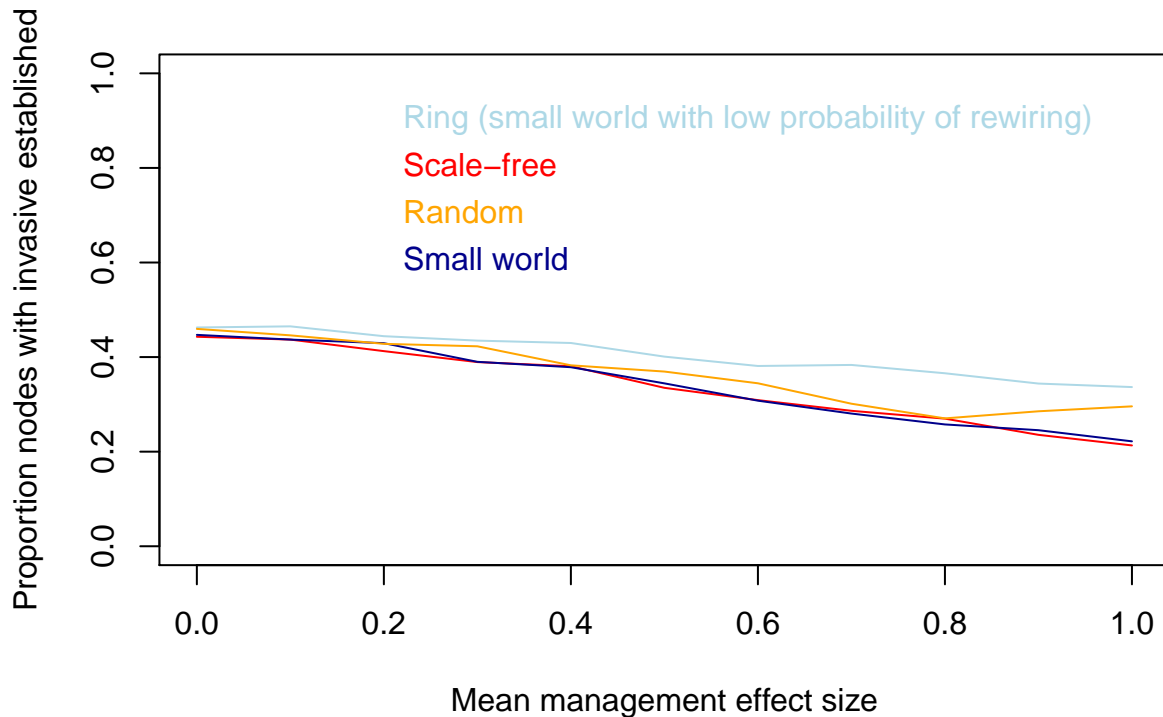
The ring network (a small world network with low probability of rewiring to create links across the ring) results in slower movement of communication about the technology, so increasing the management effect size has less effect on bioentity establishment. The small world network (with higher probabiltiy of rewiring) tends to have more rapid spread of information so that its system is more responsive to increasing the management effect size.

Experiment 2C

In experiment 2C, during monitoring and evaluation of the project, suppose that the observations are consistent with the initial conceptualization of the project, but the project is performing at the low end of the initial frequency distribution of likely outcomes. If efforts are increased to enhance the probability of technology adoption, perhaps through subsidies or policies to increase uptake, what increase in adoption rates would be necessary to keep progress in the system on track?

```
sens.exp2c <-
  INAscene(
  nreals = 20,
  ntimesteps = 10,
  doplot = F,
  readgeocoords = F,
  geocoords = NA,
  numnodes = 50,
  xrange = c(0, 50),
  yrange = c(0, 50),
  randgeo = T,
  readinitinfo = F,
  initinfo = NA,
  initinfo.norp = 'prop',
  initinfo.n = NA,
  initinfo.p = 0.05,
```

```
    initinfo.dist = 'random',
    readinitbio = F,
    initbio = NA,
    initbio.norp = 'prop',
    initbio.n = NA,
    initbio.p = 0.05,
    initbio.dist = 'upedge',
    readseam = F,
    seam = NA,
    seamdist = 'powerlaw',
    seamrandp = NA,
    seampla = 1,
    seamplb = 0.5,
    readbpam = F,
    bpam = NA,
    bpamdist = 'powerlaw',
    bpamrandp = NA,
    bpampla = 1,
    bpamplb = 0.5,
    readprobadoptvec = F,
    probadoptvec = NA,
    probadoptmean = seq(from = 0, to = 1, by = 0.1),
    probadoptsd = 0.2,
    readprobestabvec = F,
    probestabvec = NA,
    probestabmean = 0.5,
    probestabsd = 0.2,
    maneffdir = 'decrease_estab',
    maneffmean = 0.5,
    maneffsd = 0.2,
    usethreshman = F,
    maneffthresh = NA,
    sampeffort = 2
  )
```

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```

```
jt2 <- sens.exp2c$multout

# plot the proportion invasive established versus the mean probability of tech
# adoption

plot(
```

```
  jt2$probadoptmean,
  jt2$mestab,
  xlab = 'Mean probability of adoption',
  ylab = 'Proportion nodes with invasive established',
  ylim = c(0, 1),
  col = 'red',
  pch = 16
  )
lines(jt2$probadoptmean, jt2$mestab, col='red')

# also indicate the 95th and 5th percentile

lines(jt2$probadoptmean, jt2$estab95, col='red', lty=2)
lines(jt2$probadoptmean, jt2$estab5, col='red', lty=2)
```
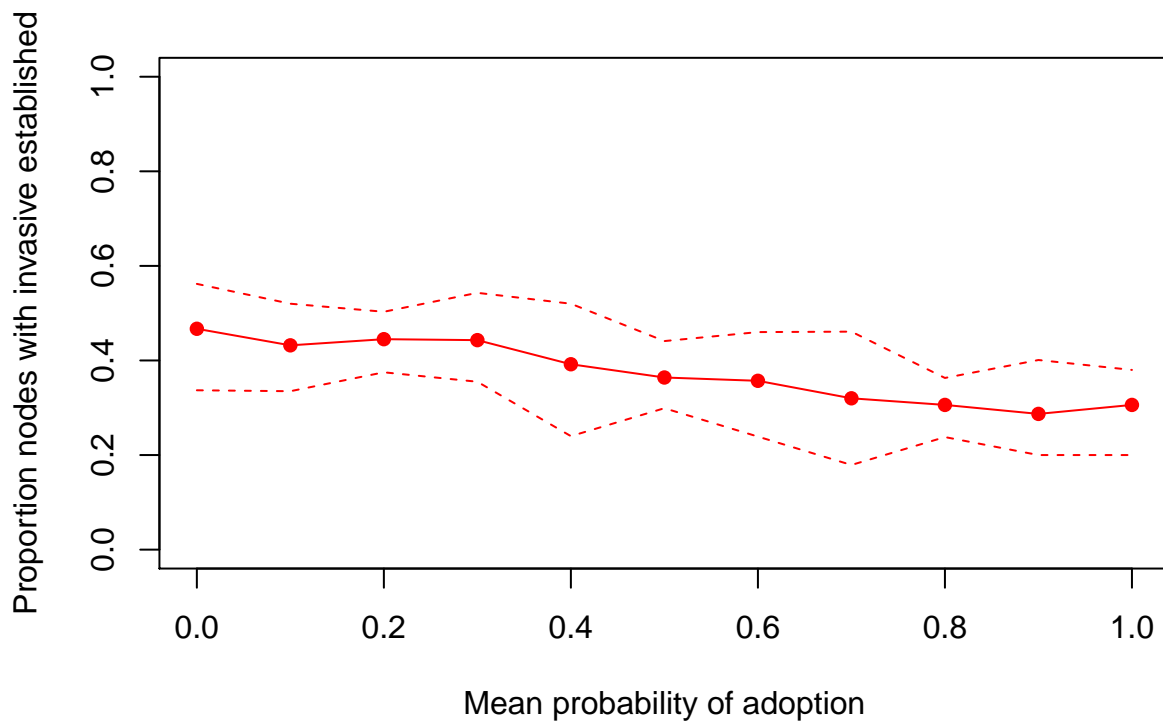


```
# plot the proportion adopting technology versus the mean probability of tech
# adoption

plot(
  jt2$probadoptmean,
  jt2$mdec,
  xlab = 'Mean probability of adoption',
  ylab = 'Proportion nodes with decision to adopt technology',
  ylim = c(0, 1),
  col = 'darkblue',
  pch = 16
  )
lines(jt2$probadoptmean, jt2$mdec, col='darkblue')

# also indicate the 95th and 5th percentile
```

```
lines(jt2$probadoptmean, jt2$dec95, col='darkblue', lty=2)
lines(jt2$probadoptmean, jt2$dec5, col='darkblue', lty=2)
```
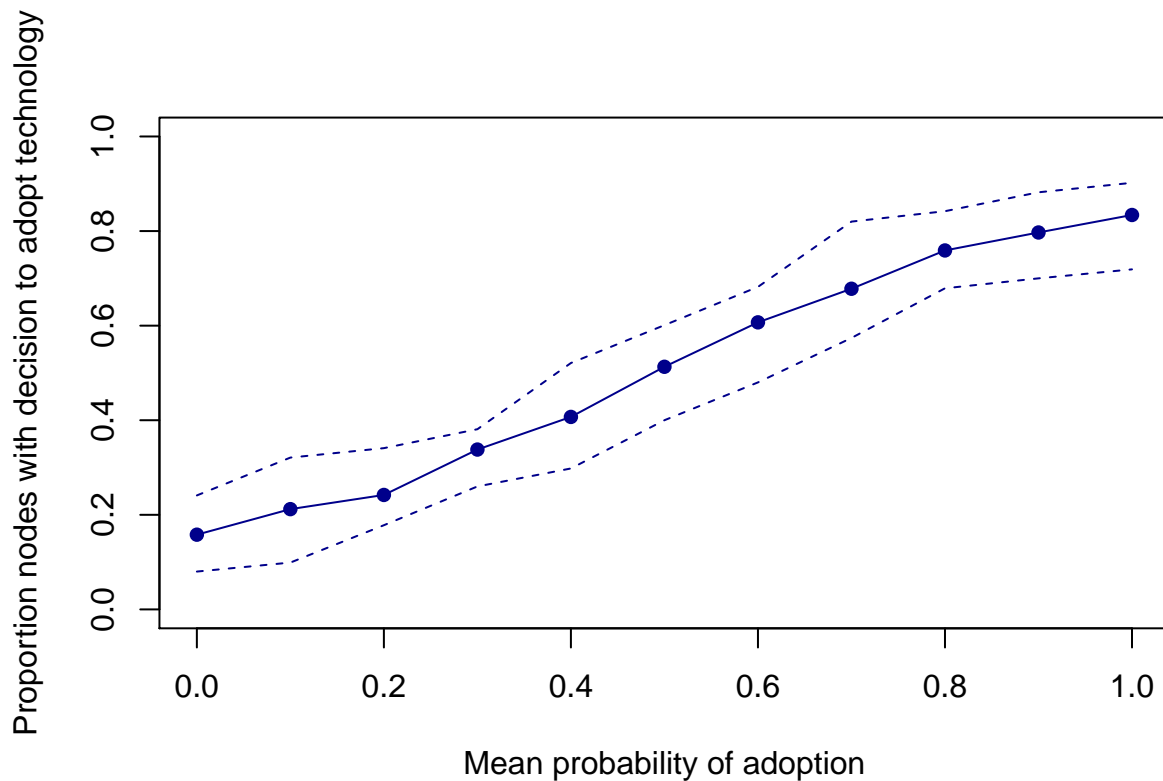

In the above system, even though adoption rates do increase substantially as expected by increasing the mean adoption rate, the influence of other components results in a limited effect of increasing the mean adoption rate on the establishment rate. Other changes would be need to bring the establishment rate lower.

Example 1D

In experiment 1D, at the conclusion of the project, the success of the project is evaluated in terms of the current status of the species, of course, and also evaluated in terms of how long the benefits of the project last for successful regional management of the species. If adoption rates decline without project inputs (such as subsidies or educational campaigns), what happens to the species over time? Can increased management effect size make up for reductions in adoption? In this example, the mean management effect size and the mean probability of adoption are considered together.

The next commands also explore some different approaches to plotting the results

```
sens.exp2d <-
  INAscene(
  nreals = 30,
  ntimesteps = 10,
  doplot = F,
  outputvol = 'less',
  readgeocoords = F,
  geocoords = NA,
  numnodes = 50,
  xrange = c(0, 50),
```

```r
          yrange = c(0, 50),
          randgeo = T,
          readinitinfo = F,
          initinfo = NA,
          initinfo.norp = 'prop',
          initinfo.n = NA,
          initinfo.p = 0.05,
          initinfo.dist = 'random',
          readinitbio = F,
          initbio = NA,
          initbio.norp = 'prop',
          initbio.n = NA,
          initbio.p = 0.05,
          initbio.dist = 'upedge',
          readseam = F,
          seam = NA,
          seamdist = 'powerlaw',
          seamrandp = NA,
          seampla = 1,
          seamplb = 0.5,
          readbpam = F,
          bpam = NA,
          bpamdist = 'powerlaw',
          bpamrandp = NA,
          bpampla = 1,
          bpamplb = 0.5,
          readprobadoptvec = F,
          probadoptvec = NA,
          probadoptmean = seq(from = 0, to = 1, by = 0.1),
          probadoptsd = 0.2,
          readprobestabvec = F,
          probestabvec = NA,
          probestabmean = 0.5,
          probestabsd = 0.2,
          maneffdir = 'decrease_estab',
          maneffmean = seq(from = 0, to = 1, by = 0.1),
          maneffsd = 0.2,
          usethreshman = F,
          maneffthresh = NA,
          sampeffort = 2
          )
```

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```
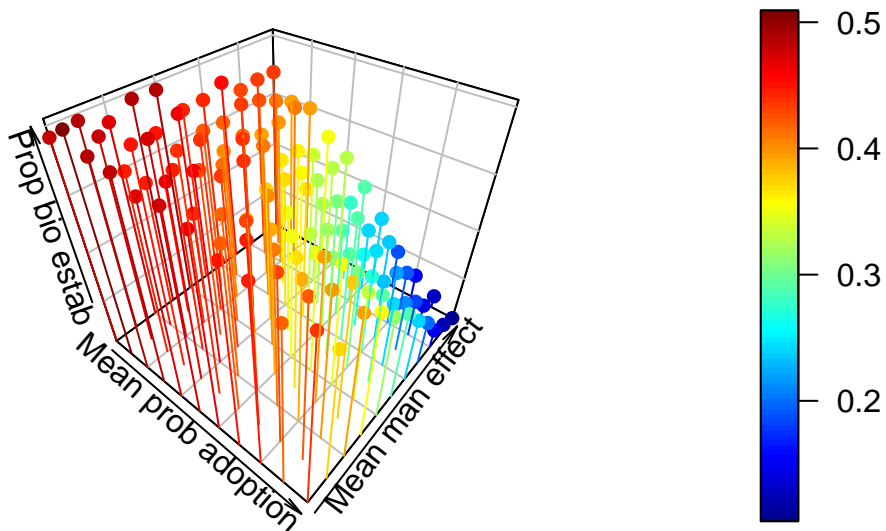
```
## [1] "ending parameter combination 120"
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```

```
jt2 <- sens.exp2d$multout
```

```
plot3D::scatter3D(
  x = jt2$probadoptmean,
  y = jt2$maneffmean,
  z = jt2$mestab,
  pch = 16,
  xlab = 'Mean prob adoption',
  ylab = 'Mean man effect',
  zlab = 'Prop bio estab',
  bty = 'b2',
  type = 'h'
  )
```



```
newz <- matrix(-99,nrow=length(unique(jt2$probadoptmean)),
               ncol=length(unique(jt2$maneffmean)))

for(i in 1:length(unique(jt2$probadoptmean))) {
  for (j in 1:length(unique(jt2$maneffmean))) {
  newz[i, j] <-
  jt2$mestab[jt2$probadoptmean == unique(jt2$probadoptmean)[i] &
  jt2$maneffmean == unique(jt2$maneffmean)[j]]
  }
  }

plot3D::hist3D(
  x = unique(jt2$probadoptmean),
  y = unique(jt2$maneffmean),
  z = newz,
  xlab = 'Mean prob adoption',
  ylab = 'Mean man effect',
  zlab = 'Prop bio estab'
```
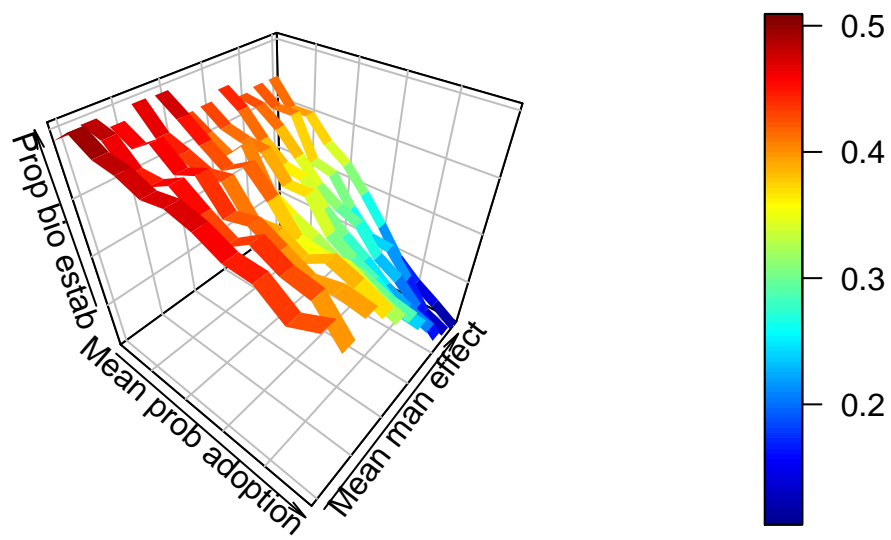
```
  )
```
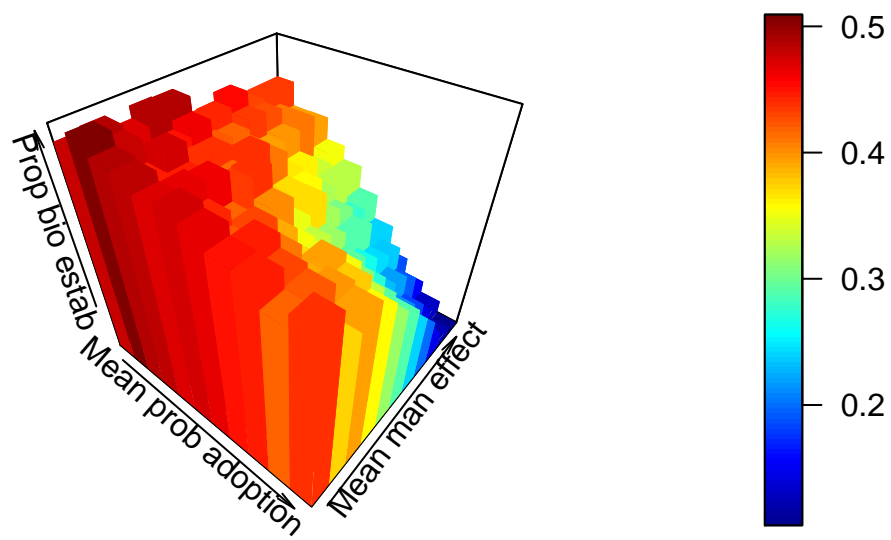


```
plot3D::ribbon3D(
  x = unique(jt2$probadoptmean),
  y = unique(jt2$maneffmean),
  z = newz,
  xlab = 'Mean prob adoption',
  ylab = 'Mean man effect',
  zlab = 'Prop bio estab',
  bty = 'b2'
  )
```



```
plot3D::persp3D(
  x = unique(jt2$probadoptmean),
  y = unique(jt2$maneffmean),
  z = newz,
  xlab = 'Mean prob adoption',
  ylab = 'Mean man effect',
```

```
  zlab = 'Prop bio estab',
  bty = 'b2',
  ticktype = 'detailed',
  theta = 130,
  phi = 0,
  zlim = c(0, 1)
  )
```
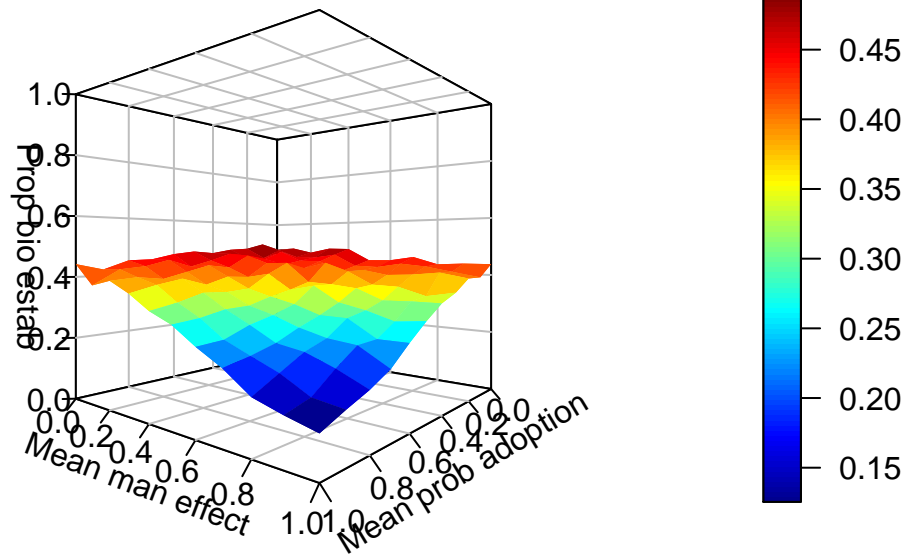


```
image(
  x = unique(jt2$probadoptmean),
  y = unique(jt2$maneffmean),
  z = newz,
  xlab = 'Mean probability of adoption',
  ylab = 'Mean management effect'
  )
```
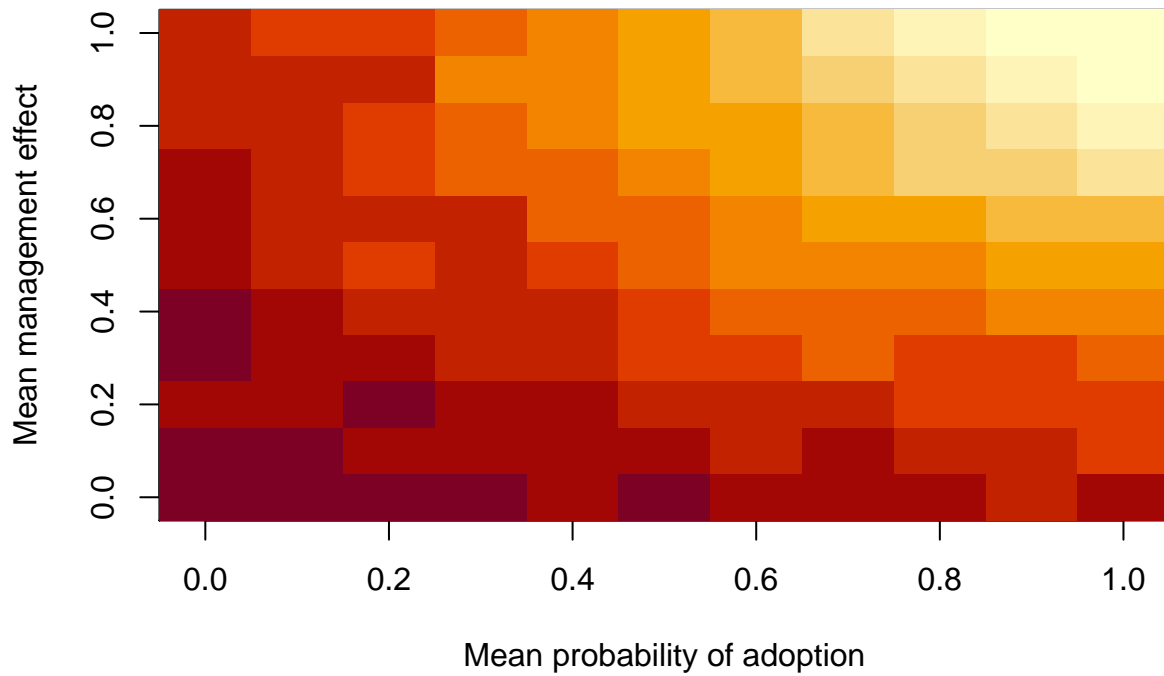
```
ggtemp <-
  as.data.frame(cbind(jt2$probadoptmean, jt2$maneffmean, jt2$mestab))
  names(ggtemp) <- c('probadoptmean', 'maneffmean', 'Estab')

ggplot(data = ggtemp, aes(probadoptmean, maneffmean, fill = Estab)) +
    geom_tile() +
    xlab("Mean probability of adoption") +
    ylab("Mean management effect")
```
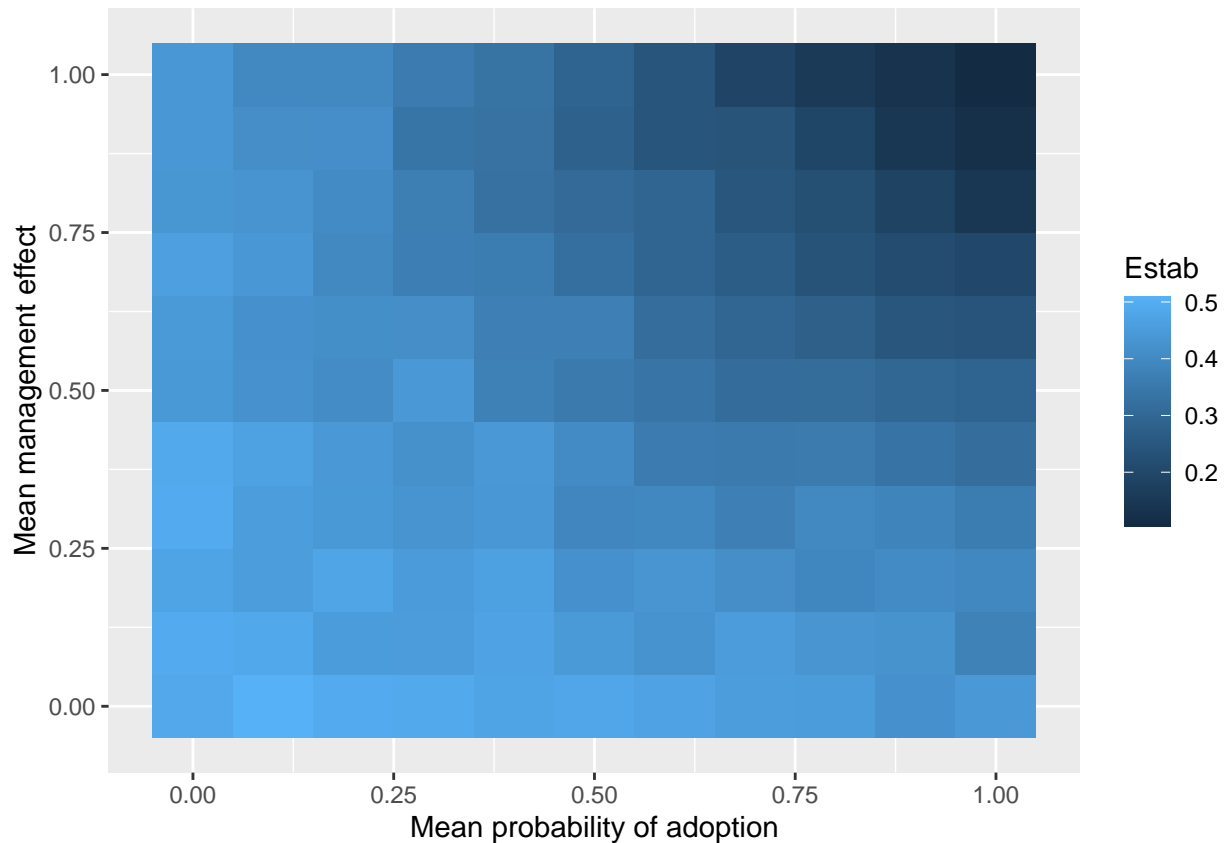
If an establishment proportion of, say, 0.2 was acceptable across 10 time steps, then high levels of both the mean probability of adoption and the mean management effect would be needed.

Let's also consider a similar case, but where the goal is to increase establishment of the bioentity.

```
sens.exp2di <-
  INAscene(
  nreals = 20,
  ntimesteps = 10,
  doplot = F,
  readgeocoords = F,
  geocoords = NA,
  numnodes = 50,
  xrange = c(0, 50),
  yrange = c(0, 50),
  randgeo = T,
  readinitinfo = F,
  initinfo = NA,
  initinfo.norp = 'prop',
  initinfo.n = NA,
  initinfo.p = 0.05,
  initinfo.dist = 'random',
  readinitbio = F,
  initbio = NA,
  initbio.norp = 'prop',
  initbio.n = NA,
  initbio.p = 0.05,
  initbio.dist = 'upedge',
```

```
readseam = F,
seam = NA,
seamdist = 'powerlaw',
seamrandp = NA,
seampla = 1,
seamplb = 0.5,
readbpam = F,
bpam = NA,
bpamdist = 'powerlaw',
bpamrandp = NA,
bpampla = 1,
bpamplb = 0.5,
readprobadoptvec = F,
probadoptvec = NA,
probadoptmean = seq(from = 0, to = 1, by = 0.1),
probadoptsd = 0.2,
readprobestabvec = F,
probestabvec = NA,
probestabmean = 0.5,
probestabsd = 0.2,
maneffdir = 'increase_estab',
maneffmean = seq(from = 0, to = 1, by = 0.1),
maneffsd = 0.2,
usethreshman = F,
maneffthresh = NA,
sampeffort = 2
)
```

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```

```r
jt2 <- sens.exp2di$multout

newz <- matrix(-99,nrow=length(unique(jt2$probadoptmean)),
               ncol=length(unique(jt2$maneffmean)))

for(i in 1:length(unique(jt2$probadoptmean))) {
  for (j in 1:length(unique(jt2$maneffmean))) {
  newz[i, j] <-
  jt2$mestab[jt2$probadoptmean == unique(jt2$probadoptmean)[i] &
  jt2$maneffmean == unique(jt2$maneffmean)[j]]
  }
```
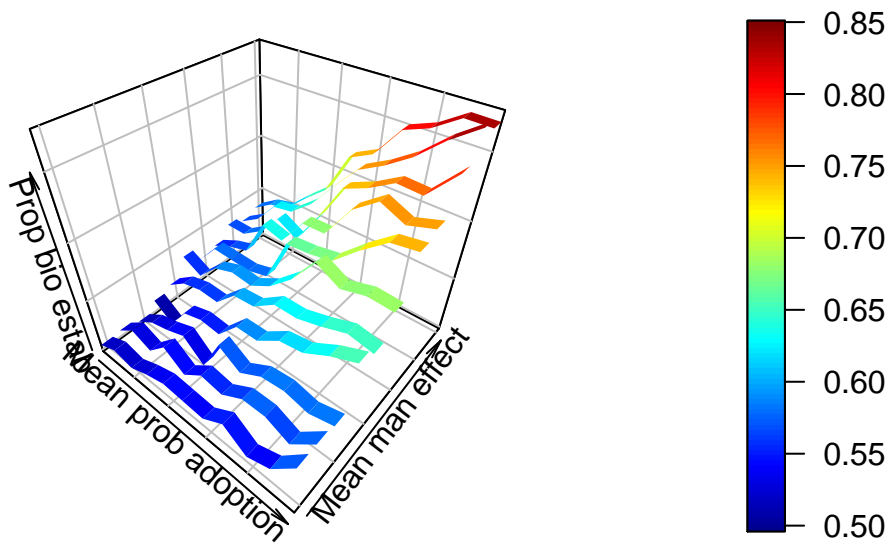
```
  }

plot3D::ribbon3D(
  x = unique(jt2$probadoptmean),
  y = unique(jt2$maneffmean),
  z = newz,
  xlab = 'Mean prob adoption',
  ylab = 'Mean man effect',
  zlab = 'Prop bio estab',
  bty = 'b2'
  )
```
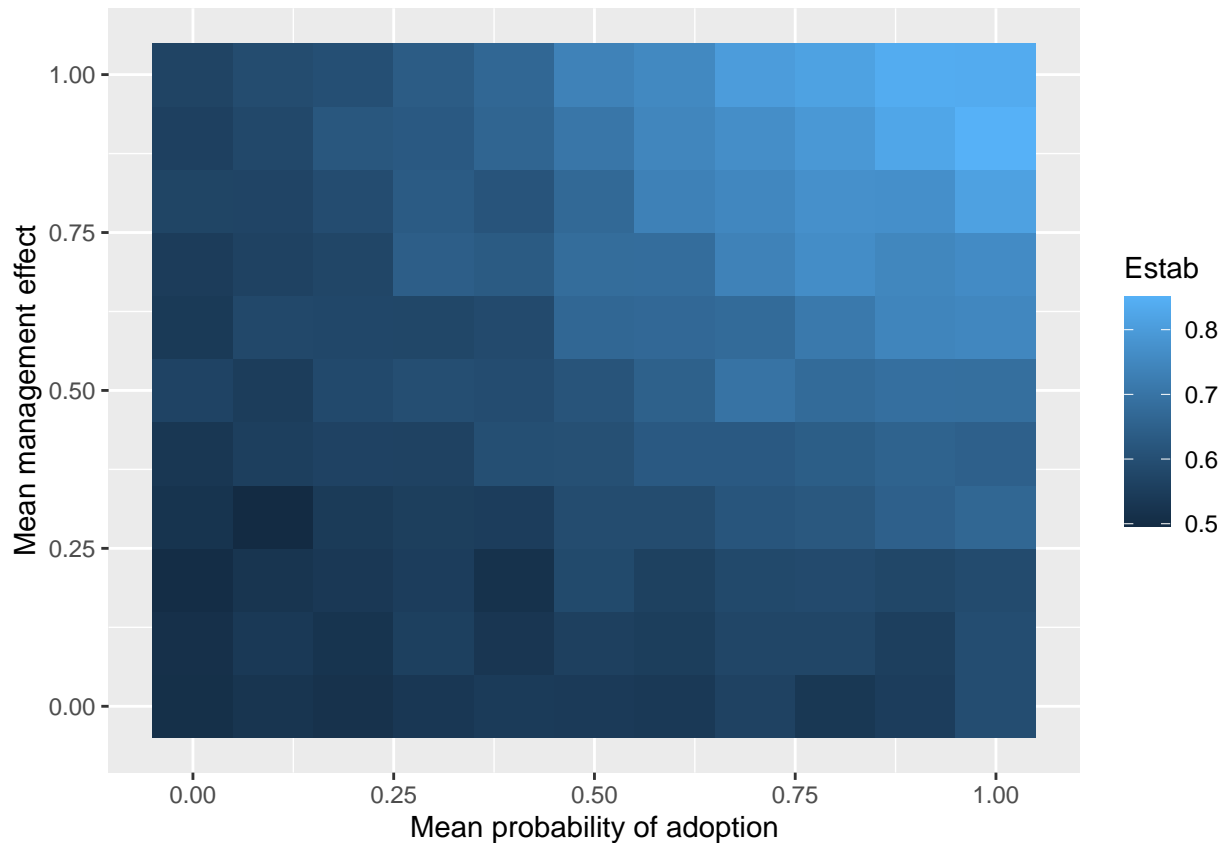


```
ggtemp <-
  as.data.frame(cbind(jt2$probadoptmean, jt2$maneffmean, jt2$mestab))
names(ggtemp) <- c('probadoptmean', 'maneffmean', 'Estab')

ggplot(data = ggtemp, aes(probadoptmean, maneffmean, fill = Estab)) +
  geom_tile() +
  xlab("Mean probability of adoption") +
  ylab("Mean management effect")
```

Uncertainty quantification

In another case, suppose there is less information available about a system. Uncertainty quantification can help to clarify the level of confidence in outcomes (as illustrated in Andersen et al. 2019). Uncertainty quantification and evaluation of the outcomes for changes to the system may be evaluated similarly, with uncertainty quantification most relevant to components of the system for which it is difficult to collect data.

For this example case study, the following analyses show how system outcomes vary as a key parameter varies.

Changing the probability of the bioentity moving greater distances

The following plots show the effect of changing the power law parameter which determines the probability of movement as a function of distance between nodes. (As b gets larger, there are fewer links.) Suppose there is uncertainty about the dispersal parameter for the bioentity and interest in understanding the effect of changing it on the outcome.

```
sens.bpamplb <-
  INAscene(
  nreals = 50,
  ntimesteps = 3,
  doplot = F,
  readgeocoords = F,
  geocoords = NA,
  numnodes = 50,
  xrange = c(0, 50),
```

```r
    yrange = c(0, 50),
    randgeo = T,
    readinitinfo = F,
    initinfo = NA,
    initinfo.norp = 'num',
    initinfo.n = 5,
    initinfo.p = NA,
    initinfo.dist = 'random',
    readinitbio = F,
    initbio = NA,
    initbio.norp = 'num',
    initbio.n = 5,
    initbio.p = NA,
    initbio.dist = 'random',
    readseam = F,
    seam = NA,
    seamdist = 'powerlaw',
    seamrandp = NA,
    seampla = 1,
    seamplb = 1,
    readbpam = F,
    bpam = NA,
    bpamdist = 'powerlaw',
    bpamrandp = NA,
    bpampla = 1,
    bpamplb = seq(0, 2, 0.1),
    readprobadoptvec = F,
    probadoptvec = NA,
    probadoptmean = 0.7,
    probadoptsd = 0.2,
    readprobestabvec = F,
    probestabvec = NA,
    probestabmean = 0.5,
    probestabsd = 0.2,
    maneffdir = 'decrease_estab',
    maneffmean = 0.9,
    maneffsd = 0.2,
    usethreshman = T,
    maneffthresh = 0.3,
    sampeffort = 2
    )
```

```
## [1] "ending parameter combination 1"
## [1] "ending parameter combination 2"
## [1] "ending parameter combination 3"
## [1] "ending parameter combination 4"
## [1] "ending parameter combination 5"
## [1] "ending parameter combination 6"
## [1] "ending parameter combination 7"
## [1] "ending parameter combination 8"
## [1] "ending parameter combination 9"
## [1] "ending parameter combination 10"
## [1] "ending parameter combination 11"
```

```
## [1] "ending parameter combination 12"
## [1] "ending parameter combination 13"
## [1] "ending parameter combination 14"
## [1] "ending parameter combination 15"
## [1] "ending parameter combination 16"
## [1] "ending parameter combination 17"
## [1] "ending parameter combination 18"
## [1] "ending parameter combination 19"
## [1] "ending parameter combination 20"
## [1] "ending parameter combination 21"
```

```r
jt2 <- sens.bpamplb$multout
plot(
jt2$bpamplb,
jt2$mestab,
xlab = 'Power law parameter b in ad^(-b) for dispersal links',
ylab = 'Proportion nodes with bioentity',
xlim = c(0, 2),
ylim = c(0, 1),
type = 'l'
)
```
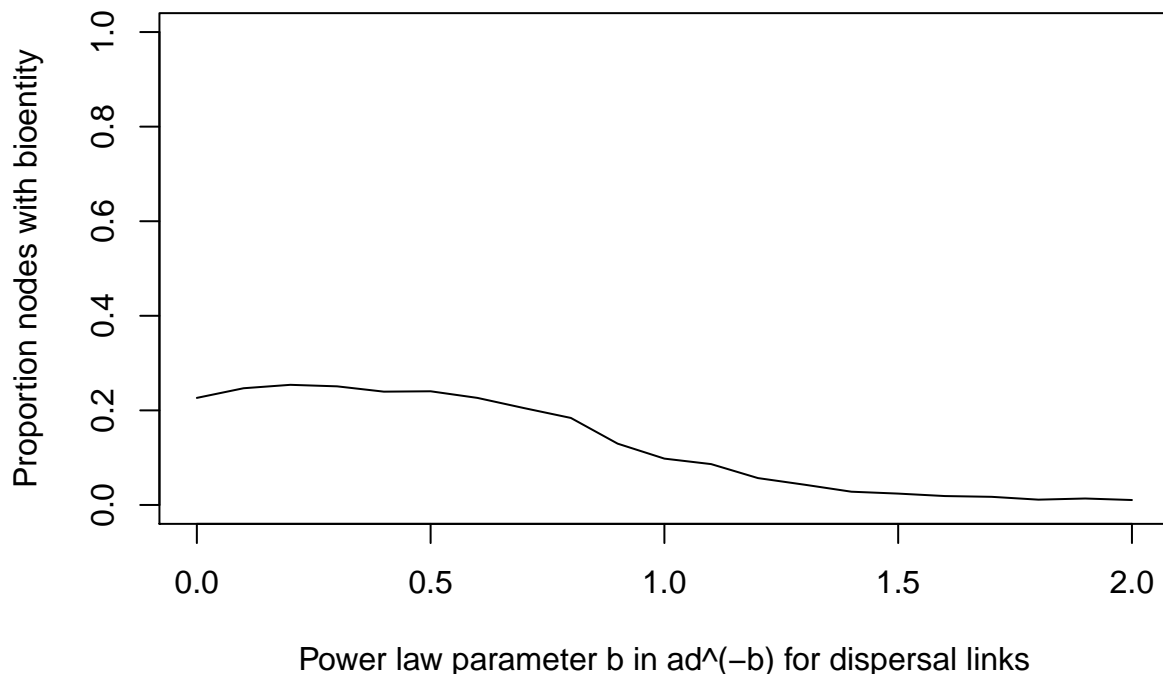

For this scenario, When the inverse power law parameter b is below 0.8, the outcome for bioentity establishment is fairly consistent across values of b. Likewise, when the parameter b is above 1.2, the outcomes is farily consistent across values of b. For b in 0.8 to 1.2, more precise estimates of the parameter could help to evaluate the likely outcomes.

References

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Garrett, K. A. 2021. Impact network analysis and the INA R package: Decision support for regional management interventions. Methods in Ecology and Evolution, in press.

Wickham, H., J. Hester, and W. Chang. devtools: Tools to Make Developing R Packages Easier. 2020. R package version 2.3.0. https://CRAN.R-project.org/package=devtools