INA-INAscene-adaptation

K. A. Garrett

University of Florida

Experiment 3 - Adaptation scenario analysis in INAscene

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 (Garrett 2021).

The code below assumes that the INA package has been installed from GitHub.

```
library(INA)

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)
```

The following examples illustrate the types of questions from Experiment 3 in Garrett 2021.

This experiment illustrates an analysis of how system components can be modified to compensate for global change factors such as climate change. Other similar challenges to the system might be changes in invasive population genotypes that make them better able to establish (antibiotic/pesticide resistance, adaptation to host resistance, adaptation to climate conditions, etc.). In this scenario analysis, global change effects are represented by changes in environmental conduciveness to establishment or persistence of a species, reflected in the probability of establishment. The scenario starts with a set of default model parameters. For simplicity, underlying environmental conduciveness is the same at all nodes for a given time step, so that the mean probability of establishment is the same at each land unit node.

Experiment 3A Adaptation for sustainability - press stressor

In the 'adaptation for sustainability' scenario, conduciveness to establishment increases and remains steady over time, as a press stressor. The probability of establishment at a baseline of 0.5 is compared to a new scenario with the probability of establishment at 0.9, where this is the probability of establishment without management.

```r
sens.exp3a.maneffmean.5 <-
  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 = 1,
  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 = seq(0, 1, 0.1),
  probestabsd = 0.2,
  maneffdir = 'decrease_estab',
  maneffmean = 0.5,
  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.exp3a.maneffmean.5$multout

jt2$probestabmean # the probabilities of establishment that were evaluated
```

```
##  [1] 0.0 0.1 0.2 0.3 0.4 0.5 0.6 0.7 0.8 0.9 1.0
```

```r
jt2$mestab # the resulting mean establishment rates
```

```
##  [1] 0.001 0.002 0.023 0.054 0.099 0.160 0.244 0.363 0.432 0.493 0.568
```

```r
# Plot how the mean establishment proportion is a function of the mean
# probability of establishment

plot(
  jt2$probestabmean,
  jt2$mestab,
  xlab = 'Mean probalilty of establishment',
  ylab = 'Proportion nodes with invasive established',
  ylim = c(0, 1),
  col = 'red',
  pch = 16
  )
  lines(jt2$probestabmean, jt2$mestab, col = 'red')

# also indicate the 95th percentile

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

# also indicate the 5th percentile

lines(jt2$probestabmean, jt2$estab5, col='red', lty=2)
```
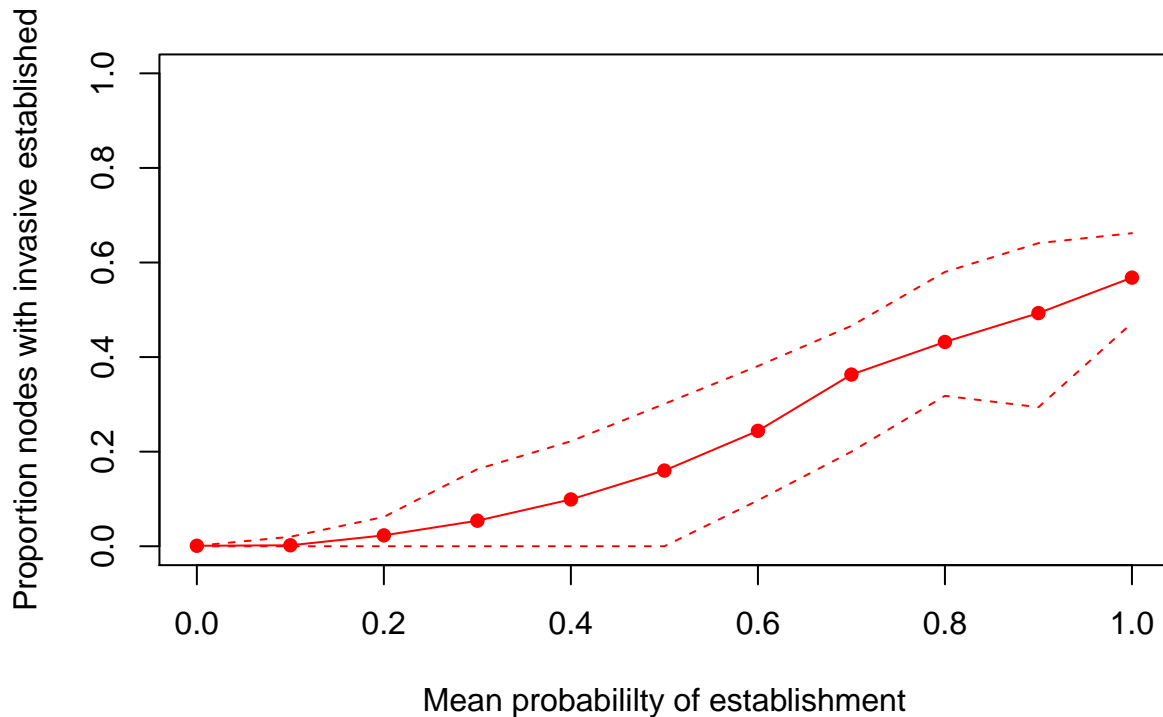
Under the previous environmental condition scenario, the mean probability of establishment, 0.5, resulted in a proportion of around 0.2 with establishment. For a new probability of establishment of 0.9, the proportion nodes with establishment is around 0.5.

What corresponding change in the potential adaptation parameters would be needed to bring the resulting rate of establishment down to 0.5 even when the establishment probability is 0.9?

Consider modifying the management effect size mean, through a better management technology.

First, what was the response to changing the management effect size mean in the old environment?

```
sens.exp3a.probestabmean.5 <-
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 = 1,
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 = 0.2,
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.exp3a.probestabmean.5$multout
```

```
jt2$maneffmean # the set of management effect means
```

```
##  [1] 0.0 0.1 0.2 0.3 0.4 0.5 0.6 0.7 0.8 0.9 1.0
```

```
jt2$mestab # the resulting mean establishment rates
```

```
##  [1] 0.219 0.233 0.262 0.225 0.145 0.191 0.159 0.133 0.120 0.109 0.099
```

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

plot(
  jt2$maneffmean,
  jt2$mestab,
  xlab = 'Management effect mean',
  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)
```
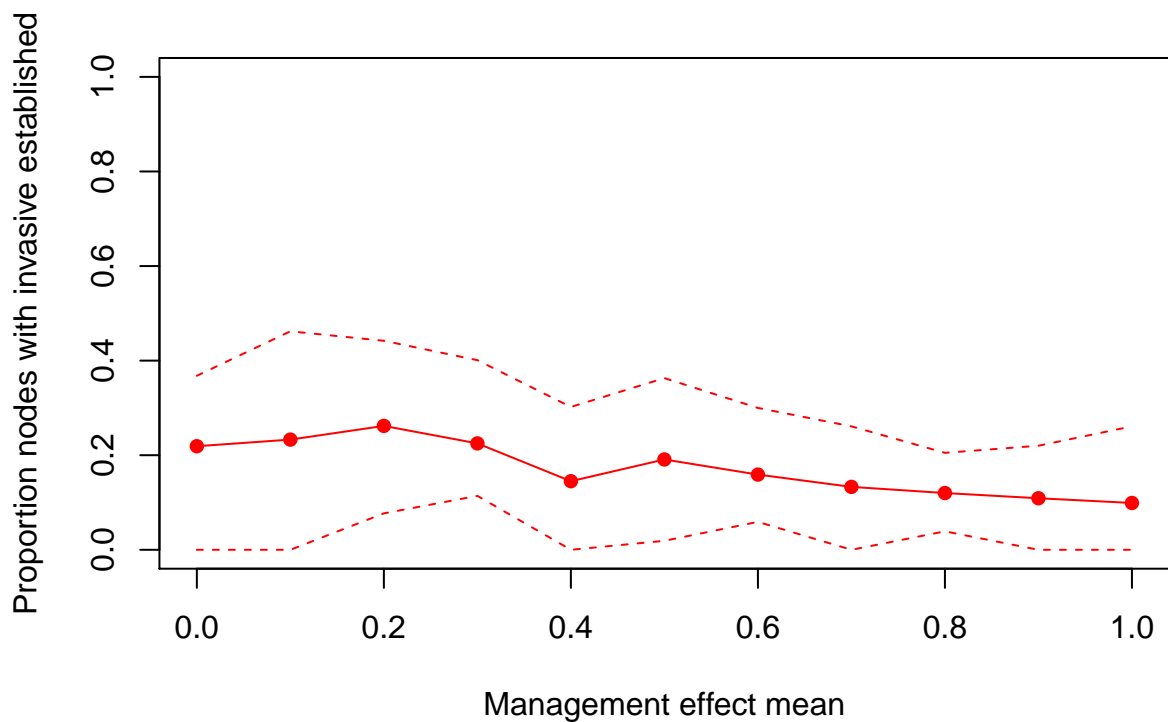


```r
# scenario where the probability of establishment probestabmean=0.9 and the
# management effect size mean maneffmean is being varied

sens.exp3a.probestabmean.9 <-
  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 = 1,
  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 = 0.9,
  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.exp3a.probestabmean.9$multout

jt2$maneffmean # the management effect means that were evaluated
```

```
##  [1] 0.0 0.1 0.2 0.3 0.4 0.5 0.6 0.7 0.8 0.9 1.0
```

```r
jt2$mestab # the resulting mean establishment rates
```

```
##  [1] 0.667 0.665 0.571 0.593 0.558 0.477 0.460 0.393 0.367 0.321 0.313
```

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

plot(
  jt2$maneffmean,
  jt2$mestab,
  xlab = 'Management effect mean',
  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)
```
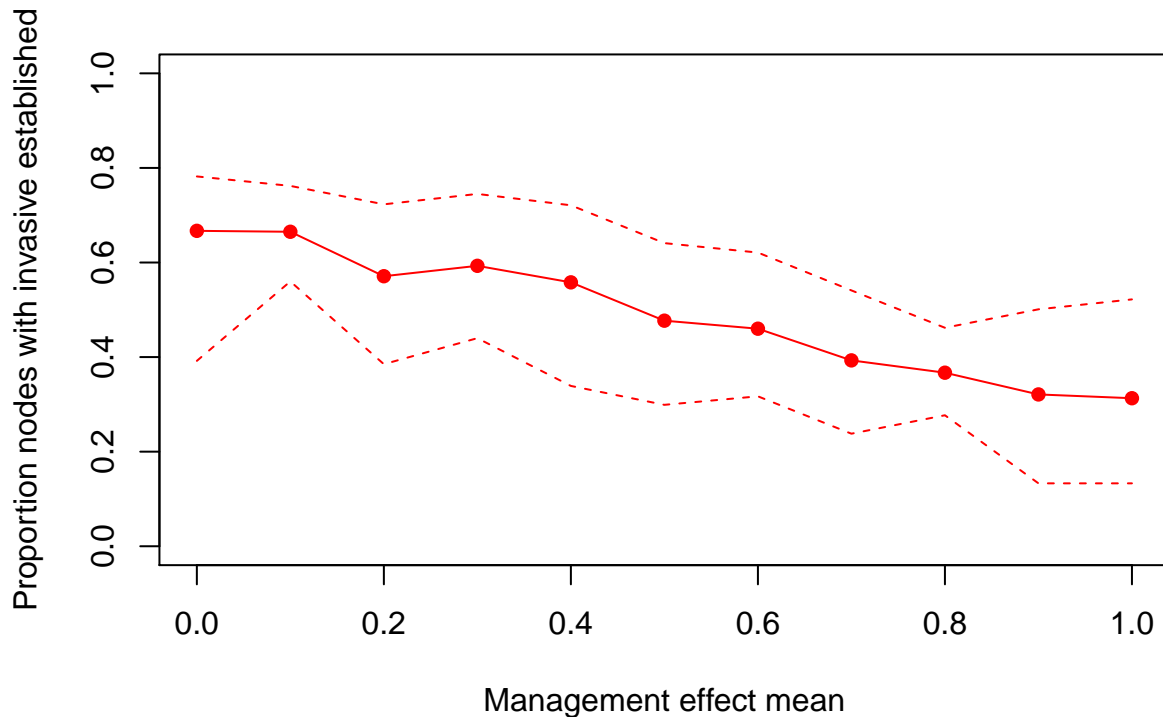
Increasing the mean management effect alone is not sufficient to sustain an invasion proportion of approximately 0.2. Even at manneffmean=1.0, the proportion establishment is somewhat greater.

What about modifying the probability of adoption along with the mean management effect, to try to achieve sustainability in the new climate scenario?

```
# scenario where the probability of establishment probestabmean=0.9 and the
# probability of adoption probadoptmean and the management effect mean
# maneffmean are both being varied

sens.exp3a.probestabmean.9a <-
  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 = 1,
  readbpam = F,
  bpam = NA,
  bpamdist = 'powerlaw',
  bpamrandp = NA,
  bpampla = 1,
  bpamplb = 1,
  readprobadoptvec = F,
  probadoptvec = NA,
  probadoptmean = seq(0, 1, 0.1),
  probadoptsd = 0.2,
  readprobestabvec = F,
  probestabvec = NA,
  probestabmean = 0.9,
  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"
## [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"
## [1] "ending parameter combination 22"
## [1] "ending parameter combination 23"
## [1] "ending parameter combination 24"
```

```
## [1] "ending parameter combination 25"
## [1] "ending parameter combination 26"
## [1] "ending parameter combination 27"
## [1] "ending parameter combination 28"
## [1] "ending parameter combination 29"
## [1] "ending parameter combination 30"
## [1] "ending parameter combination 31"
## [1] "ending parameter combination 32"
## [1] "ending parameter combination 33"
## [1] "ending parameter combination 34"
## [1] "ending parameter combination 35"
## [1] "ending parameter combination 36"
## [1] "ending parameter combination 37"
## [1] "ending parameter combination 38"
## [1] "ending parameter combination 39"
## [1] "ending parameter combination 40"
## [1] "ending parameter combination 41"
## [1] "ending parameter combination 42"
## [1] "ending parameter combination 43"
## [1] "ending parameter combination 44"
## [1] "ending parameter combination 45"
## [1] "ending parameter combination 46"
## [1] "ending parameter combination 47"
## [1] "ending parameter combination 48"
## [1] "ending parameter combination 49"
## [1] "ending parameter combination 50"
## [1] "ending parameter combination 51"
## [1] "ending parameter combination 52"
## [1] "ending parameter combination 53"
## [1] "ending parameter combination 54"
## [1] "ending parameter combination 55"
## [1] "ending parameter combination 56"
## [1] "ending parameter combination 57"
## [1] "ending parameter combination 58"
## [1] "ending parameter combination 59"
## [1] "ending parameter combination 60"
## [1] "ending parameter combination 61"
## [1] "ending parameter combination 62"
## [1] "ending parameter combination 63"
## [1] "ending parameter combination 64"
## [1] "ending parameter combination 65"
## [1] "ending parameter combination 66"
## [1] "ending parameter combination 67"
## [1] "ending parameter combination 68"
## [1] "ending parameter combination 69"
## [1] "ending parameter combination 70"
## [1] "ending parameter combination 71"
## [1] "ending parameter combination 72"
## [1] "ending parameter combination 73"
## [1] "ending parameter combination 74"
## [1] "ending parameter combination 75"
## [1] "ending parameter combination 76"
## [1] "ending parameter combination 77"
## [1] "ending parameter combination 78"
```

```
## [1] "ending parameter combination 79"
## [1] "ending parameter combination 80"
## [1] "ending parameter combination 81"
## [1] "ending parameter combination 82"
## [1] "ending parameter combination 83"
## [1] "ending parameter combination 84"
## [1] "ending parameter combination 85"
## [1] "ending parameter combination 86"
## [1] "ending parameter combination 87"
## [1] "ending parameter combination 88"
## [1] "ending parameter combination 89"
## [1] "ending parameter combination 90"
## [1] "ending parameter combination 91"
## [1] "ending parameter combination 92"
## [1] "ending parameter combination 93"
## [1] "ending parameter combination 94"
## [1] "ending parameter combination 95"
## [1] "ending parameter combination 96"
## [1] "ending parameter combination 97"
## [1] "ending parameter combination 98"
## [1] "ending parameter combination 99"
## [1] "ending parameter combination 100"
## [1] "ending parameter combination 101"
## [1] "ending parameter combination 102"
## [1] "ending parameter combination 103"
## [1] "ending parameter combination 104"
## [1] "ending parameter combination 105"
## [1] "ending parameter combination 106"
## [1] "ending parameter combination 107"
## [1] "ending parameter combination 108"
## [1] "ending parameter combination 109"
## [1] "ending parameter combination 110"
## [1] "ending parameter combination 111"
## [1] "ending parameter combination 112"
## [1] "ending parameter combination 113"
## [1] "ending parameter combination 114"
## [1] "ending parameter combination 115"
## [1] "ending parameter combination 116"
## [1] "ending parameter combination 117"
## [1] "ending parameter combination 118"
## [1] "ending parameter combination 119"
## [1] "ending parameter combination 120"
## [1] "ending parameter combination 121"
```

```r
jt2 <- sens.exp3a.probestabmean.9a$multout
```

```r
jt2$probadoptmean # the probabilities of adoption that were evaluated
```

```
##   [1] 0.0 0.1 0.2 0.3 0.4 0.5 0.6 0.7 0.8 0.9 1.0 0.0 0.1 0.2 0.3 0.4 0.5 0.6
##  [19] 0.7 0.8 0.9 1.0 0.0 0.1 0.2 0.3 0.4 0.5 0.6 0.7 0.8 0.9 1.0 0.0 0.1 0.2
##  [37] 0.3 0.4 0.5 0.6 0.7 0.8 0.9 1.0 0.0 0.1 0.2 0.3 0.4 0.5 0.6 0.7 0.8 0.9
##  [55] 1.0 0.0 0.1 0.2 0.3 0.4 0.5 0.6 0.7 0.8 0.9 1.0 0.0 0.1 0.2 0.3 0.4 0.5
##  [73] 0.6 0.7 0.8 0.9 1.0 0.0 0.1 0.2 0.3 0.4 0.5 0.6 0.7 0.8 0.9 1.0 0.0 0.1
##  [91] 0.2 0.3 0.4 0.5 0.6 0.7 0.8 0.9 1.0 0.0 0.1 0.2 0.3 0.4 0.5 0.6 0.7 0.8
```

```
## [109] 0.9 1.0 0.0 0.1 0.2 0.3 0.4 0.5 0.6 0.7 0.8 0.9 1.0
```

```
jt2$mestab # the resulting mean establishment rates
```

```
##    [1] 0.745 0.719 0.700 0.709 0.686 0.669 0.624 0.624 0.590 0.627 0.634 0.752
##   [13] 0.730 0.692 0.688 0.616 0.673 0.652 0.603 0.628 0.576 0.547 0.736 0.709
##   [25] 0.699 0.650 0.663 0.660 0.606 0.563 0.551 0.540 0.560 0.702 0.670 0.684
##   [37] 0.630 0.636 0.612 0.584 0.517 0.567 0.494 0.457 0.664 0.659 0.626 0.615
##   [49] 0.579 0.533 0.501 0.471 0.435 0.368 0.432 0.682 0.641 0.635 0.616 0.520
##   [61] 0.486 0.431 0.400 0.369 0.318 0.308 0.676 0.638 0.613 0.553 0.479 0.455
##   [73] 0.401 0.351 0.303 0.291 0.275 0.628 0.644 0.566 0.558 0.477 0.407 0.334
##   [85] 0.327 0.231 0.203 0.177 0.613 0.574 0.563 0.500 0.424 0.354 0.304 0.256
##   [97] 0.192 0.132 0.133 0.632 0.576 0.545 0.457 0.388 0.318 0.281 0.212 0.165
## [109] 0.153 0.115 0.636 0.584 0.517 0.427 0.345 0.324 0.246 0.177 0.128 0.130
## [121] 0.104
```

```
# Plot how the mean establishment proportion is a function of the probability of
# adoption and management effect mean

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$maneffmean)[j]]
  }
  }
ribbon3D(
  x = unique(jt2$probadoptmean),
  y = unique(jt2$maneffmean),
  z = newz,
  xlab = 'Mean prob adoption',
  ylab = 'Mean man effect',
  zlab = 'Prop bio estab',
  bty = 'b2'
  )
```
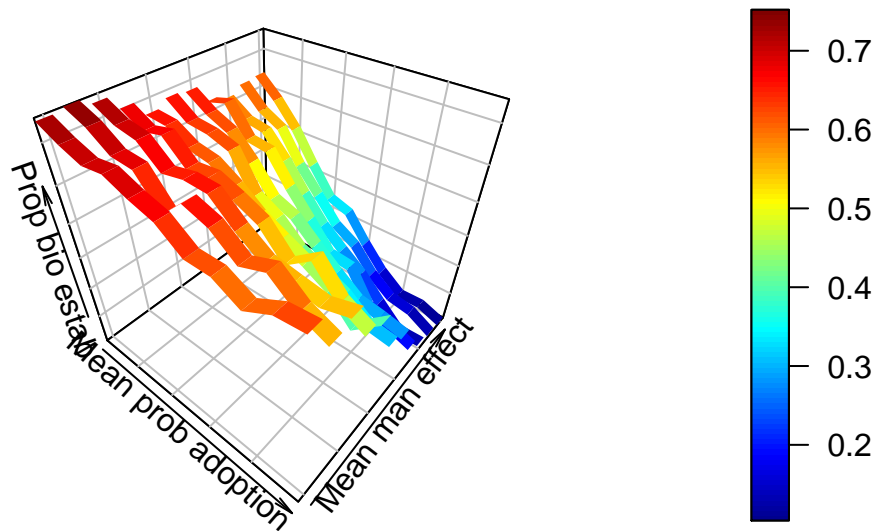
The dark blue region indicates the range of combinations of the mean probability of adoption and the management effect mean that would be required to make the system sustainable under an increase from 0.5 probability of establishment to 0.9 probability of establishment (probabilities in the absence of management). The x- and y-axes run from 0 to 1.

A heatmap version of this plot:

```
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")
```
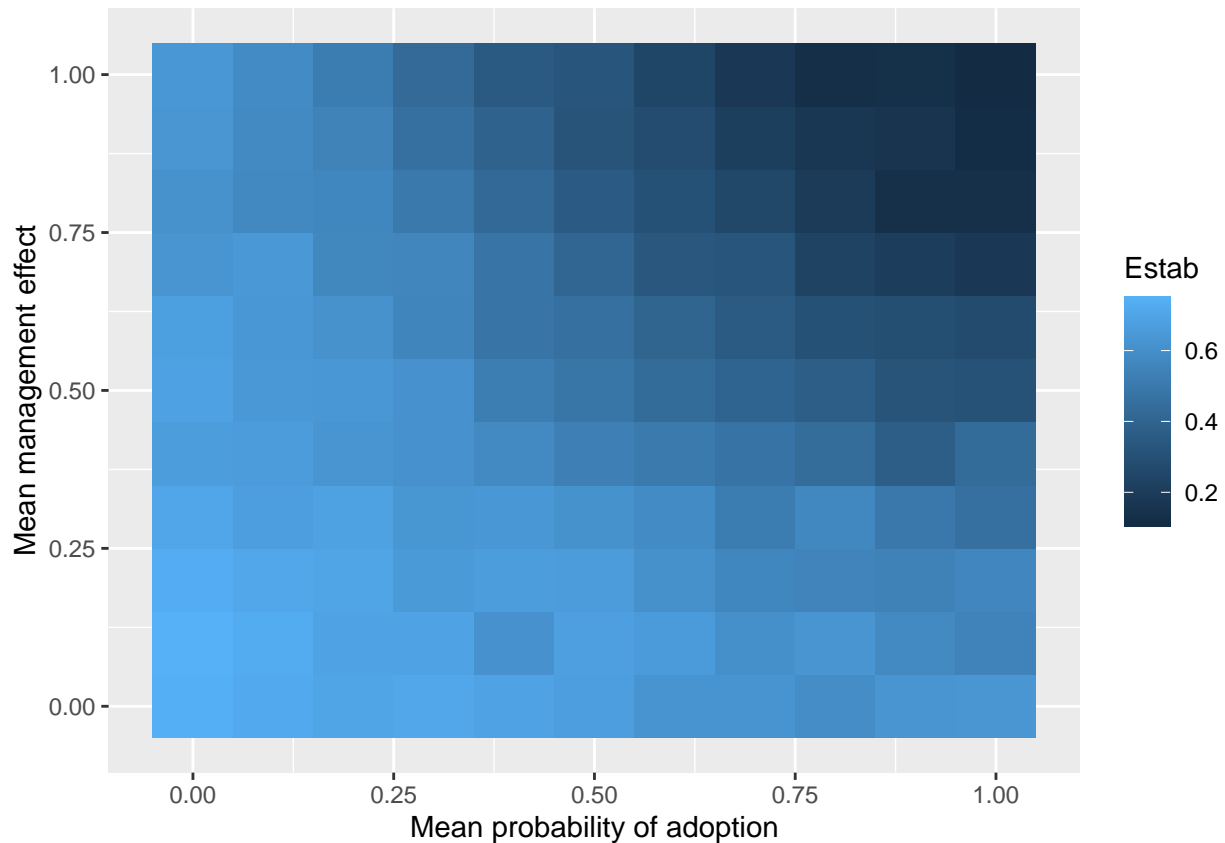
Experiment 3B - Adaptation function for sustainability

Again, suppose we are adapting to the scenario where, due to an environmental change and/or change in the bioentity, the mean probability of establishment (in the absence of management) increases from 0.5 to a higher probability. We would like to keep the 'observed' establishment rate below 0.2 for sustainable management.

Based on the previous analysis, we know we will probably need to increase both the mean adoption probability and the mean management effect. Suppose we can increase the mean management effect to 0.8. Then we can consider the 'adaptation function' for sustainability in terms of what mean adoption rate is necessary to keep the 'observed' establishment rate below 0.2.

```
sens.exp3b <-
  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 = 1,
  readbpam = F,
  bpam = NA,
  bpamdist = 'powerlaw',
  bpamrandp = NA,
  bpampla = 1,
  bpamplb = 1,
  readprobadoptvec = F,
  probadoptvec = NA,
  probadoptmean = seq(0, 1, 0.1),
  probadoptsd = 0.2,
  readprobestabvec = F,
  probestabvec = NA,
  probestabmean = seq(0.5, 1, 0.1),
  probestabsd = 0.2,
  maneffdir = 'decrease_estab',
  maneffmean = 0.8,
  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"
## [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"
## [1] "ending parameter combination 22"
## [1] "ending parameter combination 23"
## [1] "ending parameter combination 24"
## [1] "ending parameter combination 25"
## [1] "ending parameter combination 26"
## [1] "ending parameter combination 27"
## [1] "ending parameter combination 28"
## [1] "ending parameter combination 29"
## [1] "ending parameter combination 30"
## [1] "ending parameter combination 31"
## [1] "ending parameter combination 32"
## [1] "ending parameter combination 33"
## [1] "ending parameter combination 34"
## [1] "ending parameter combination 35"
## [1] "ending parameter combination 36"
## [1] "ending parameter combination 37"
## [1] "ending parameter combination 38"
## [1] "ending parameter combination 39"
## [1] "ending parameter combination 40"
## [1] "ending parameter combination 41"
## [1] "ending parameter combination 42"
## [1] "ending parameter combination 43"
## [1] "ending parameter combination 44"
## [1] "ending parameter combination 45"
## [1] "ending parameter combination 46"
## [1] "ending parameter combination 47"
## [1] "ending parameter combination 48"
## [1] "ending parameter combination 49"
## [1] "ending parameter combination 50"
## [1] "ending parameter combination 51"
## [1] "ending parameter combination 52"
## [1] "ending parameter combination 53"
## [1] "ending parameter combination 54"
## [1] "ending parameter combination 55"
## [1] "ending parameter combination 56"
## [1] "ending parameter combination 57"
## [1] "ending parameter combination 58"
## [1] "ending parameter combination 59"
## [1] "ending parameter combination 60"
## [1] "ending parameter combination 61"
## [1] "ending parameter combination 62"
## [1] "ending parameter combination 63"
## [1] "ending parameter combination 64"
## [1] "ending parameter combination 65"
## [1] "ending parameter combination 66"
```

```r
jt2 <- sens.exp3b$multout
```

```r
# Plot how the mean establishment proportion is a function of the probability of
```

```r
# adoption mean, separately for each level of the probability of establishment
# mean

# These are the 'observed' mean establishment proportions corresponding to the
# levels of the mean probability of adoption, in separate vectors by the
# probabilities of establishment running from 0.5 to 1.0
mestab0.5 <- jt2$mestab[jt2$probestabmean==0.5]
mestab0.6 <- jt2$mestab[jt2$probestabmean==0.6]
mestab0.7 <- jt2$mestab[jt2$probestabmean==0.7]
mestab0.8 <- jt2$mestab[jt2$probestabmean==0.8]
mestab0.9 <- jt2$mestab[jt2$probestabmean==0.9]
mestab1.0 <- jt2$mestab[jt2$probestabmean==1.0]
probadoptmean.frac <- jt2$probadoptmean[jt2$probestabmean==1.0]
# This last command can be used because the parameter values are evaluated from
# smaller to larger

plot(
  probadoptmean.frac,
  mestab0.5,
  xlab = 'Mean probability of adoption',
  ylab = 'Proportion nodes with invasive established',
  ylim = c(0, 1),
  col = 'orchid1',
  type = 'l'
  )
lines(probadoptmean.frac, mestab0.6, col='orchid2')
lines(probadoptmean.frac, mestab0.7, col='orchid3')
lines(probadoptmean.frac, mestab0.8, col='darkorchid1')
lines(probadoptmean.frac, mestab0.9, col='darkorchid2')
lines(probadoptmean.frac, mestab1.0, col='darkorchid3')
text(x=1, y=0.4, labels='= 0.5', pos=2, col='orchid1')
text(x=1, y=0.5, labels='= 0.6', pos=2, col='orchid2')
text(x=1, y=0.6, labels='= 0.7', pos=2, col='orchid3')
text(x=1, y=0.7, labels='= 0.8', pos=2, col='darkorchid1')
text(x=1, y=0.8, labels='= 0.9', pos=2, col='darkorchid2')
text(
  x = 1,
  y = 0.9,
  labels = 'Probability of establishment in absence of management = 1.0',
  pos = 2,
  col = 'darkorchid3'
  )
```
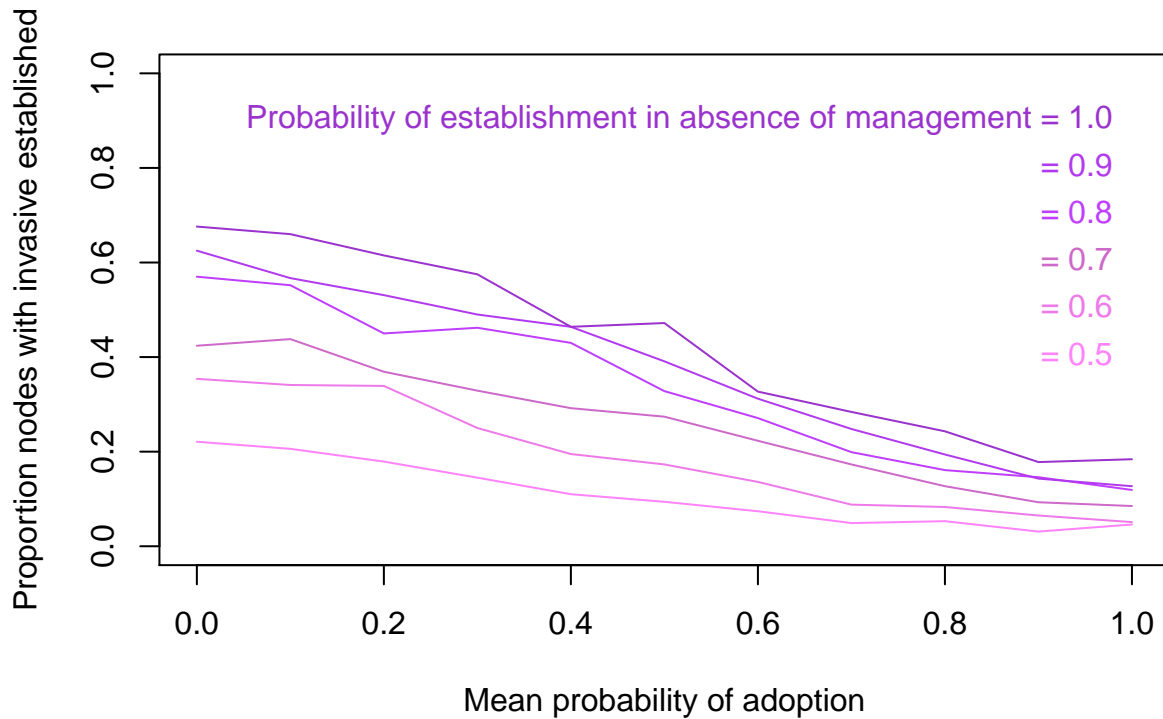
Next considering the adaptation function:

```r
# Now creating the plot of the adaptation function

# for each value of the probability of establishment from 0.5 to 1
# find the minimum probability of adoption required to keep the
# 'observed' establishment proportion below 0.2

probadoptrequired <- 1:6

probadoptrequired[1] <- min(probadoptmean.frac[mestab0.5 < 0.2])
probadoptrequired[2] <- min(probadoptmean.frac[mestab0.6 < 0.2])
probadoptrequired[3] <- min(probadoptmean.frac[mestab0.7 < 0.2])
probadoptrequired[4] <- min(probadoptmean.frac[mestab0.8 < 0.2])
probadoptrequired[5] <- min(probadoptmean.frac[mestab0.9 < 0.2])
probadoptrequired[6] <- min(probadoptmean.frac[mestab1.0 < 0.2])

plot(
  seq(0.5, 1.0, 0.1),
  probadoptrequired,
  xlab = 'Mean probability of establishment in absence of management',
  ylab = 'Mean adoption rate required',
  xlim = c(0, 1),
  ylim = c(0, 1),
  type = 'l',
  main = 'Adaptation function for sustainability',
  col = 'turquoise3',
  lwd = 3
  )
```
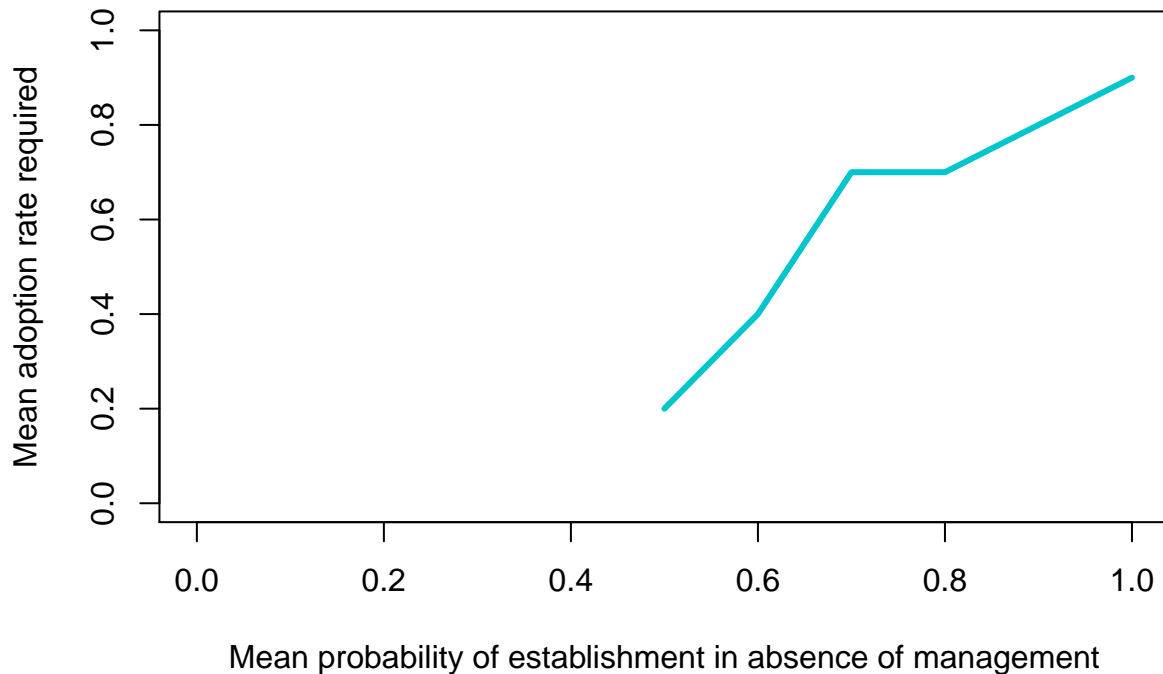
Adaptation function for sustainability

This figure shows the technology adoption rate required to keep the mean 'observed' establishment rate below 0.2, as the probability of establishment (in the absence of management) increases from the baseline of 0.5. This assumes the mean management effect has already been increased to 0.8.

In a plot of bioentity success versus impact network parameter, the line indicating the required adaptation is interpreted as demarcating the 'zone of adaptation for sustainability'.

Experiment 3C - Adaptation for resilience

In the 'adaptation for resilience' scenario, as a pulse stressor, a baseline starting proportion of nodes infected of 0.05 is compared to a new scenario where the starting proportion is 0.50.

```
# Scenario with 0.05 proportion of nodes infected at the beginning of management
# (as already seen), and the probability of establishment probestabmean=0.5 (not
# elevated)

sens.exp3c.05 <-
  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 = '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,
    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 = 0.2,
    maneffdir = 'decrease_estab',
    maneffmean = 0.5,
    maneffsd = 0.2,
    usethreshman = F,
    maneffthresh = NA,
    sampeffort = NA
    )
```

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

```
jt2 <- sens.exp3c.05$multout

jt2$mestab # the resulting mean establishment
```

```
## [1] 0.1558
```

```
jt2$estab5 # the 5th percentile of establishment
```

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

```r
jt2$estab95 # the 95th percentile of establishment
```

```
## [1] 0.32
```

Now a scenario where a climate event has acted as a pulse stressor, and the starting conditions are at 0.5 proportion invaded rather than 0.05.

```r
# Scenario with 0.05 proportion of nodes infected at the beginning of management
# (as already seen), and the probability of establishment probestabmean=0.5 (not
# elevated)

sens.exp3c.5 <-
  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 = 'prop',
  initinfo.n = NA,
  initinfo.p = 0.05,
  initinfo.dist = 'random',
  readinitbio = F,
  initbio = NA,
  initbio.norp = 'prop',
  initbio.n = NA,
  initbio.p = 0.5,
  initbio.dist = 'upedge',
  readseam = F,
  seam = NA,
  seamdist = 'powerlaw',
  seamrandp = NA,
  seampla = 1,
  seamplb = 1,
  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 = 0.2,
  maneffdir = 'decrease_estab',
  maneffmean = 0.5,
  maneffsd = 0.2,
  usethreshman = F,
  maneffthresh = NA,
  sampeffort = NA
  )
```

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

```
jt2 <- sens.exp3c.5$multout

jt2$mestab # the resulting mean establishment
```

```
## [1] 0.2588
```

```
jt2$estab5 # the 5th percentile of establishment
```

```
## [1] 0.12
```

```
jt2$estab95 # the 95th percentile of establishment
```

```
## [1] 0.381
```

The mean proportion establishment increased from around 0.15 to around 0.25 with the pulse stressor that increased the starting proportion established. The scenario allows for a reduction in establishment from the initial pulse stress population of 0.50 to around 0.25 over 5 time steps.

What increase in the mean probability of technology adoption would be needed to bring the mean 'observed' establishment back down to 0.15 for the same scenario?

```
# Scenario with the probability of establishment probestabmean=0.5 , for
# multiple levels of probadoptmean

sens.exp3c.5 <-
  INAscene(
  nreals = 40,
  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,
```

```r
  initinfo.dist = 'random',
  readinitbio = F,
  initbio = NA,
  initbio.norp = 'prop',
  initbio.n = NA,
  initbio.p = 0.5,
  initbio.dist = 'upedge',
  readseam = F,
  seam = NA,
  seamdist = 'powerlaw',
  seamrandp = NA,
  seampla = 1,
  seamplb = 1,
  readbpam = F,
  bpam = NA,
  bpamdist = 'powerlaw',
  bpamrandp = NA,
  bpampla = 1,
  bpamplb = 1,
  readprobadoptvec = F,
  probadoptvec = NA,
  probadoptmean = seq(0, 1, 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 = 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.exp3c.5$multout

# Plot how the mean establishment proportion is a function of the mean
# probability of technology adoption

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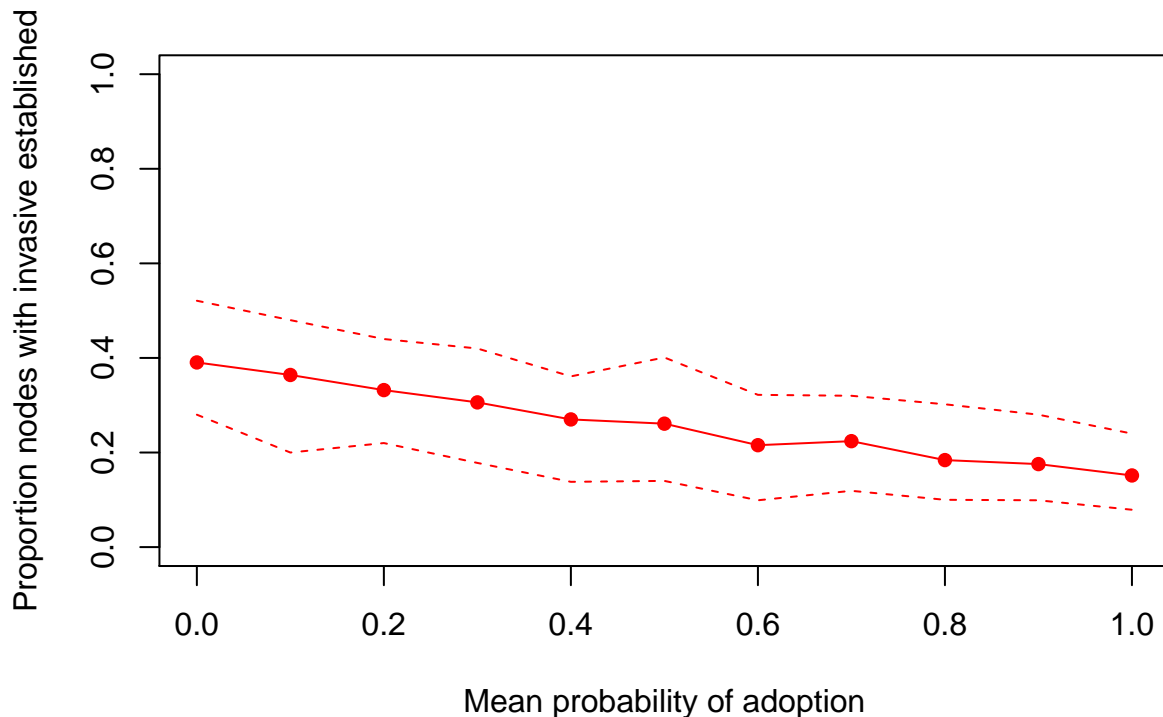
```
  jt2$probadoptmean,
  jt2$mestab,
  xlab = 'Mean probability of adoption',
  ylab = 'Proportion nodes with invasive established',
  ylim = c(0, 1),
  col = 'red',
  pch = 16
  )
lines(jt2$probadoptmean, jt2$mestab, col='red')

# also indicate the 95th percentile

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

# also indicate the 5th percentile

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


If there is 100% adoption, the proportion nodes with the bioentity is brought down to around 0.2, so additional adaptations would be necessary to have the mean proportion nodes reduced to 0.15

Experiment 3D - Adaptation function for resilience

The adaptation function for resilience indicates the adaptation required in terms of modifying one of the system parameters potentially under managers' direct control. The adaptation is in response to a pulse stressor that results in an unusually high proportion of locations with an invasive bioentity. What adaptation is necessary to bring the proportion locations with the bioentity established below 0.2 during the time steps considered? Suppose the management effect mean is brought up to 0.9. What is the adaptation function for resilience, based on adaptation through modifying the mean technology adoption probability?

```r
# Scenario with the probability of establishment probestabmean=0.5, and
# probestabmean=0.5, with maneffmean=0.9.  For a range of starting proportions
# for establishment of the bioentity (initbio.p=seq(0.05,0.55,0.1)), what is the
# effect of a range of values of propadoptmean (seq(0,1,0.1))?

sens.exp3d <-
  INAscene(
  nreals = 40,
  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 = seq(0.05, 0.55, 0.1),
  initbio.dist = 'upedge',
  readseam = F,
  seam = NA,
  seamdist = 'powerlaw',
  seamrandp = NA,
  seampla = 1,
  seamplb = 1,
  readbpam = F,
  bpam = NA,
  bpamdist = 'powerlaw',
  bpamrandp = NA,
  bpampla = 1,
  bpamplb = 1,
  readprobadoptvec = F,
  probadoptvec = NA,
  probadoptmean = seq(0, 1, 0.1),
  probadoptsd = 0.2,
  readprobestabvec = F,
  probestabvec = NA,
  probestabmean = 0.5,
  probestabsd = 0.2,
  maneffdir = 'decrease_estab',
  maneffmean = 0.9,
  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"
## [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"
## [1] "ending parameter combination 22"
## [1] "ending parameter combination 23"
## [1] "ending parameter combination 24"
## [1] "ending parameter combination 25"
## [1] "ending parameter combination 26"
## [1] "ending parameter combination 27"
## [1] "ending parameter combination 28"
## [1] "ending parameter combination 29"
## [1] "ending parameter combination 30"
## [1] "ending parameter combination 31"
## [1] "ending parameter combination 32"
## [1] "ending parameter combination 33"
## [1] "ending parameter combination 34"
## [1] "ending parameter combination 35"
## [1] "ending parameter combination 36"
## [1] "ending parameter combination 37"
## [1] "ending parameter combination 38"
## [1] "ending parameter combination 39"
## [1] "ending parameter combination 40"
## [1] "ending parameter combination 41"
## [1] "ending parameter combination 42"
## [1] "ending parameter combination 43"
## [1] "ending parameter combination 44"
## [1] "ending parameter combination 45"
## [1] "ending parameter combination 46"
## [1] "ending parameter combination 47"
## [1] "ending parameter combination 48"
## [1] "ending parameter combination 49"
## [1] "ending parameter combination 50"
```

```
## [1] "ending parameter combination 51"
## [1] "ending parameter combination 52"
## [1] "ending parameter combination 53"
## [1] "ending parameter combination 54"
## [1] "ending parameter combination 55"
## [1] "ending parameter combination 56"
## [1] "ending parameter combination 57"
## [1] "ending parameter combination 58"
## [1] "ending parameter combination 59"
## [1] "ending parameter combination 60"
## [1] "ending parameter combination 61"
## [1] "ending parameter combination 62"
## [1] "ending parameter combination 63"
## [1] "ending parameter combination 64"
## [1] "ending parameter combination 65"
## [1] "ending parameter combination 66"
```

```r
jt2 <- sens.exp3d$multout

# Plot how the mean 'observed' establishment proportion is a function of the
# probability of adoption mean, separately for each level of the starting
# proportion of nodes with the bioentity established

# These are the 'observed' mean establishment proportions corresponding to the
# levels of the starting proportion of nodes with establishment, in separate
# vectors by the starting proportion of nodes with establishment running from
# 0.05 to 0.55
mestab0.05 <- jt2$mestab[round(jt2$initbio.p, digits=10)==0.05]
mestab0.15 <- jt2$mestab[round(jt2$initbio.p, digits=10)==0.15]
mestab0.25 <- jt2$mestab[round(jt2$initbio.p, digits=10)==0.25]
mestab0.35 <- jt2$mestab[round(jt2$initbio.p, digits=10)==0.35]
mestab0.45 <- jt2$mestab[round(jt2$initbio.p, digits=10)==0.45]
mestab0.55 <- jt2$mestab[round(jt2$initbio.p, digits=10)==0.55]
probadoptmean.frac.p <- jt2$probadoptmean[round(jt2$initbio.p, digits=10)==0.55]

# note that the round command was used because of probablems with 0.15 being off
# by 2.775558e-17

# the last command in the set can be used because the parameter values are
# evaluated from smaller to larger

plot(
  probadoptmean.frac.p,
  mestab0.05,
  xlab = 'Mean probability of adoption',
  ylab = 'Proportion nodes starting with bioentity established',
  ylim = c(0, 1),
  col = 'orchid1',
  type = 'l'
  )
lines(probadoptmean.frac.p, mestab0.15, col='orchid2')
lines(probadoptmean.frac.p, mestab0.25, col='orchid3')
lines(probadoptmean.frac.p, mestab0.35, col='darkorchid1')
lines(probadoptmean.frac.p, mestab0.45, col='darkorchid2')
```
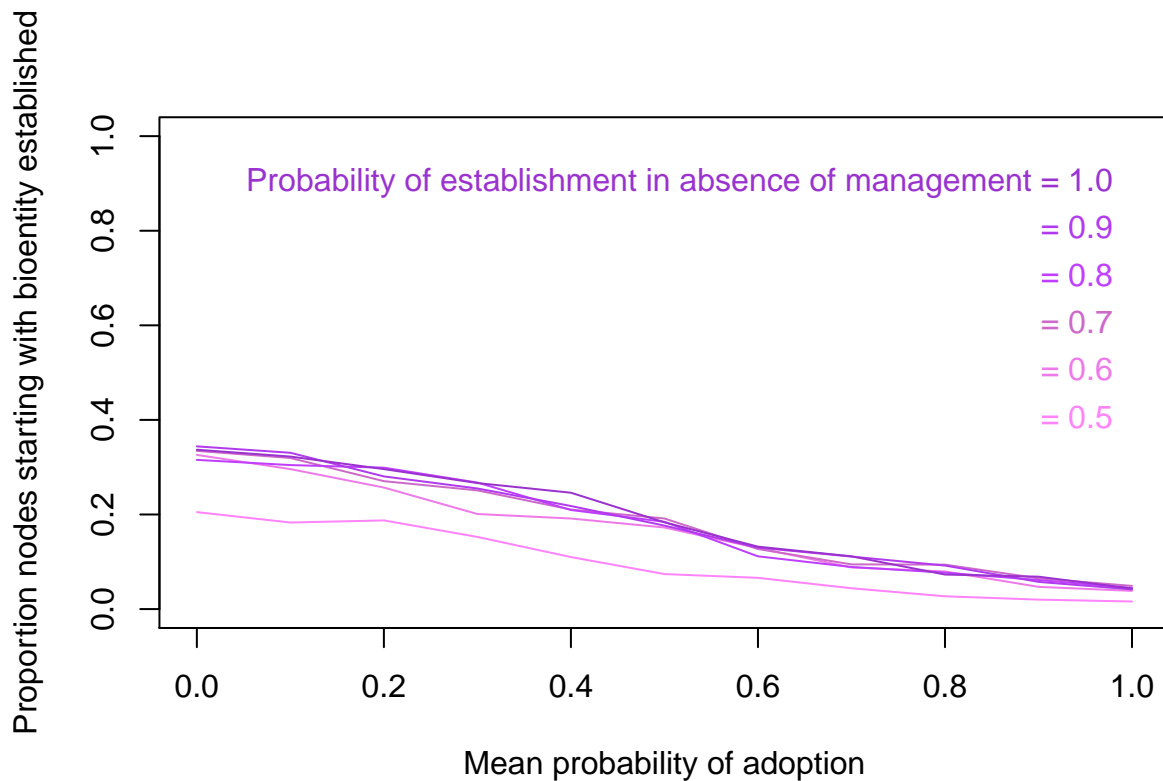
```r
lines(probadoptmean.frac.p, mestab0.55, col='darkorchid3')
text(x=1, y=0.4, labels='= 0.5', pos=2, col='orchid1')
text(x=1, y=0.5, labels='= 0.6', pos=2, col='orchid2')
text(x=1, y=0.6, labels='= 0.7', pos=2, col='orchid3')
text(x=1, y=0.7, labels='= 0.8', pos=2, col='darkorchid1')
text(x=1, y=0.8, labels='= 0.9', pos=2, col='darkorchid2')
text(
  x = 1,
  y = 0.9,
  labels = 'Probability of establishment in absence of management = 1.0',
  pos = 2,
  col = 'darkorchid3'
  )
```


Next the adaptation function for this scenario:

```r
# Now creating the plot of the adaptation function

# for each value of the initial proportion establishment from 0.05 to 0.50
# find the minimum probability of adoption required to keep the
# 'observed' establishment proportion below 0.2

probadoptrequired.p <- 1:6

probadoptrequired.p[1] <- min(probadoptmean.frac[mestab0.05 < 0.2])
probadoptrequired.p[2] <- min(probadoptmean.frac[mestab0.15 < 0.2])
probadoptrequired.p[3] <- min(probadoptmean.frac[mestab0.25 < 0.2])
probadoptrequired.p[4] <- min(probadoptmean.frac[mestab0.35 < 0.2])
probadoptrequired.p[5] <- min(probadoptmean.frac[mestab0.45 < 0.2])
```
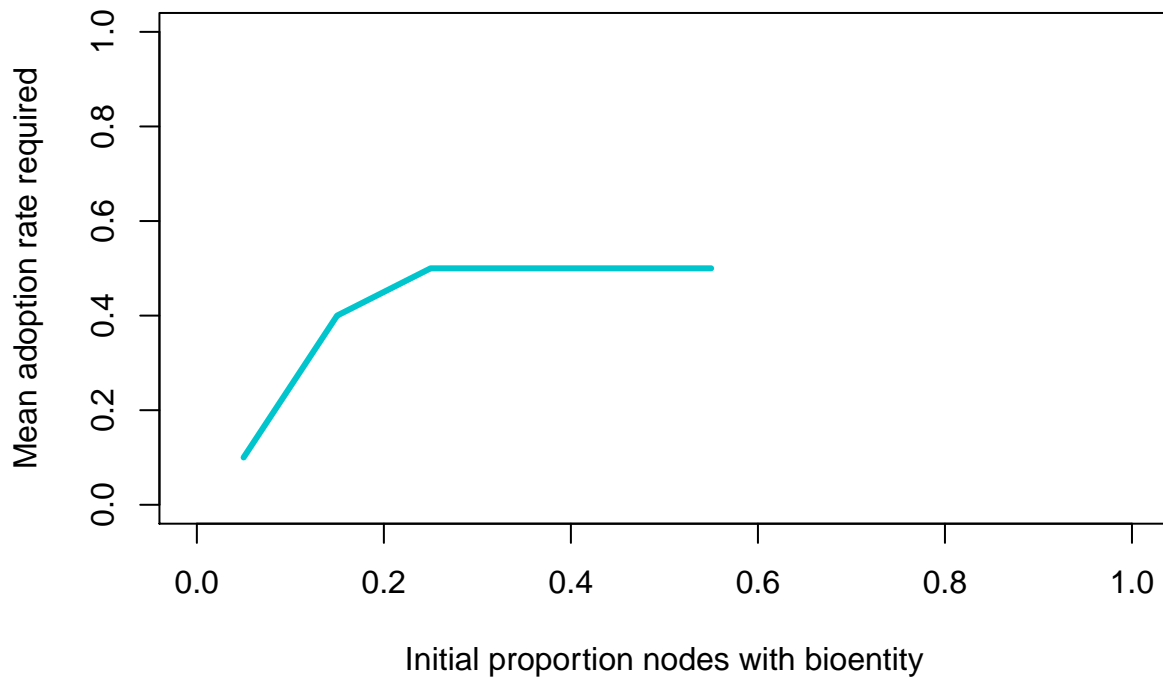
```
probadoptrequired.p[6] <- min(probadoptmean.frac[mestab0.55 < 0.2])

plot(
  seq(0.05, 0.55, 0.1),
  probadoptrequired.p,
  xlab = 'Initial proportion nodes with bioentity',
  ylab = 'Mean adoption rate required',
  xlim = c(0, 1),
  ylim = c(0, 1),
  type = 'l',
  main = 'Adaptation function for resilience',
  col = 'turquoise3',
  lwd = 3
  )
```

Adaptation function for resilience

In a plot of bioentity success versus impact network parameter, the line indicating the required adaptation is interpreted as demarcating the 'zone of adaptation for resilience'.

Science of science example

In a science of science scenario analysis, the ability of a technology to improve regional management is also influenced by the outcome of an experiment. This could represent a scenario where a research group is testing management technologies and deciding whether to promote them or not. Depending on the effort invested by the scientists in the scenario, the management effect size is estimated with greater or lesser precision. When the management effect size estimate generated by the research group is below a threshold, information about the management is not communicated, so some share of scenario realizations do not include use of the management technology. In this illustrative experiment, the threshold for communication about management rangs from 0 (communication occurs regardless of the estimated management effect) to 1 (communication

cannot occur unless there is not uncertainty about the complete effectiveness of management). In this example, the management effect mean is 0.5 and the management effect standard deviation is fairly high, also 0.5, while the sampling effort is low, 1.

```
sens.exp3s <-
  INAscene(
  nreals = 30,
  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,
  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 = 0.2,
  maneffdir = 'decrease_estab',
  maneffmean = 0.5,
  maneffsd = 0.5,
  usethreshman = T,
  maneffthresh = seq(0, 1, 0.1),
  sampeffort = 1
  )
```

```
## [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.exp3s$multout

jt2$maneffthresh # the levels of the management effect threshold that were evaluated
```

```
##  [1] 0.0 0.1 0.2 0.3 0.4 0.5 0.6 0.7 0.8 0.9 1.0
```

```r
jt2$mestab # the resulting mean establishment rates
```

```
##  [1] 0.1386667 0.1606667 0.2200000 0.1693333 0.2160000 0.1960000 0.2546667
##  [8] 0.2506667 0.2306667 0.2553333 0.2706667
```

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

plot(
  jt2$maneffthresh,
  jt2$mestab,
  xlab = 'Management effect threshold for communication',
  ylab = 'Proportion nodes with bioentity established',
  ylim = c(0, 1),
  col = 'red',
  pch = 16
  )
lines(jt2$maneffthresh, jt2$mestab, col='red')

# also indicate the 95th percentile

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

# also indicate the 5th percentile

lines(jt2$maneffthresh, jt2$estab5, col='red', lty=2)
```
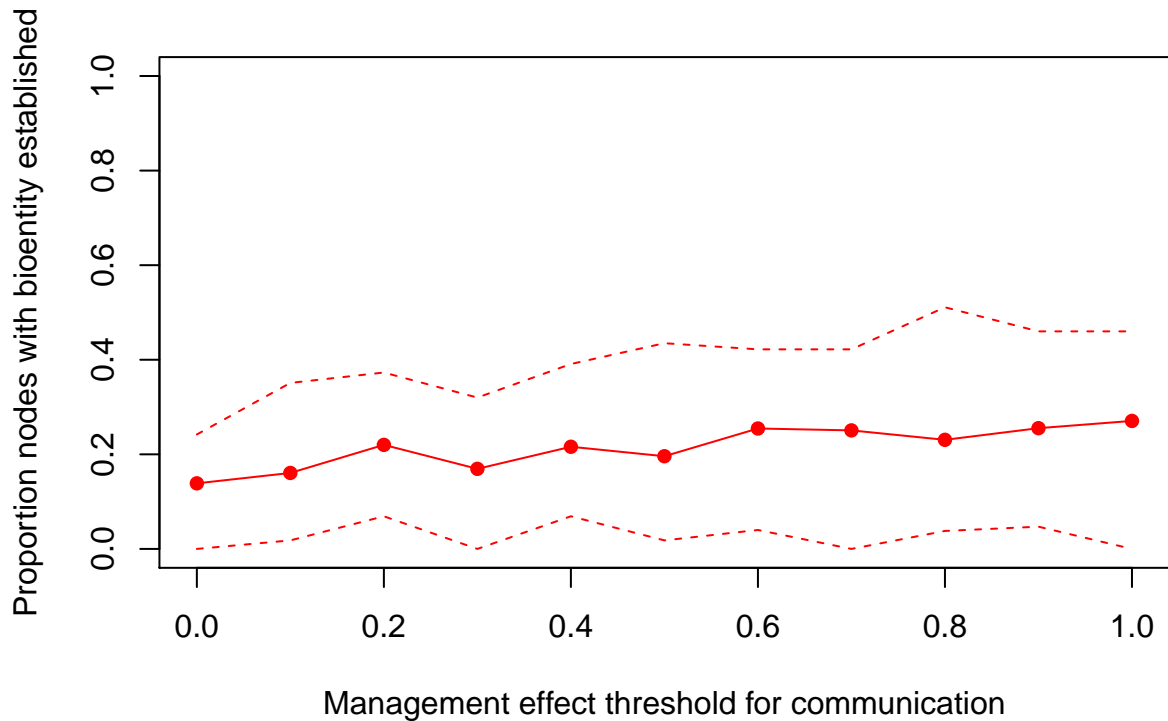
In this case, the management has only a modest regional effect on the bioentity. Consider another case where the probability of establishment in the absence of management (where the bioentity has dispersed) and the probability of technology adoption (where there has been communication about the technology) are both higher.

Note that these analyses explore the potential costs of not communicating about a technology. There are other types of costs of communicating about a technology for which the benefits have been overestimated.

```
sens.exp3s2 <-
  INAscene(
  nreals = 30,
  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,
  readbpam = F,
  bpam = NA,
  bpamdist = 'powerlaw',
  bpamrandp = NA,
  bpampla = 1,
  bpamplb = 1,
  readprobadoptvec = F,
  probadoptvec = NA,
  probadoptmean = 0.9,
  probadoptsd = 0.2,
  readprobestabvec = F,
  probestabvec = NA,
  probestabmean = 0.9,
  probestabsd = 0.2,
  maneffdir = 'decrease_estab',
  maneffmean = 0.5,
  maneffsd = 0.5,
  usethreshman = T,
  maneffthresh = seq(0, 1, 0.1),
  sampeffort = 1
  )
```

```
## [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.exp3s2$multout
```

```
jt2$maneffthresh # the levels of the management effect threshold that were evaluated
```

```
##  [1] 0.0 0.1 0.2 0.3 0.4 0.5 0.6 0.7 0.8 0.9 1.0
```

```
jt2$mestab # the resulting mean establishment rates
```

```
##  [1] 0.3346667 0.3440000 0.4040000 0.5020000 0.5326667 0.6440000 0.5600000
##  [8] 0.6320000 0.6980000 0.6940000 0.7453333
```

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

plot(
  jt2$maneffthresh,
  jt2$mestab,
  xlab = 'Management effect threshold for communication',
  ylab = 'Proportion nodes with bioentity established',
  ylim = c(0, 1),
  col = 'red',
  pch = 16
  )
lines(jt2$maneffthresh, jt2$mestab, col='red')

# also indicate the 95th percentile

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

# also indicate the 5th percentile

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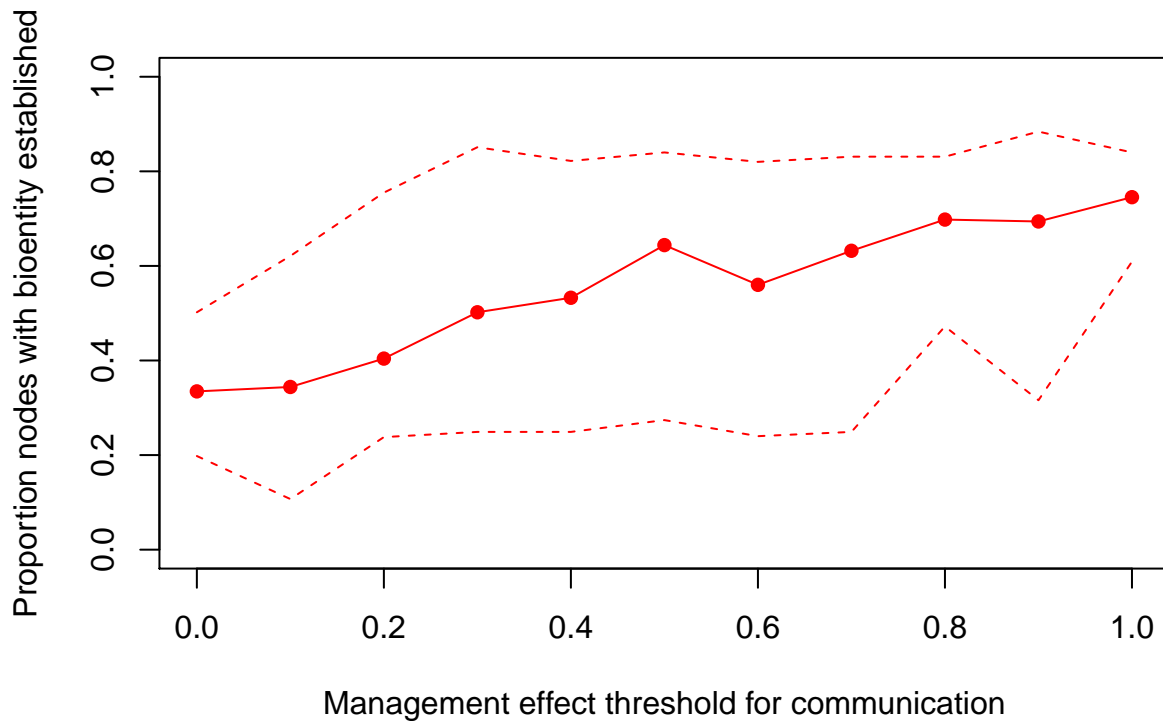

In this case, a wider range of outcomes is observed, as indicated by the 5th and 95th percentiles of the bioentity establishment.

References

For more information and references, see www.garrettlab.com/ina

Csardi, G. and T. Nepusz. 2006. The igraph software package for complex network research. InterJournal, Complex Systems: 1695. http://igraph.org

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