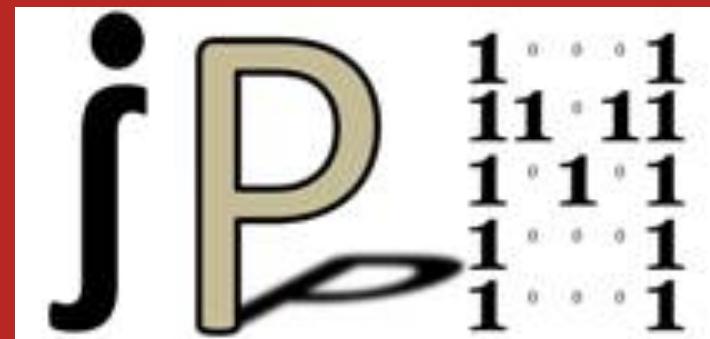


Reproduction in *IPMpack*

fun with *fecObj*



Eelke Jongejans

Radboud Universiteit



IPM: a summation of kernels

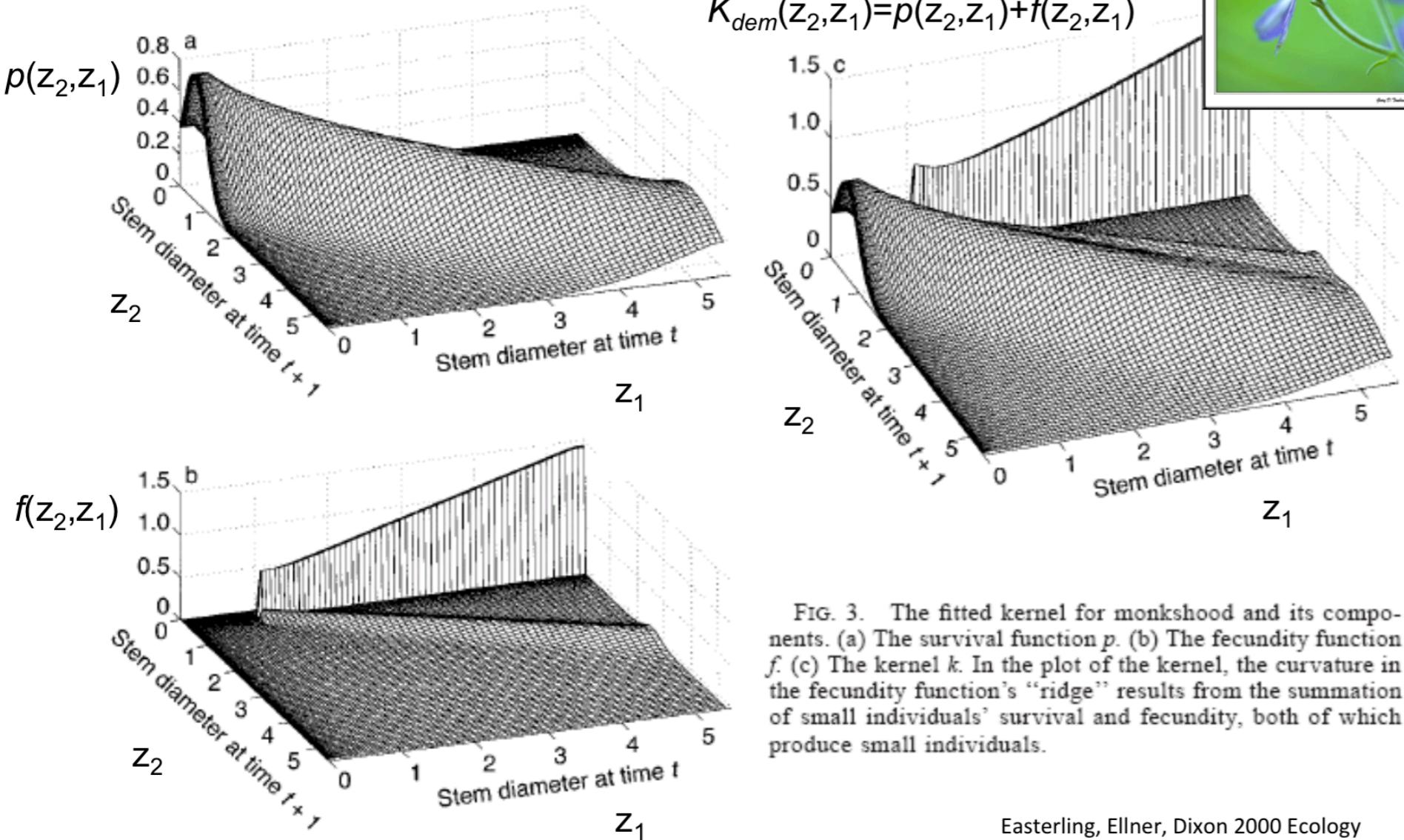


FIG. 3. The fitted kernel for monkshood and its components. (a) The survival function p . (b) The fecundity function f . (c) The kernel k . In the plot of the kernel, the curvature in the fecundity function's "ridge" results from the summation of small individuals' survival and fecundity, both of which produce small individuals.

IPM: multiple vital rates per kernel

$$n(z_2, t+1) = \int_Z K_{dem}(z_2, z_1) n(z_1, t) dz_1$$

$$K_{dem}(z_2, z_1) = p(z_2, z_1) + f(z_2, z_1)$$

$$p(z_2, z_1) = survival(z_1) \left(1 - flowering(z_1)\right) growth(z_2, z_1)$$

$$f(z_2, z_1) = survival(z_1) flowering(z_1) seedlinggrowth(z_2, z_1)$$



IPM: multiple vital rates per kernel

$$K_{\text{dem}} = \sigma(z_1)[(1 - \beta(z_1))\gamma(z_2, z_1) + \beta(z_1)\omega(z_1)\pi\phi\varepsilon\chi(z_2)]$$

Parameters of reproduction rates

- Intercept of flowering, β
- Size-slope of flowering, β
- Intercept of no. flower heads, π
- Size-slope of no. flower heads, π
- No. seeds per flower head, ω
- Seeds escaping florivory, ϕ
- Germination of fresh seeds, ε
- Mean seedling size, χ
- Variance of seedling size, χ

Elasticity values



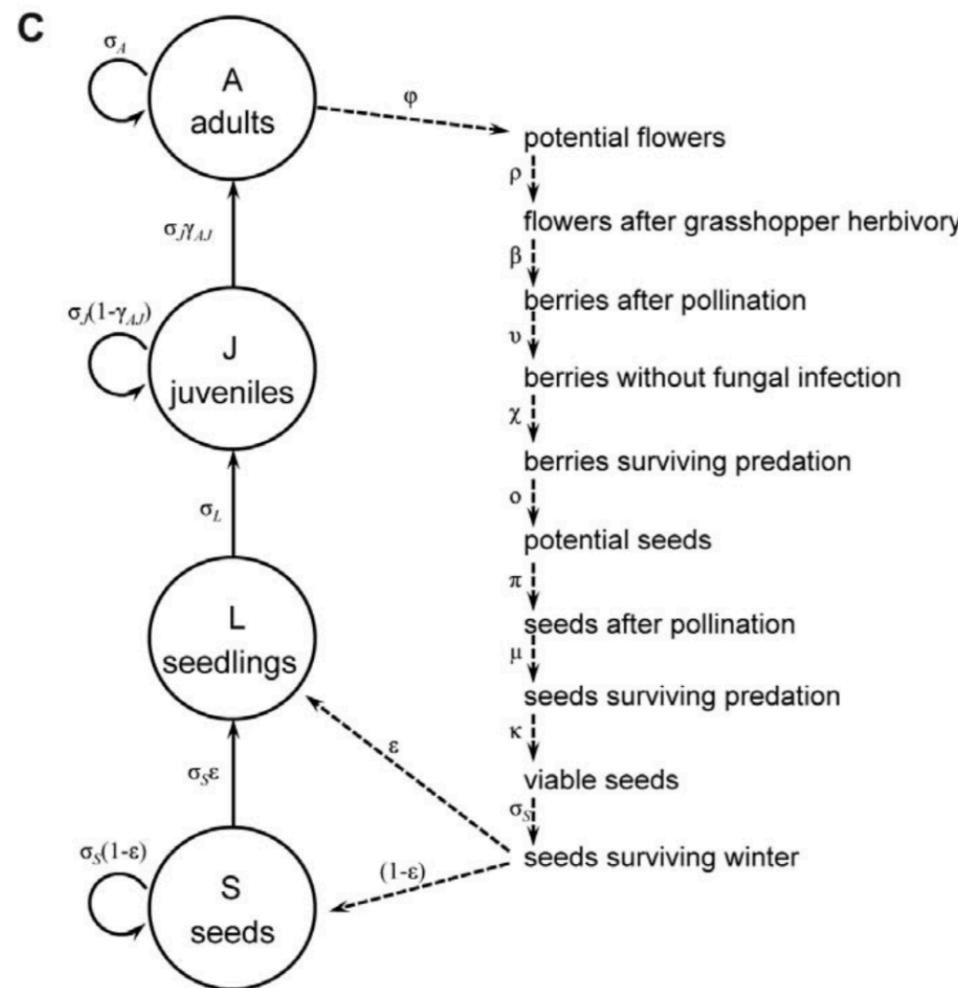


Figure 1. Huckleberry habitat and life cycle diagram. Huckleberry is sparsely distributed in primary successional sites (A), and densely distributed in secondary (B) successional sites. (C) Life cycle diagram for huckleberry. The Greek letters denote the transition rates between the consecutive steps (see Table 1).

Succisa pratensis



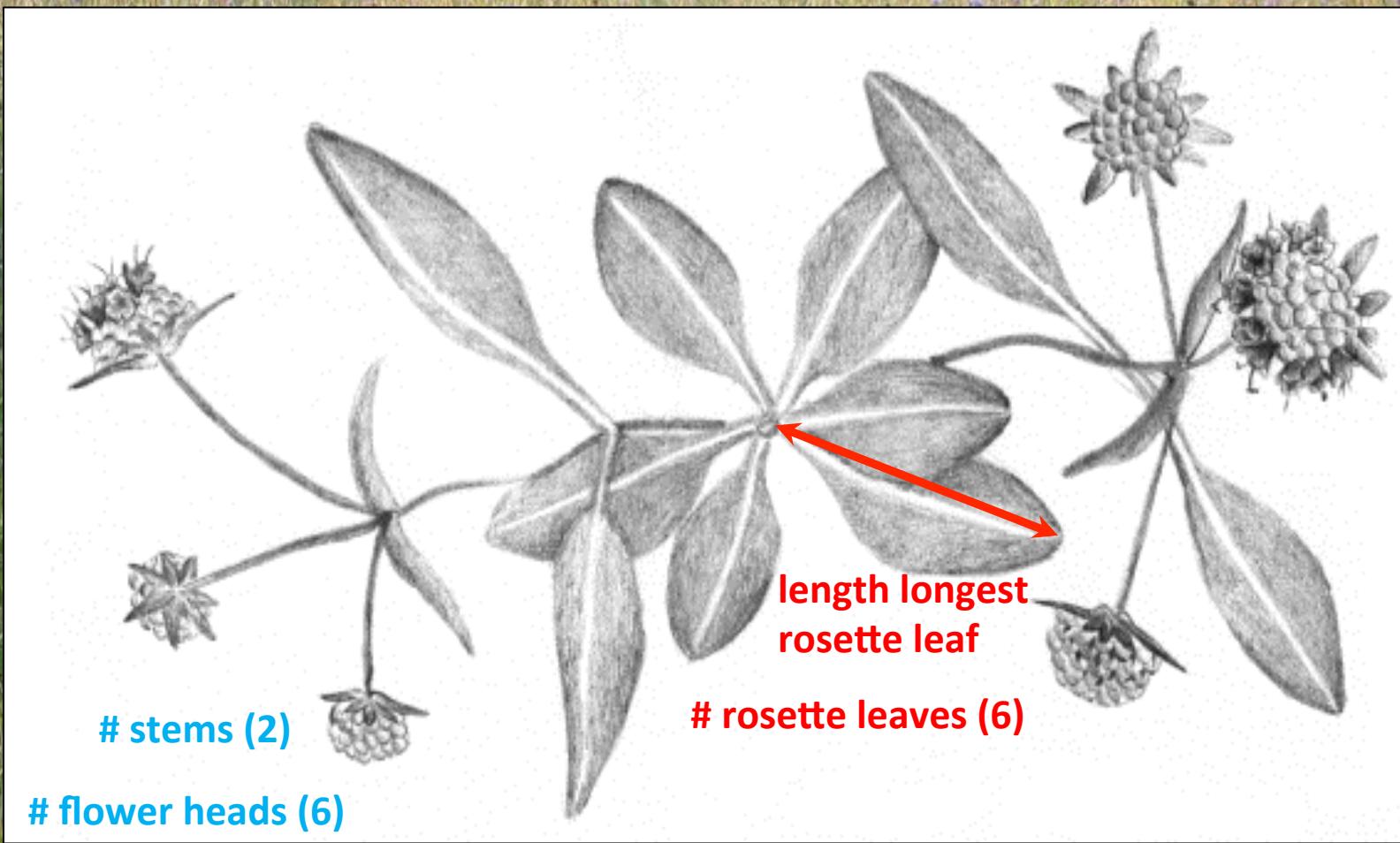
Duivelsbeet

Blauwe knoop



Extra data:

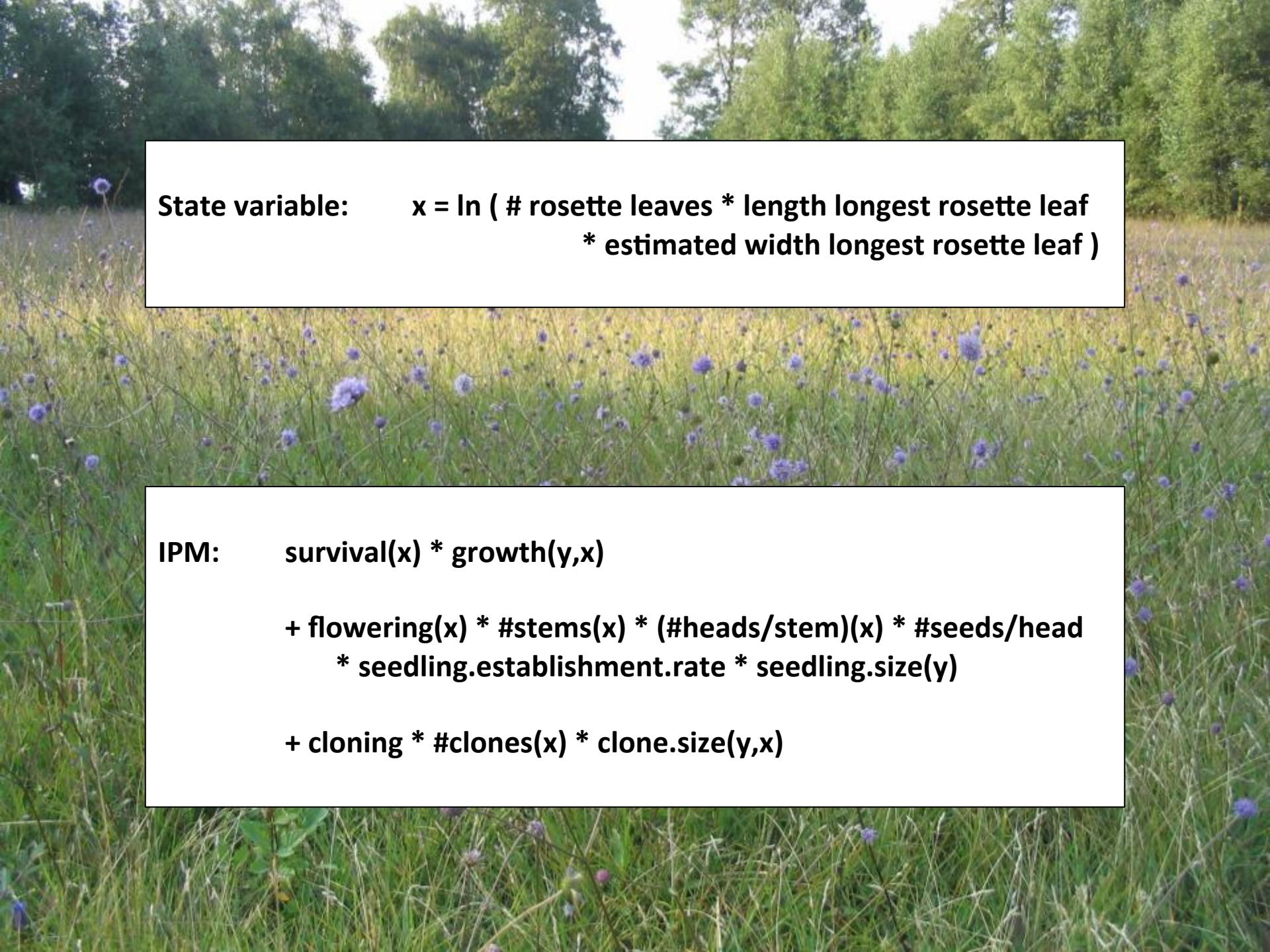
- average #seeds/head (counts) = ~50
- seedling/seed ratio (sowing experiment) = ~0.02





```
> rm(list = ls())
> require(IPMpack)
> data(dataIPMpackSuccisa)
> Sp<-dataIPMpackSuccisa
> head(Sp)
```

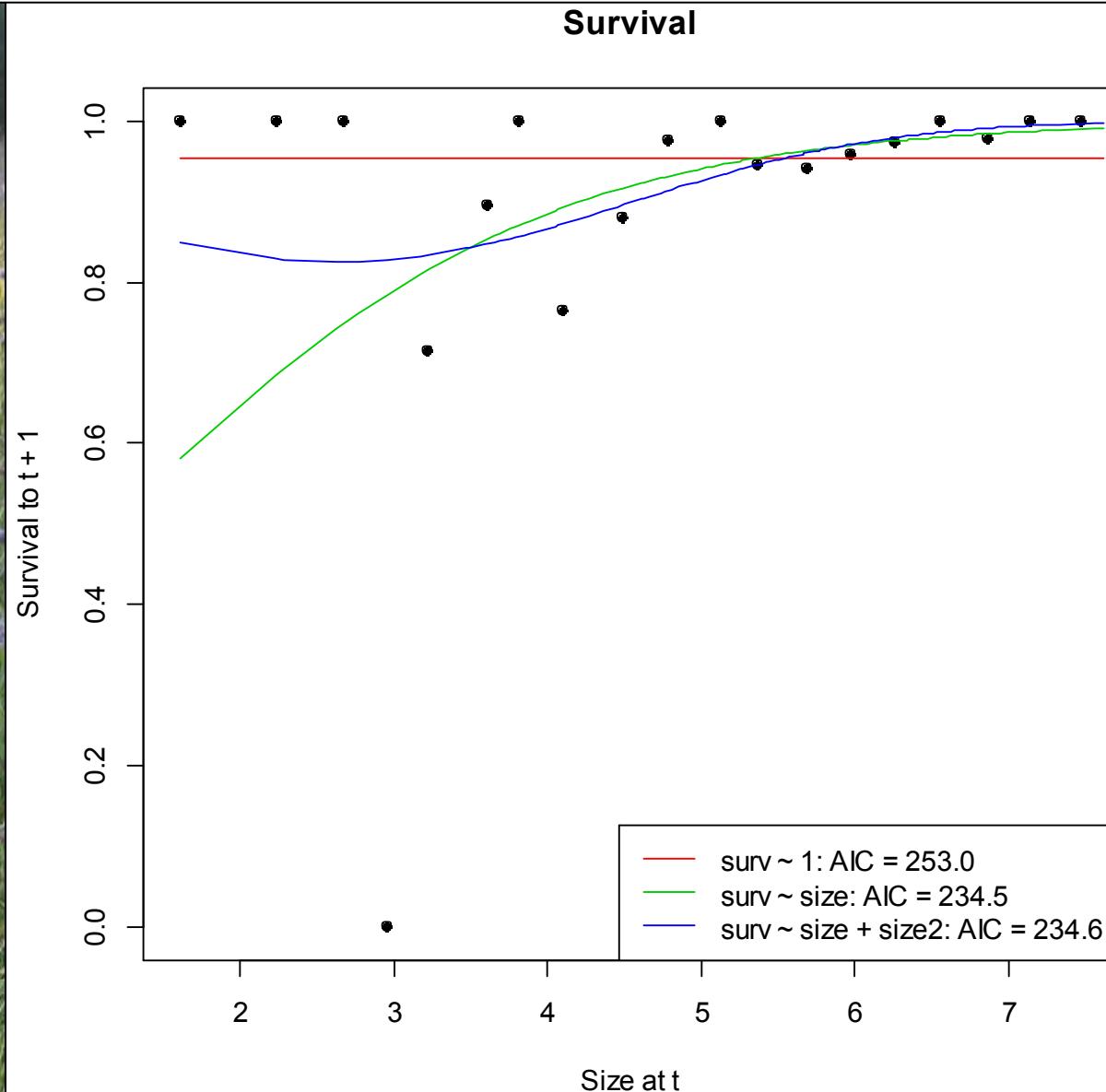
	size	sizeNext	stage	stageNext	surv	offspringNext	fec1Bolt	fec2Stem	fec3Head	fec1BoltNext	fec2StemNext	fec3HeadNext	cloning	clonesNext
1	6.282965	4.801939	continuous	continuous	1	<NA>	0	NA	NA	1	2	1.5	0	NA
2	3.472842	5.376433	continuous	continuous	1	<NA>	0	NA	NA	0	NA	NA	0	NA
3	4.902599	4.624504	continuous	continuous	1	<NA>	0	NA	NA	0	NA	NA	0	NA
4	6.074348	6.588023	continuous	continuous	1	<NA>	0	NA	NA	1	2	3.0	0	NA
5	7.218641	6.588023	continuous	continuous	1	<NA>	0	NA	NA	1	2	3.5	0	NA
6	6.937394	6.703946	continuous	continuous	1	<NA>	1	1	4	1	1	4.0	0	NA
593	5.268504	4.857953	continuous	continuous	NA	clonal	1	1	2.000000	0	NA	NA	NA	NA
742	NA	2.626464	<NA>	continuous	NA	sexual	NA	NA	NA	0	NA	NA	NA	NA



State variable: $x = \ln (\# \text{ rosette leaves} * \text{length longest rosette leaf}$
 $* \text{estimated width longest rosette leaf})$

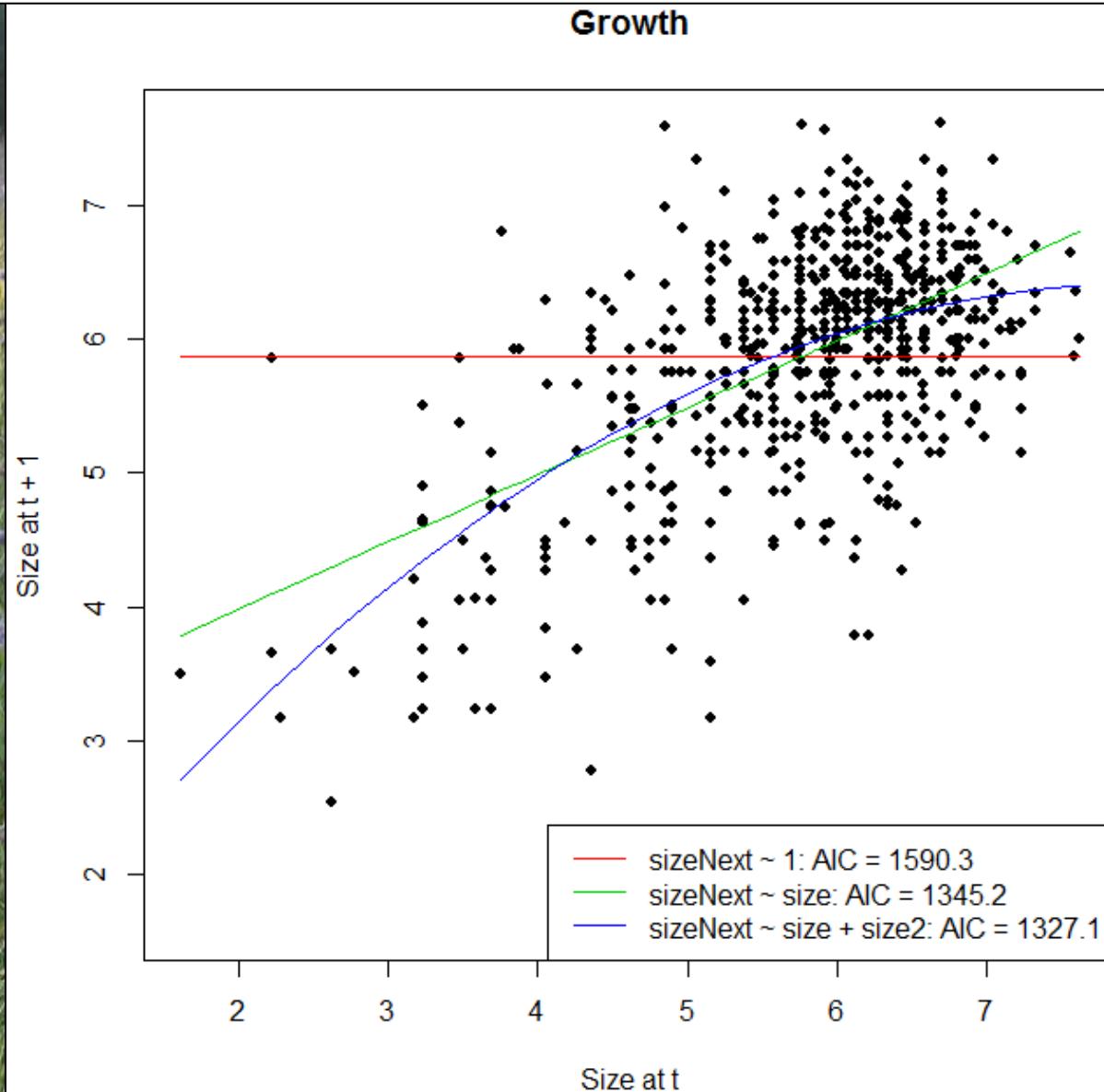
IPM: $\text{survival}(x) * \text{growth}(y, x)$
 $+ \text{flowering}(x) * \#\text{stems}(x) * (\#\text{heads/stem})(x) * \#\text{seeds/head}$
 $* \text{seedling.establishment.rate} * \text{seedling.size}(y)$
 $+ \text{cloning} * \#\text{clones}(x) * \text{clone.size}(y, x)$

```
survModelComp(dataf = Sp, makePlot = TRUE,  
               legendPos = "bottomright", mainTitle = "Survival")
```



```
so<-makeSurvObj(dataf=Sp,Formula="surv~size")
```

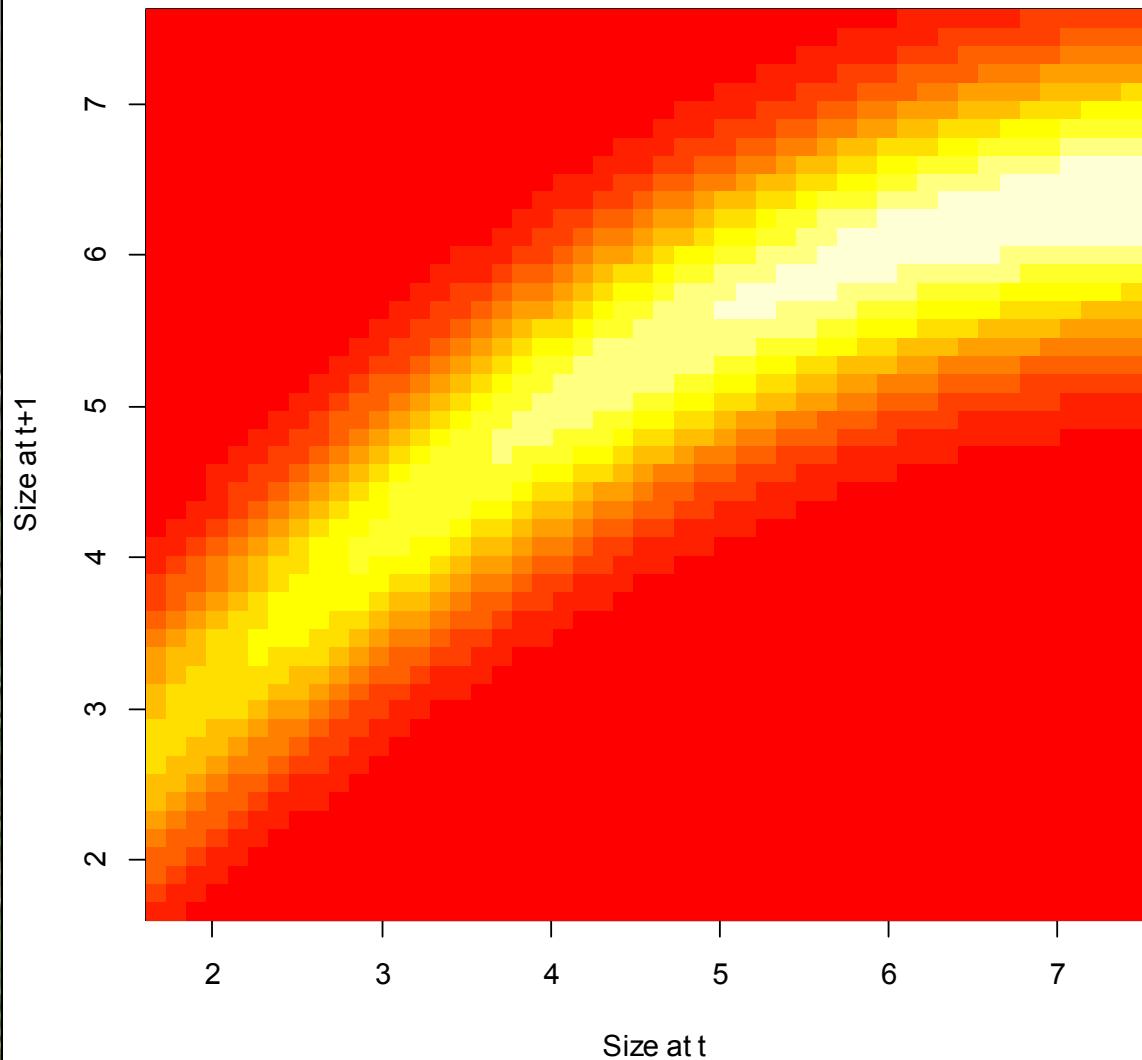
```
growthModelComp(dataf = Sp, makePlot = TRUE,  
legendPos = "bottomright", mainTitle = "Growth")
```



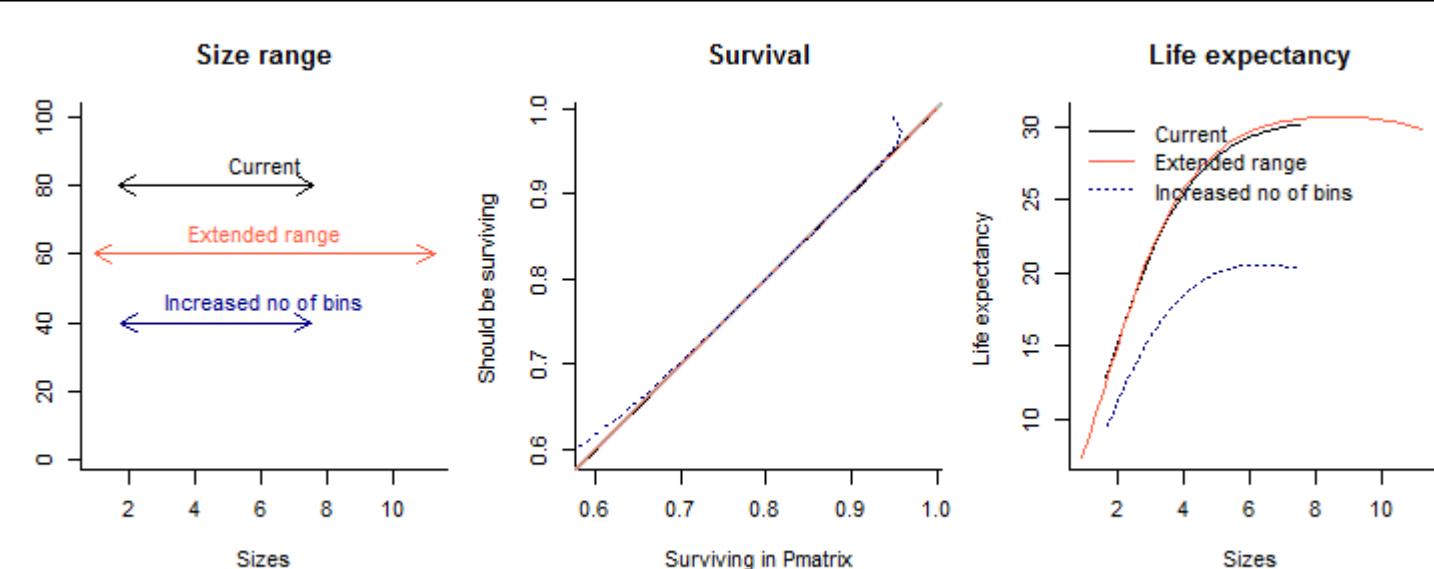
```
go<-makeGrowthObj(dataf=Sp,Formula=sizeNext~size+size2)
```

```
Pmatrix<-makeIOMPmatrix(survObj=so, growObj=go,  
minSize=min(Sp$size,na.rm=T), maxSize=max(Sp$size,na.rm=T),  
correction="constant")
```

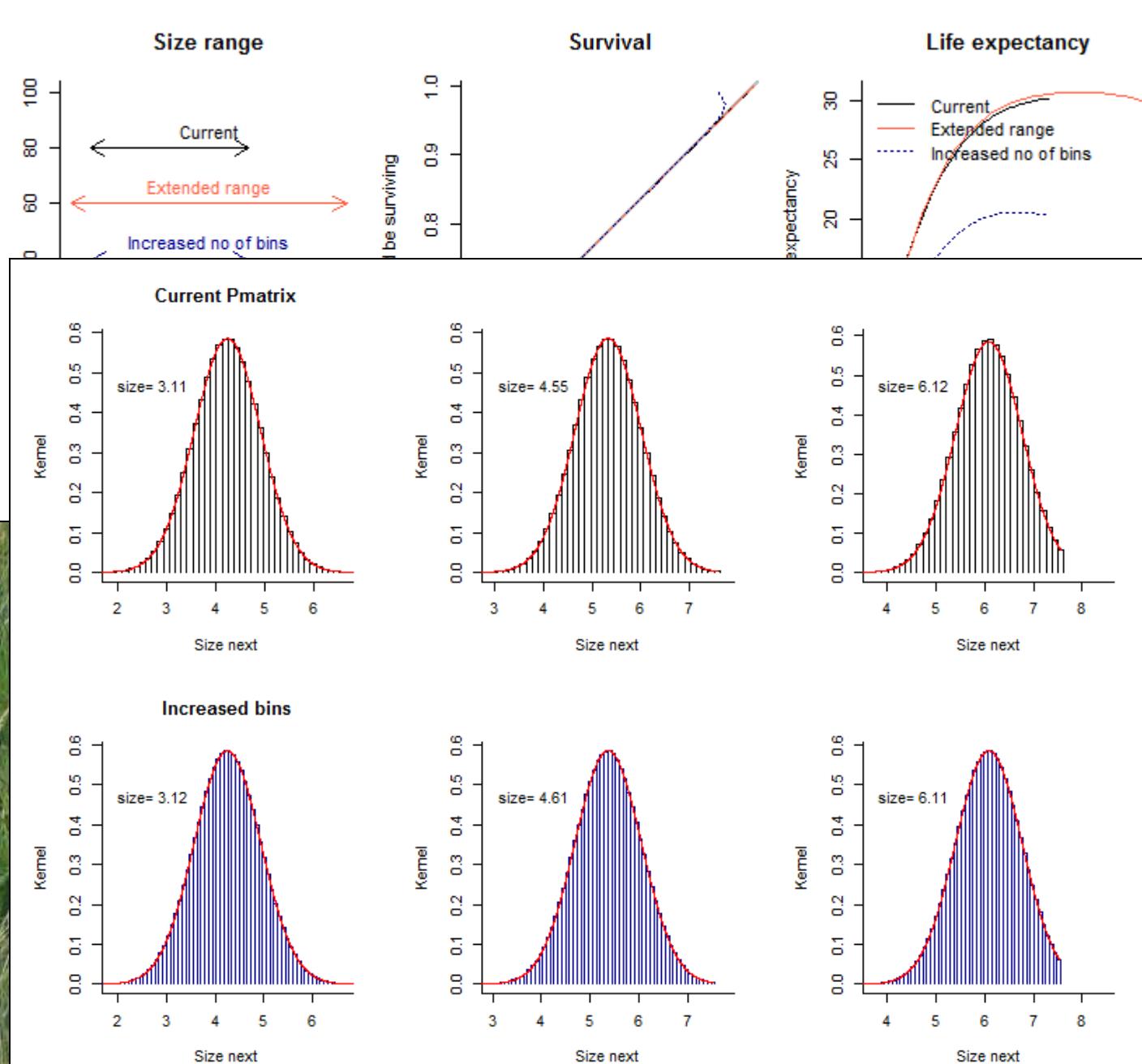
Pmatrix: survival and growth



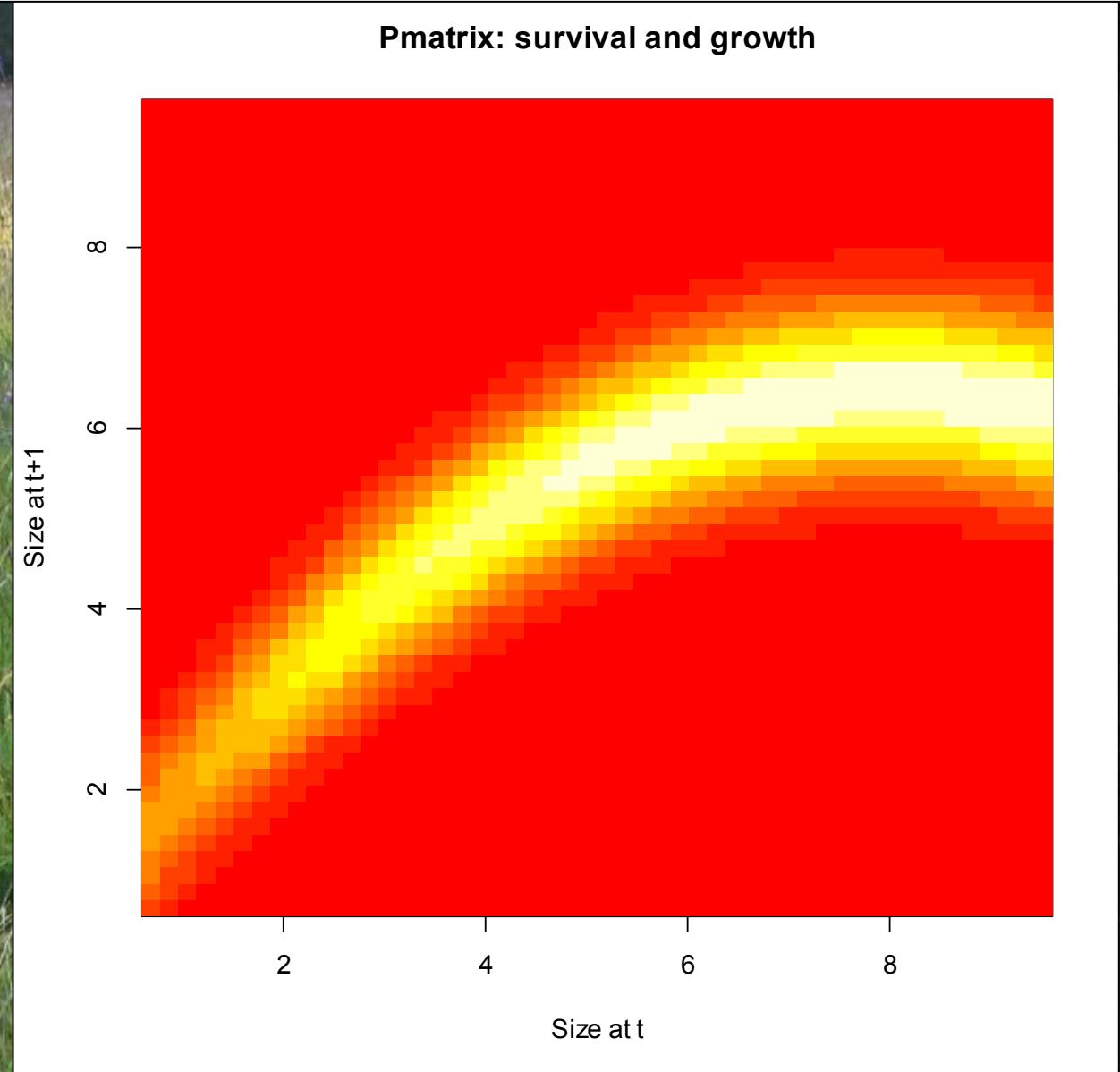
```
diagnosticsPmatrix(Pmatrix, growObj=go, survObj=so, correction="constant")
```



```
diagnosticsPmatrix(Pmatrix, growObj=go, survObj=so, correction="constant")
```

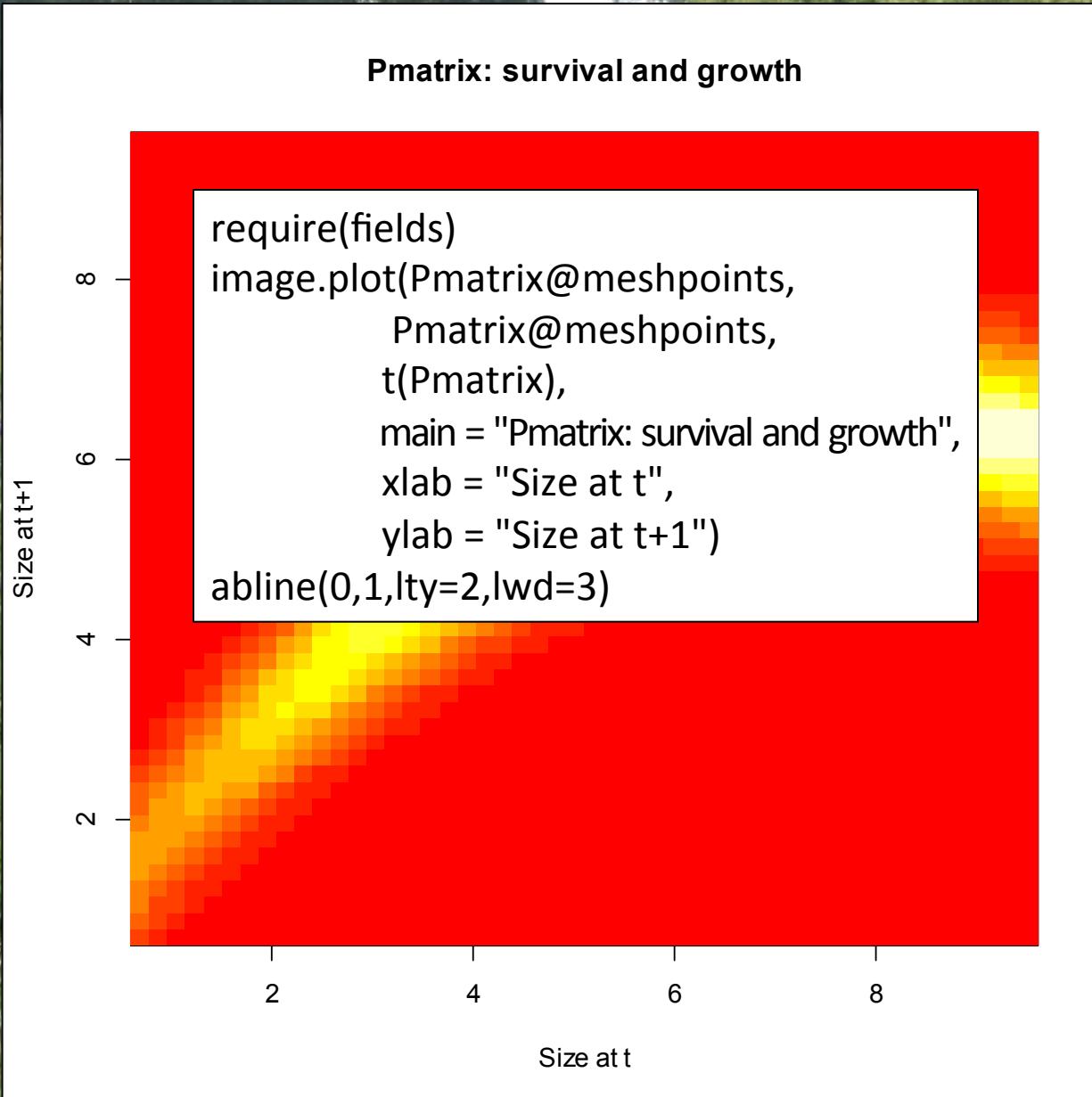


```
Pmatrix<-makeIPMPmatrix(survObj=so, growObj=go,  
minSize=min(Sp$size,na.rm=T)-1,  
maxSize=max(Sp$size,na.rm=T)+2, correction="constant")
```

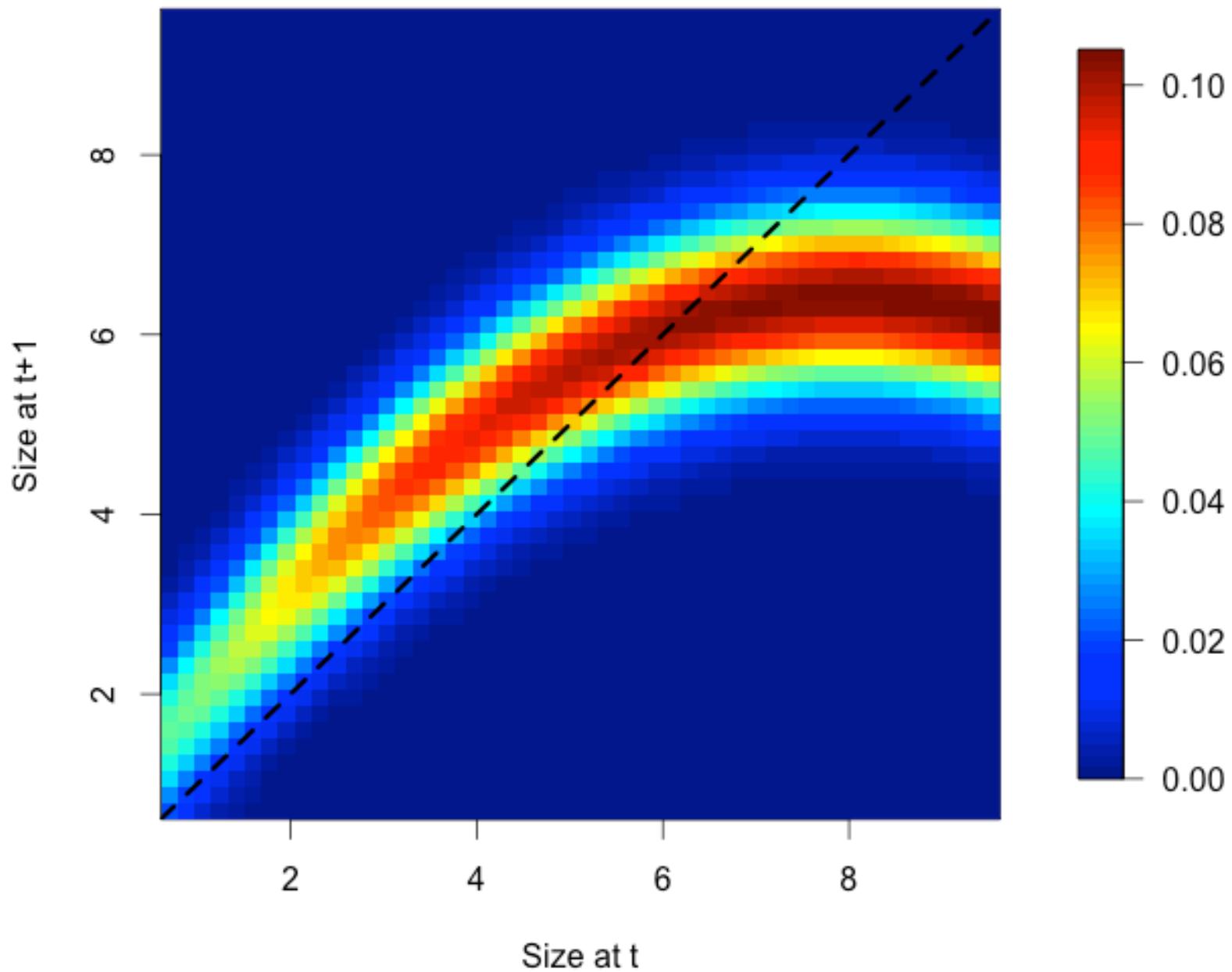


Pmatrix: survival and growth

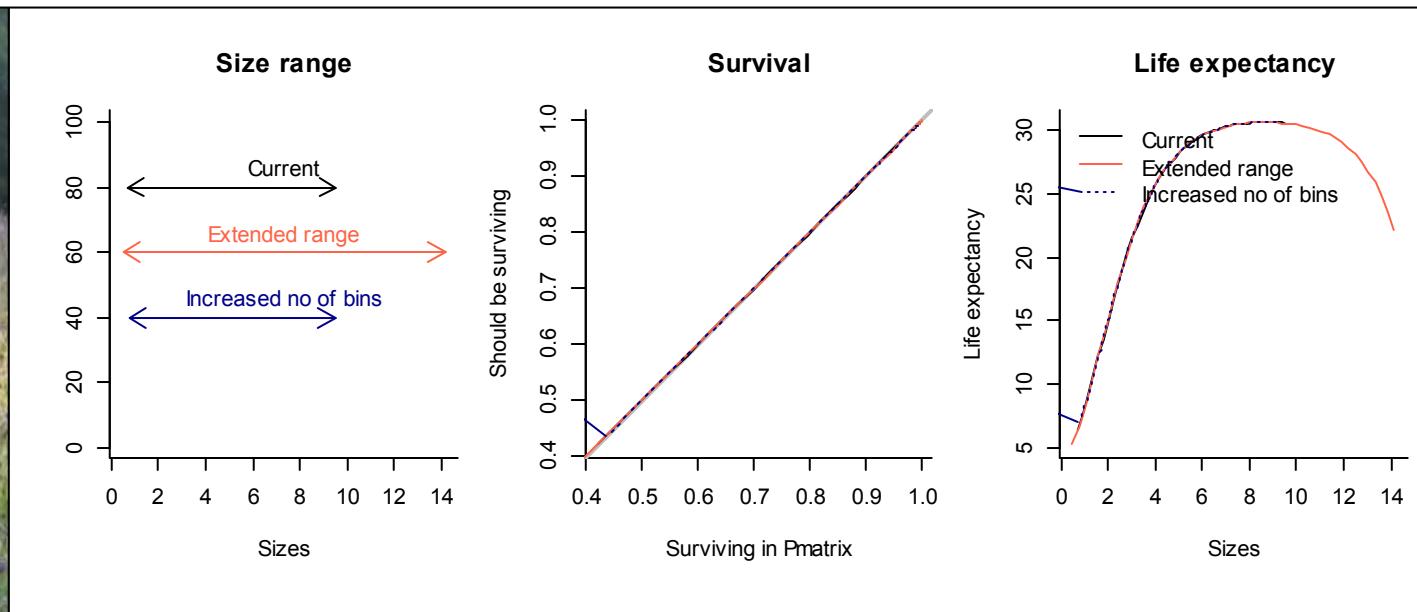
```
require(fields)
image.plot(Pmatrix@meshpoints,
           Pmatrix@meshpoints,
           t(Pmatrix),
           main = "Pmatrix: survival and growth",
           xlab = "Size at t",
           ylab = "Size at t+1")
abline(0,1,lty=2,lwd=3)
```



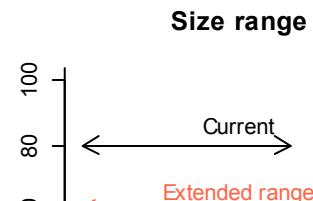
Pmatrix: survival and growth



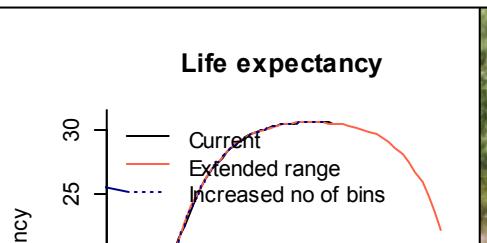
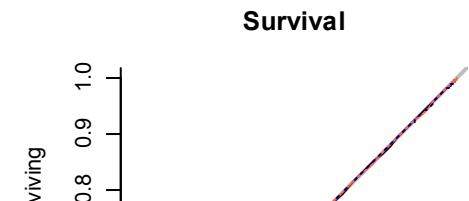
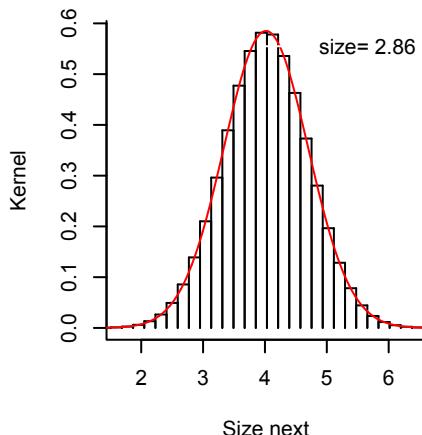
```
diagnosticsPmatrix(Pmatrix, growObj=go, survObj=so, correction="constant")
```



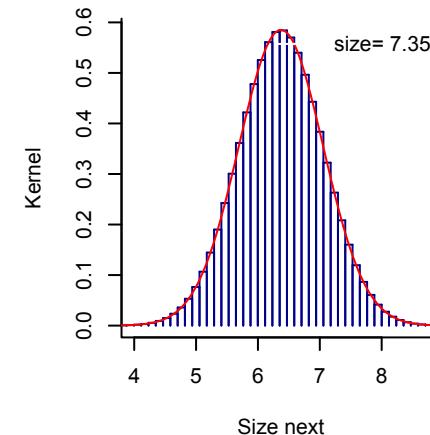
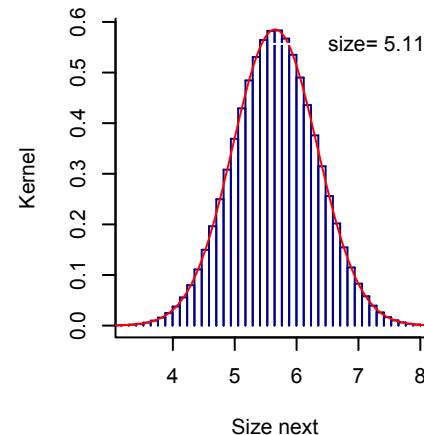
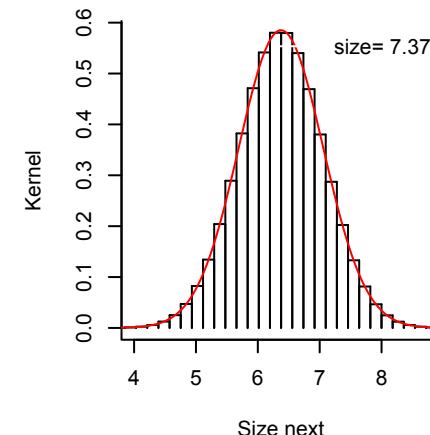
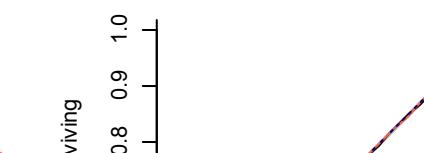
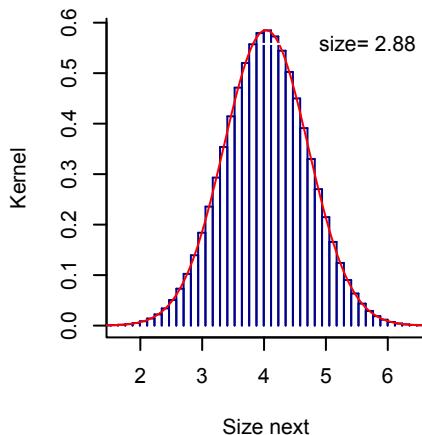
diagnosticsPmatrix(Pmatrix, growObj=go, survObj=so, correction="constant")

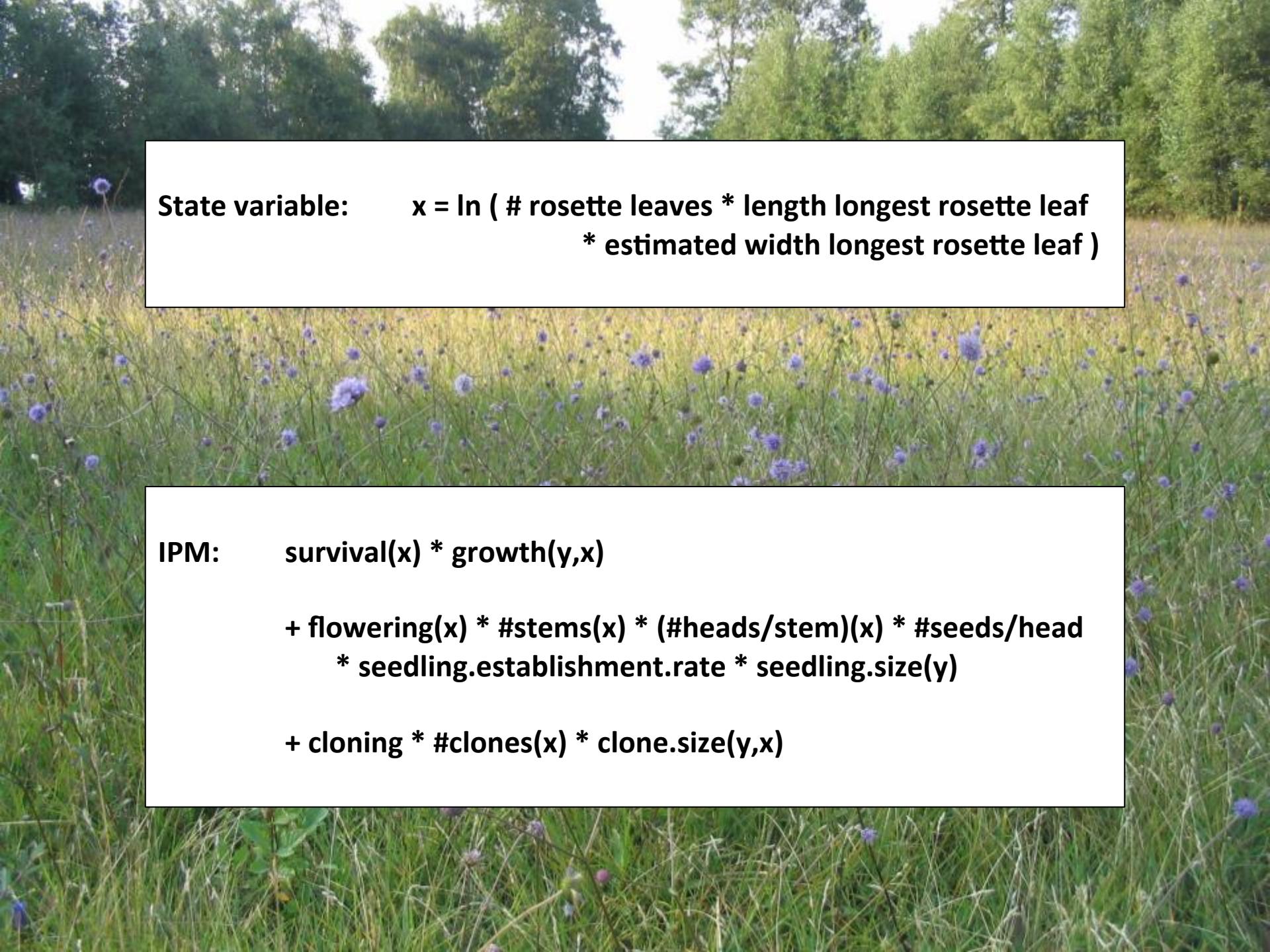


Current Pmatrix



Increased bins



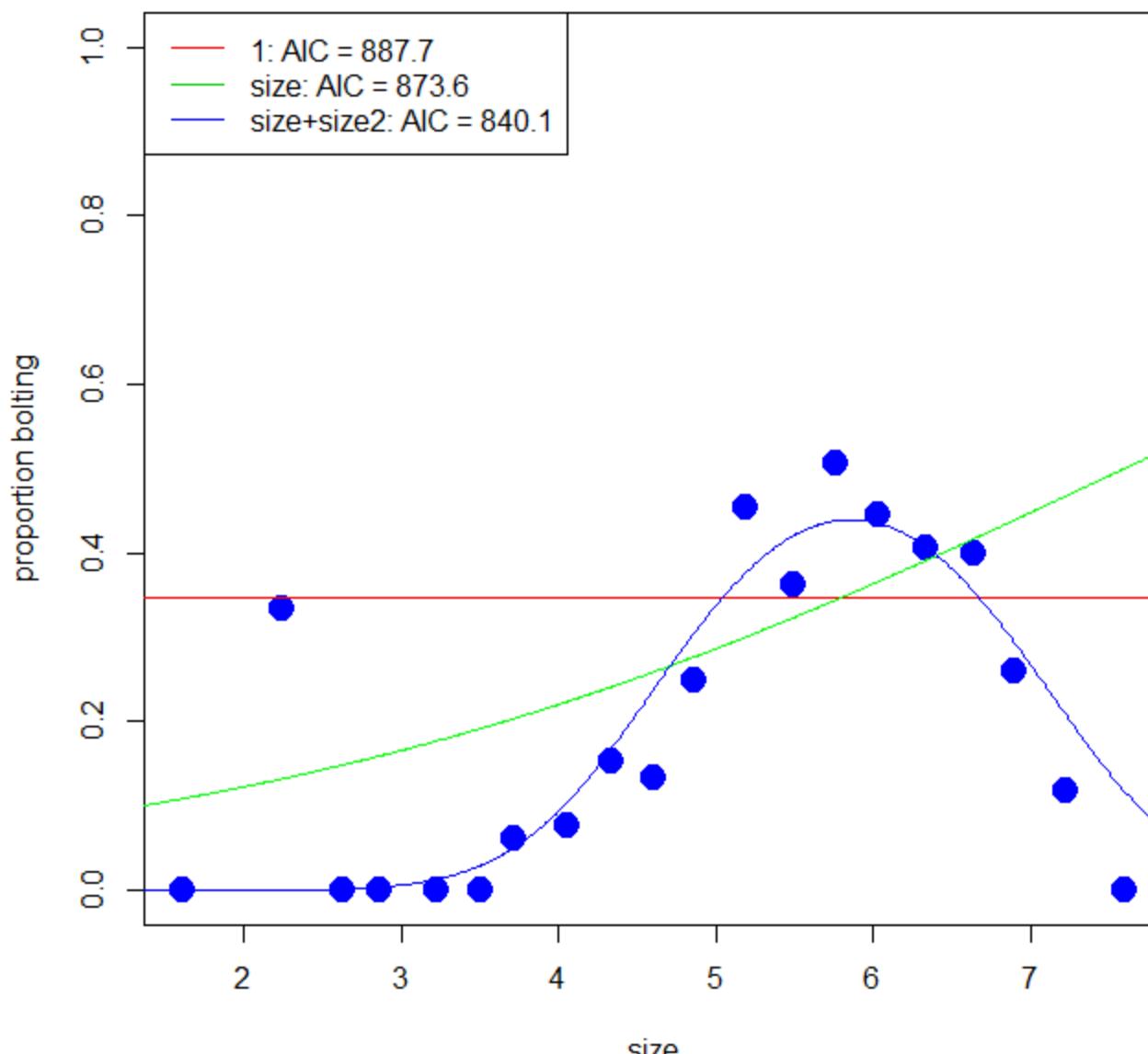


State variable: $x = \ln (\# \text{ rosette leaves} * \text{length longest rosette leaf}$
 $* \text{estimated width longest rosette leaf})$

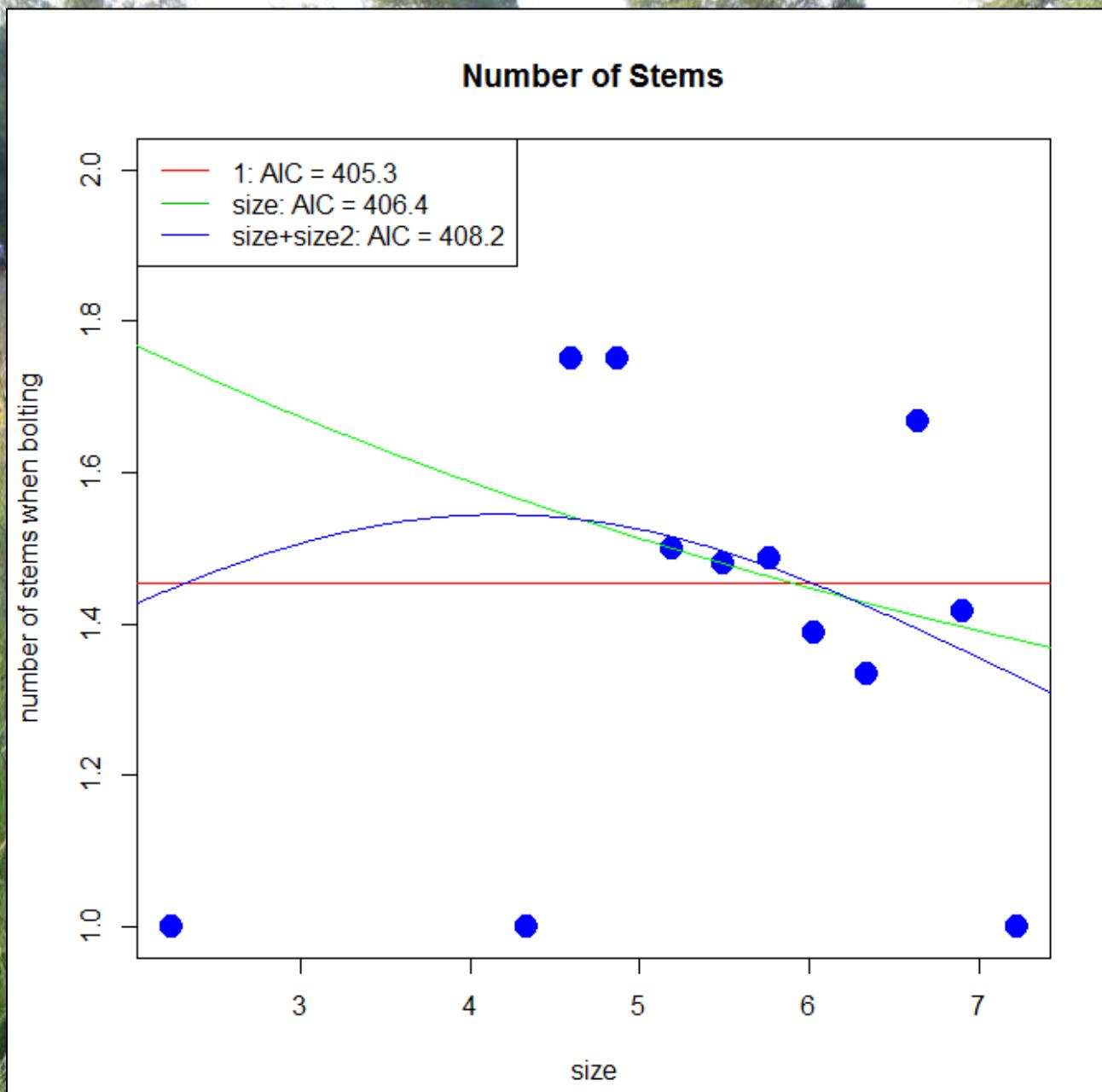
IPM: $\text{survival}(x) * \text{growth}(y, x)$
 $+ \text{flowering}(x) * \#\text{stems}(x) * (\#\text{heads/stem})(x) * \#\text{seeds/head}$
 $* \text{seedling.establishment.rate} * \text{seedling.size}(y)$
 $+ \text{cloning} * \#\text{clones}(x) * \text{clone.size}(y, x)$

fecModelComp ?

Bolting probability

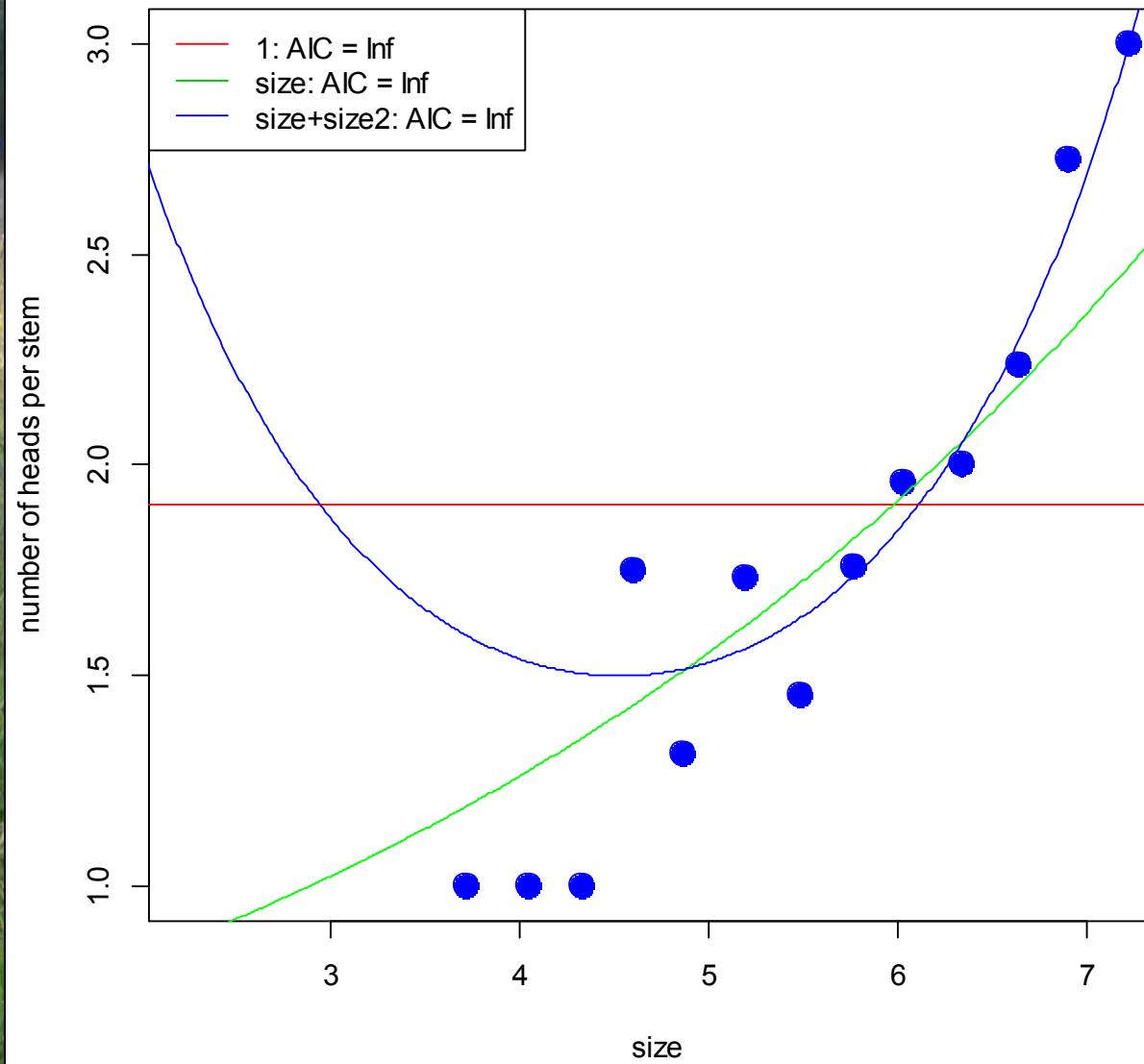


```
fo <- makeFecObj(Sp, Formula=fec1Bolt~size+size2, Family = "binomial")
```

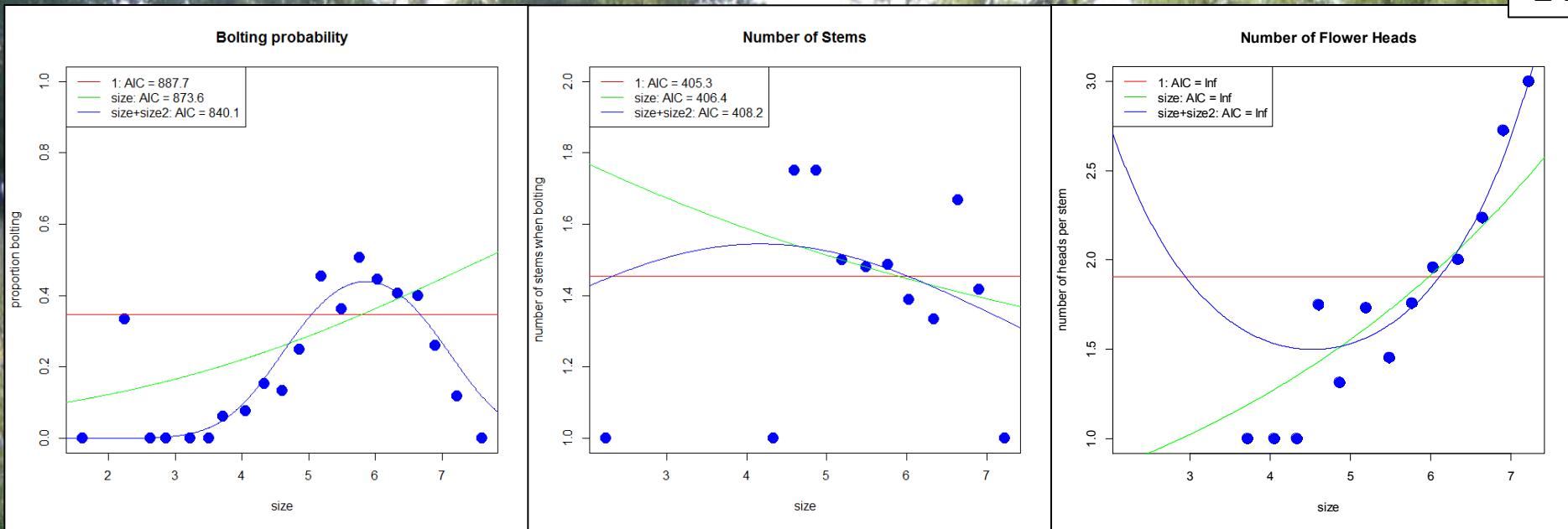


```
fo <- makeFecObj(Sp, Formula=c(fec1Bolt~size+size2, fec2Stem~1),
Family = c("binomial","poisson"), Transform = c("none",-1))
```

Number of Flower Heads



```
fo <- makeFecObj(Sp, Formula=c(fec1Bolt~size+size2,fec2Stem~1,fec3Head~size),  
Family = c("binomial","poisson","poisson"), Transform = c("none",-1,"none"))
```



```
fo <- makeFecObj(Sp, Formula=c(fec1Bolt~size+size2,fec2Stem~1,fec3Head~size),
  Family = c("binomial","poisson","poisson"),
  Transform = c("none",-1,"none"),
  fecConstants = data.frame(seedsPerHead=50,seedlingEstablishmentRate= 0.02))
```

Seedling sizes at t+1 estimated by makeFecObj: mean = 4.19, sd = 1.19

```

> fo
An object of class "fecObj"
Slot "fitFec":
[[1]]

Call: glm(formula = Formula[[i]], family = Family[i], data = dataf)

Coefficients:
(Intercept)      size      size2
-20.3088       6.8528     -0.5851

Degrees of Freedom: 685 Total (i.e. Null); 683 Residual
(91 observations deleted due to missingness)
Null Deviance: 885.7
Residual Deviance: 834.1 AIC: 840.1

[[2]]

Call: glm(formula = Formula[[i]], family = Family[i], data = dataf)

Coefficients:
(Intercept)
-0.7901

Degrees of Freedom: 237 Total (i.e. Null); 237 Residual
(539 observations deleted due to missingness)
Null Deviance: 203.9
Residual Deviance: 203.9 AIC: 405.3

[[3]]

Call: glm(formula = Formula[[i]], family = Family[i], data = dataf)

Coefficients:
(Intercept)      size
-0.6010       0.2085

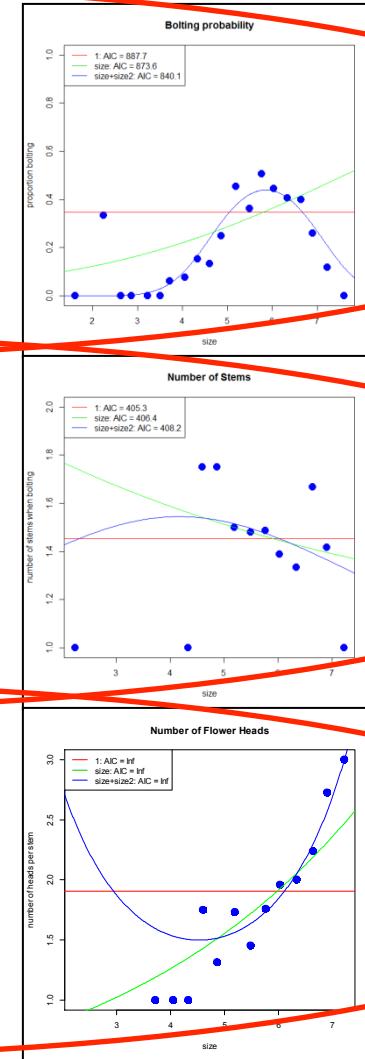
Degrees of Freedom: 237 Total (i.e. Null); 236 Residual
(539 observations deleted due to missingness)
Null Deviance: 139
Residual Deviance: 131.8 AIC: Inf

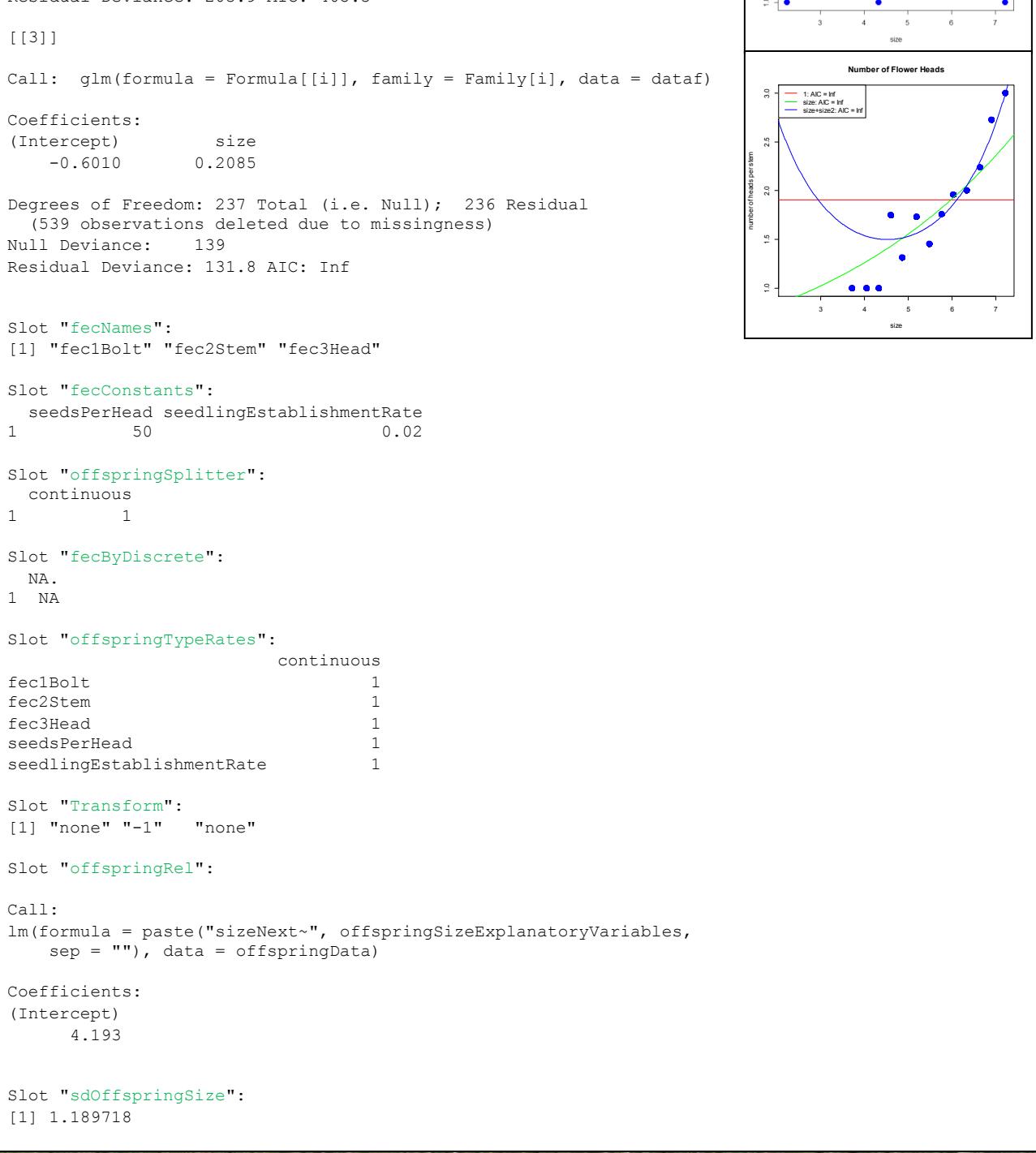
Slot "fecNames":
[1] "fec1Bolt" "fec2Stem" "fec3Head"

Slot "fecConstants":
  seedsPerHead seedlingEstablishmentRate
1                 50                      0.02

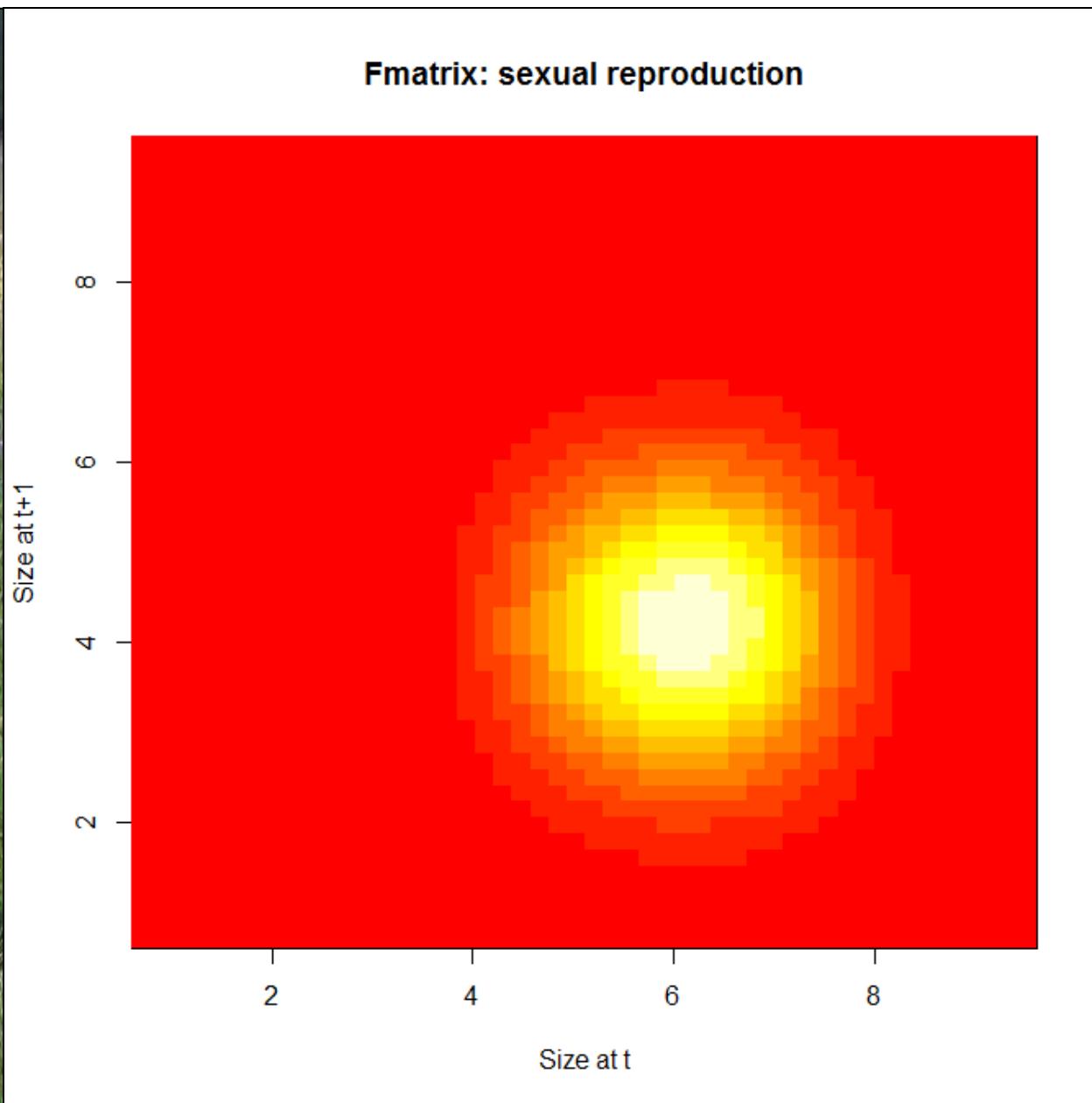
Slot "offspringSplitter":
  continuous
1                 1

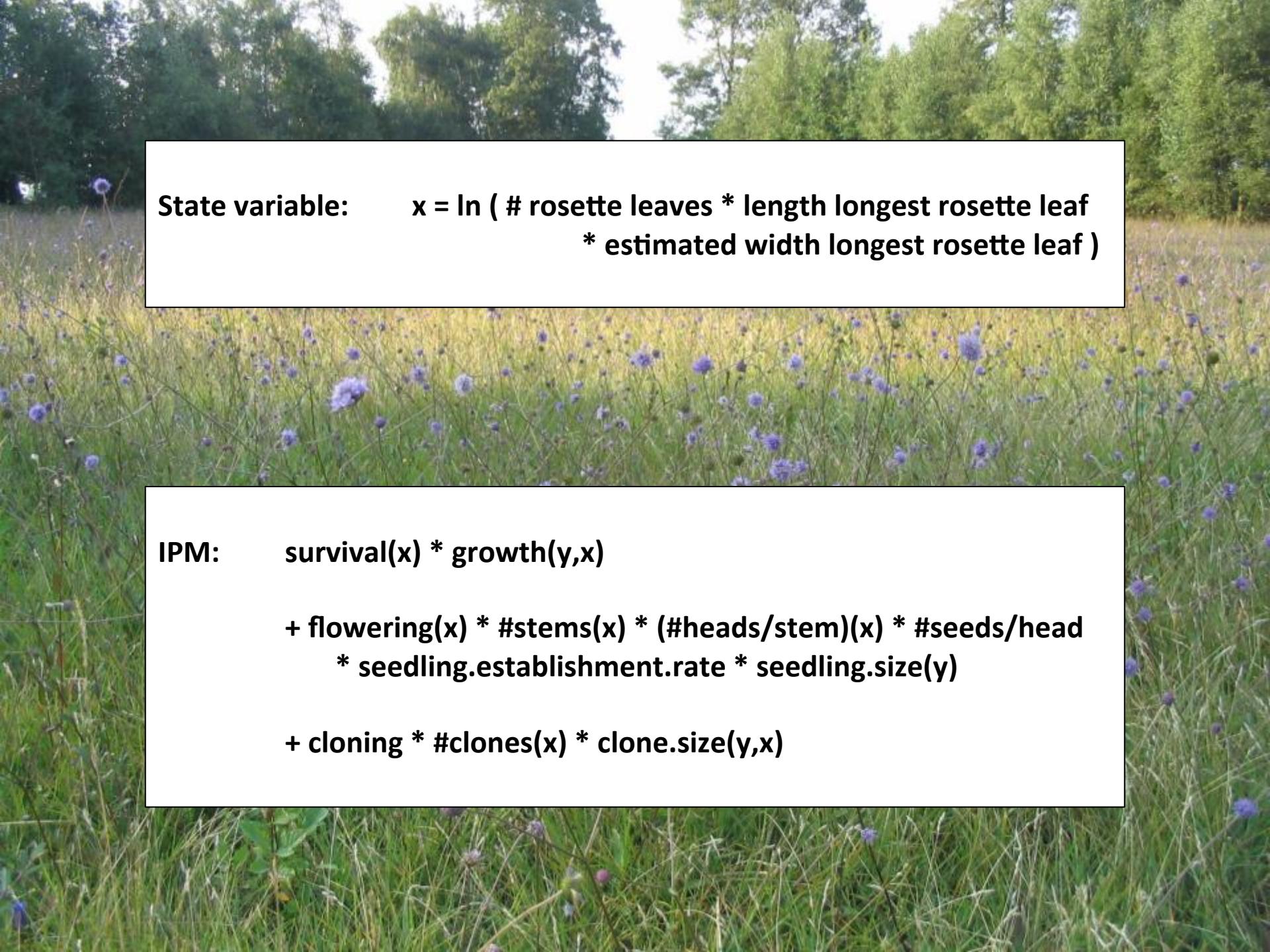
```





```
Fmatrix <- makeIPMFmatrix(fecObj=fo, minSize=min(Sp$size,na.rm=T)-1,  
maxSize=max(Sp$size,na.rm=T)+2, correction="constant")
```





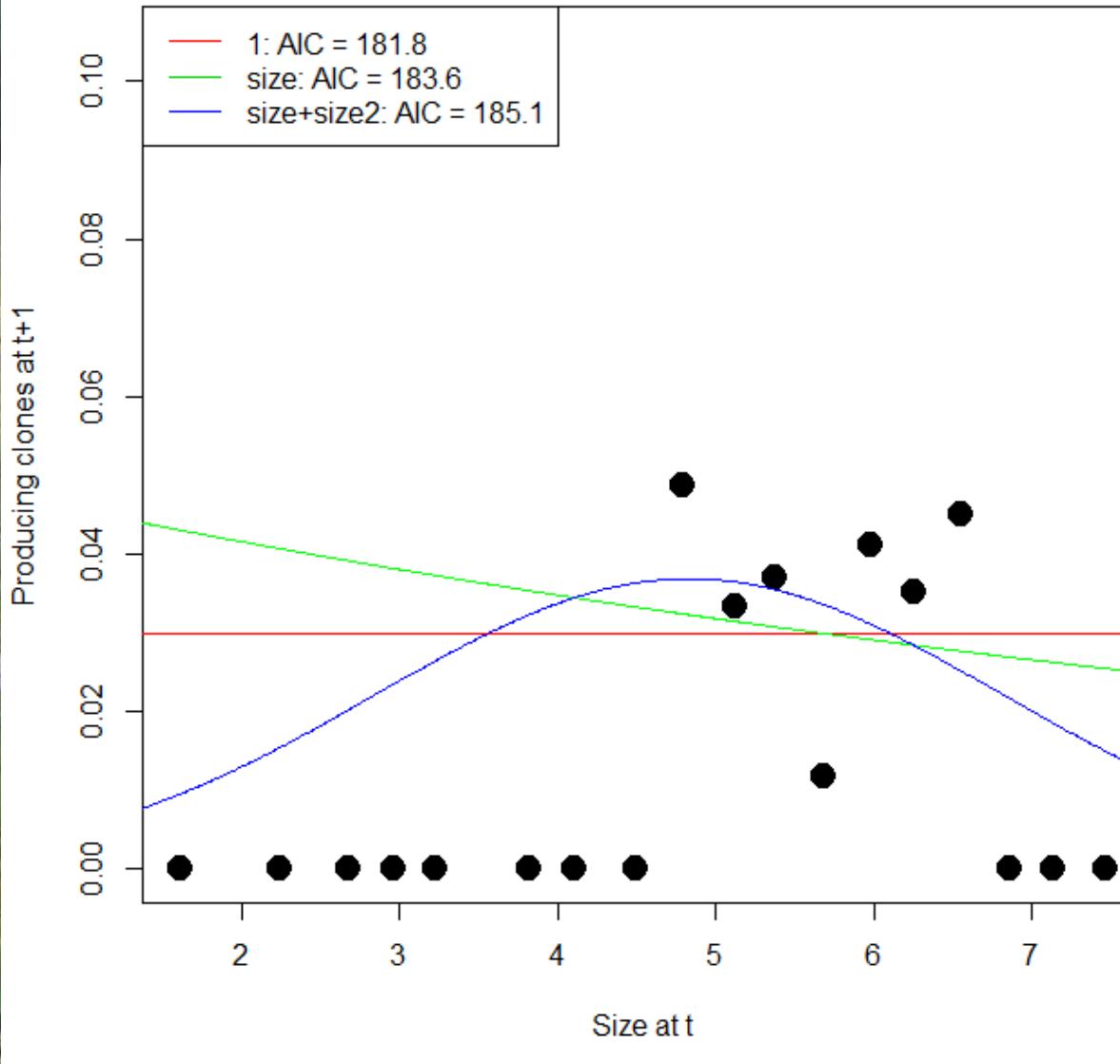
State variable: $x = \ln (\# \text{ rosette leaves} * \text{length longest rosette leaf}$
 $* \text{estimated width longest rosette leaf})$

IPM: $\text{survival}(x) * \text{growth}(y, x)$

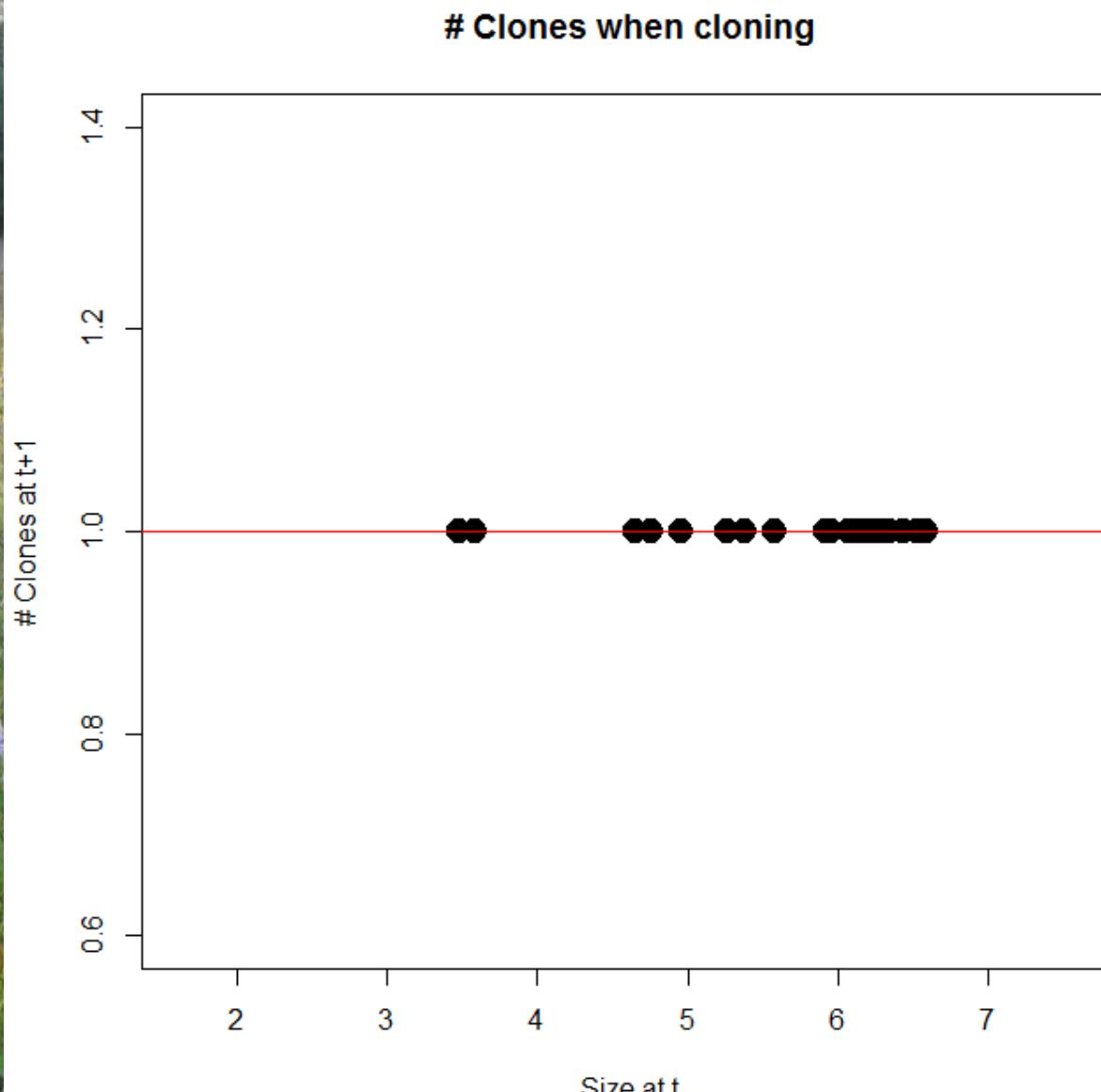
$+ \text{flowering}(x) * \#\text{stems}(x) * (\#\text{heads/stem})(x) * \#\text{seeds/head}$
 $* \text{seedling.establishment.rate} * \text{seedling.size}(y)$

$+ \text{cloning} * \#\text{clones}(x) * \text{clone.size}(y, x)$

Whether or not side rosettes are produced

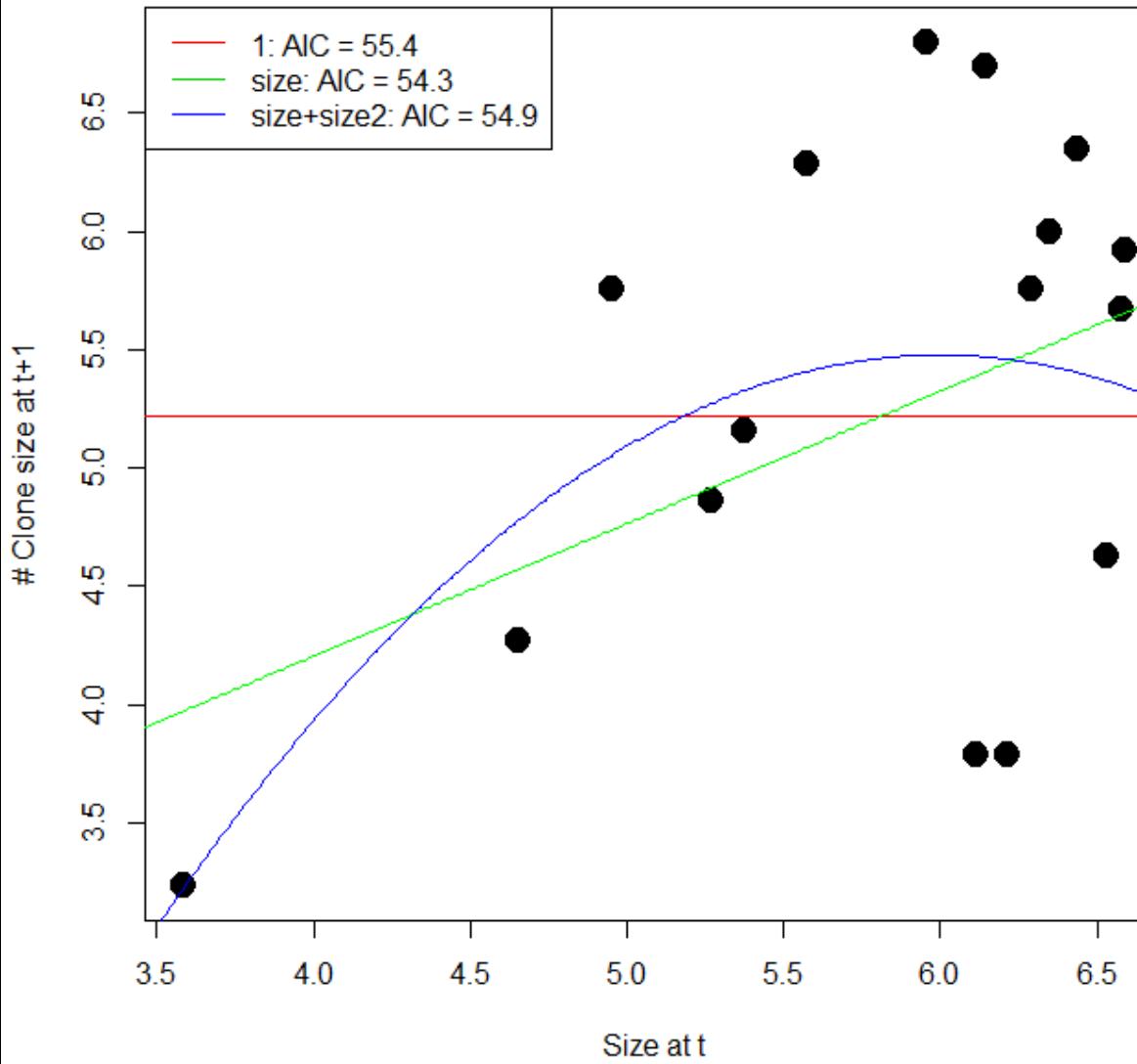


```
co <- makeClonalObj(Sp, Formula = cloning~1, Family = c("binomial"),
                      Transform=c("none"))
```



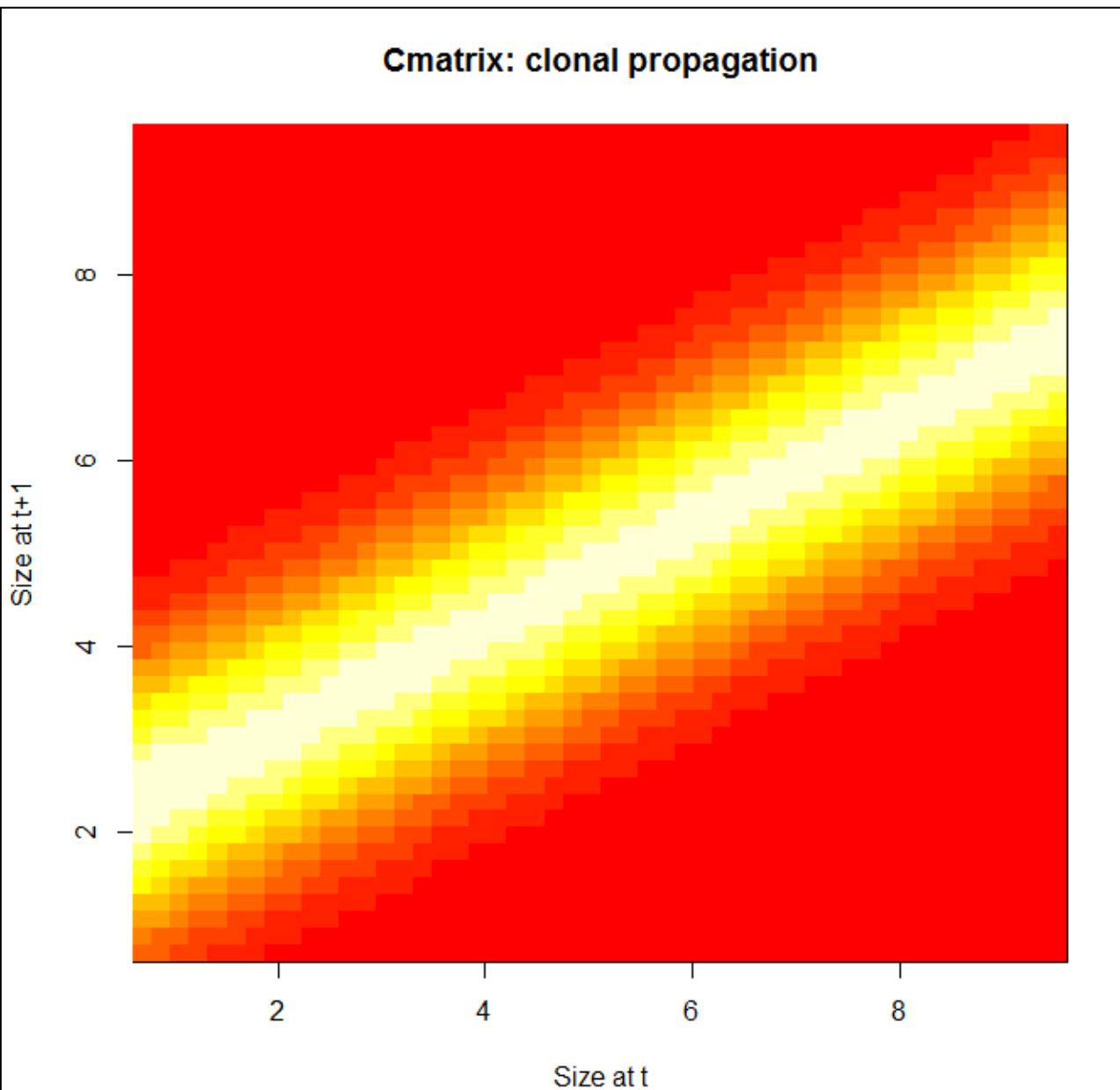
```
co <- makeClonalObj(Sp, Formula = c(cloning~1, clonesNext~1),  
Family = c("binomial","poisson"), Transform=c("none","-1"))
```

Parent - Clonal offspring size relationship

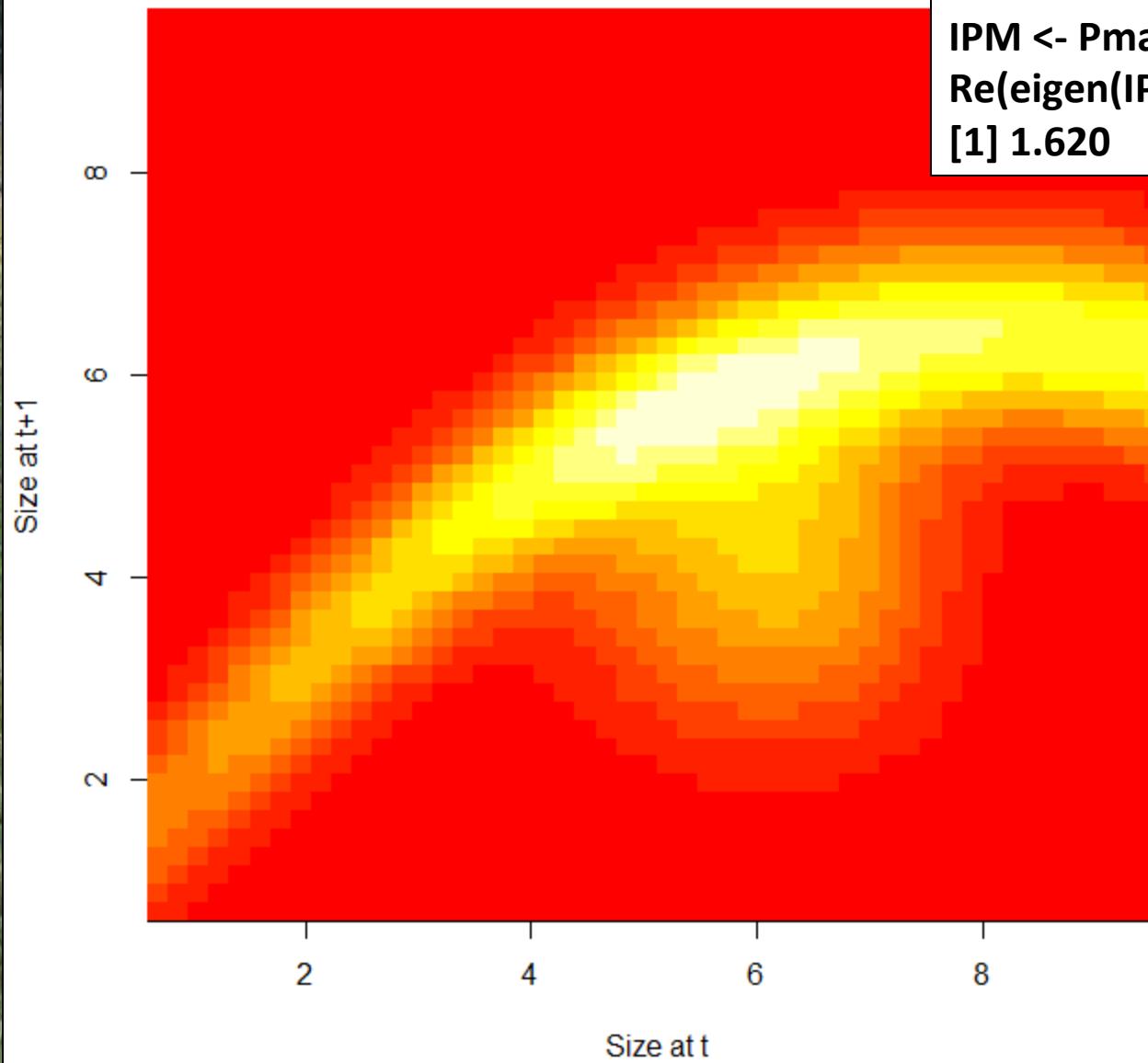


```
co <- makeClonalObj(Sp, offspringSizeExplanatoryVariables = "size",
  Formula = c(cloning~1, clonesNext~1), Family = c("binomial", "poisson"),
  Transform=c("none", "-1"))
```

```
Cmatrix <- makeIPMCmatrix(clonalObj=co, minSize=min(Sp$size,na.rm=T)-1,
                           maxSize=max(Sp$size,na.rm=T)+2, correction="constant")
```

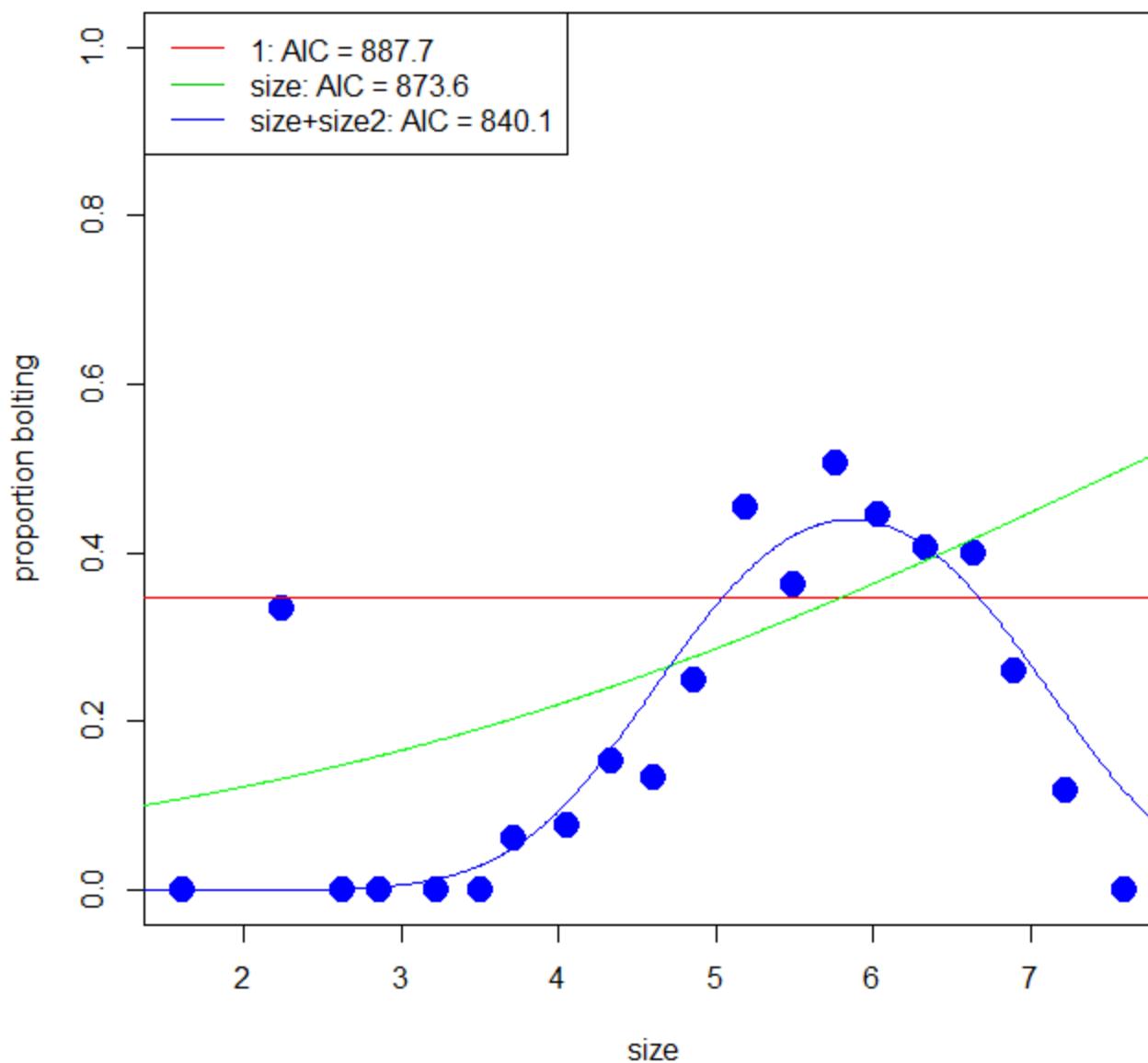


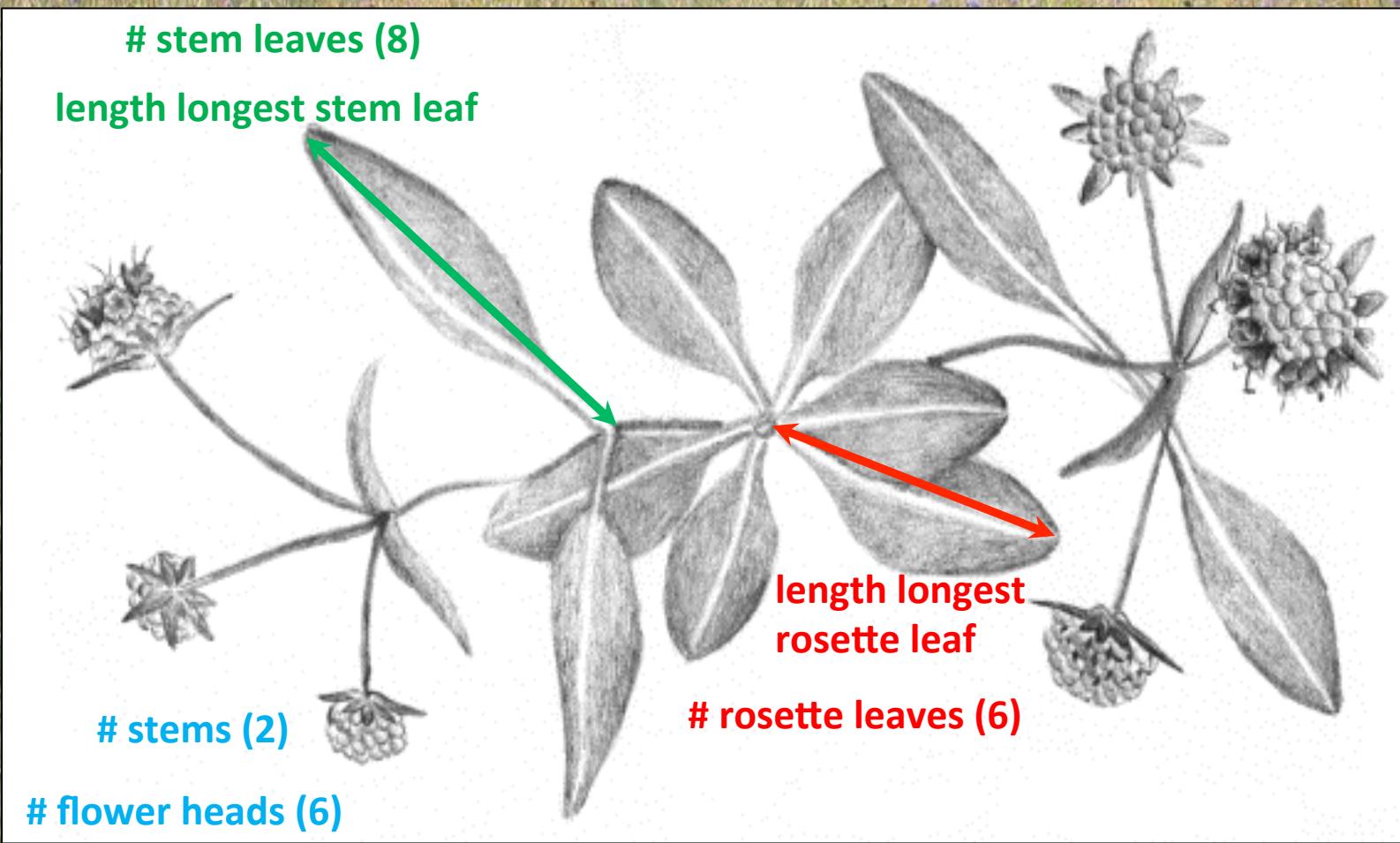
Pmatrix + Fmatrix + Cmatrix

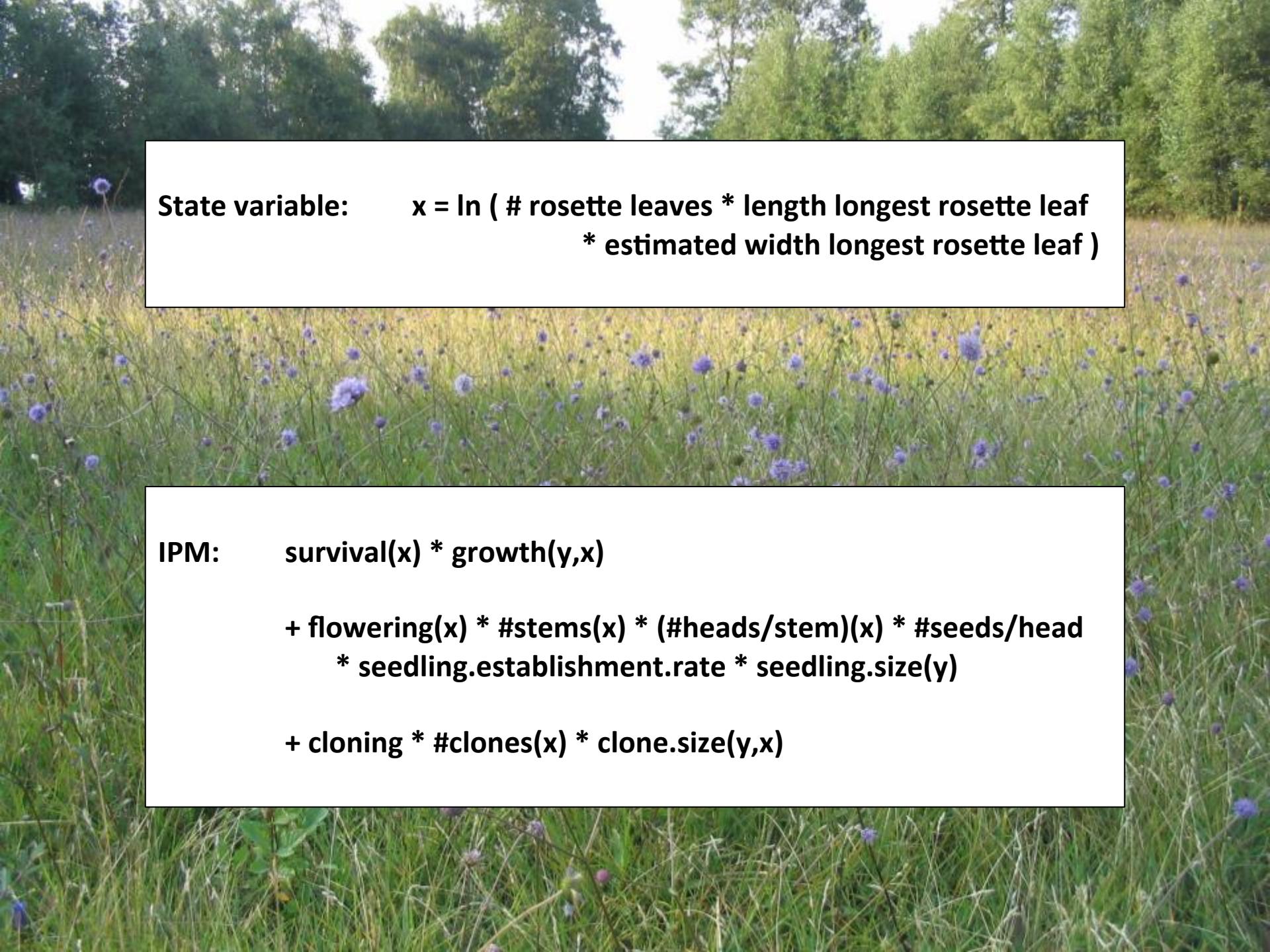


```
IPM <- Pmatrix + Fmatrix + Cmatrix  
Re(eigen(IPM)$value[1])  
[1] 1.620
```

Bolting probability







State variable: $x = \ln (\# \text{ rosette leaves} * \text{length longest rosette leaf}$
 $* \text{estimated width longest rosette leaf})$

IPM: $\text{survival}(x) * \text{growth}(y, x)$

$+ \text{flowering}(x) * \#\text{stems}(x) * (\#\text{heads/stem})(x) * \#\text{seeds/head}$
 $* \text{seedling.establishment.rate} * \text{seedling.size}(y)$

$+ \text{cloning} * \#\text{clones}(x) * \text{clone.size}(y, x)$

State variable: $x = \ln (\# \text{ leaves} * \text{length longest leaf} / \text{estimated width longest leaf})$

IPM:

$$\begin{aligned} & \text{survival}(x) * \text{growth}(y, x) \\ & + \text{flowering}(x) * \#\text{stems}(x) * (\#\text{heads/stem})(x) * \#\text{seeds/head} \\ & * \text{seedling.establishment.rate} * \text{seedling.size}(y) \\ & + \text{cloning} * \#\text{clones}(x) * \text{clone.size}(y, x) \end{aligned}$$

State variable: $x = \ln (\# \text{ leaves} * \text{length longest} * \text{estimated width longest})$ leaf
leaf)

Exercise:

Redo the vital rate model selection and IPM building with the new, above state variable.

Please use the data(dataIPMpackSuccisa2) from IPMpack

IPM: $\text{survival}(x) * \text{growth}(y,x)$
 $+ \text{flowering}(x) * \#\text{stems}(x) * (\#\text{heads/stem})(x) * \#\text{seeds/head}$
 $* \text{seedling.establishment.rate} * \text{seedling.size}(y)$
 $+ \text{cloning} * \#\text{clones}(x) * \text{clone.size}(y,x)$

Next up:

Rob with Pastel Pastures

