IPMpack:
an R package for Integral Projection Models

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Workflow for IPMpack

Import data

Data enter as a ***data frame*** with set column names

```
> library(IPMpack)
Loading required package: Matrix
Loading required package: lattice
Loading required package: MASS
Loading required package: nlme
Loading required package: mvtnorm
> dff<-generateData()
> head(dff)
      size sizeNext surv covariate covariateNext       fec      stage  stageNext
1 4.709132 4.477829    0         1             0 0.0000000 continuous continuous
2 7.381911 7.788379    1         0             0 0.1152413 continuous continuous
3 1.572960 1.933876    0         1             0 0.0000000 continuous continuous
4 4.302018 4.866706    1         0             1 0.0000000 continuous continuous
5 5.142006 4.675990    0         1             0 0.0000000 continuous continuous
6 5.116661 5.905220    0         0             1 8.5576014 continuous continuous
>
```

minimum requirement for a Tmatrix

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minimum requirement for a Tmatrix

only necessary if you have a mixture of discrete and continuous stages (defaults to all continuous)

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>
```

minimum requirement for a Tmatrix

only necessary if you have a mixture of discrete and continuous stages (defaults to all continuous)

```
> dff<-generateDataDiscrete()
> head(dff)
      size sizeNext surv      fec      stage  stageNext number
1       NA       NA    1 3.763959    dormant    dormant      1
2 5.975158 8.118134    1 0.000000 continuous continuous      1
3 9.093308       NA    0 4.603087 continuous       dead      1
4 7.410467 5.777279    1 0.000000 continuous continuous      1
5 5.627206       NA    0 0.000000 continuous       dead      1
6 5.133702 3.731515    1 0.000000 continuous continuous      1
>
```

only necessary for models with transition between discrete stages

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Loading required package: Matrix
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>
```

only necessary for models with transition between discrete stages

```
> head(dff)
      size sizeNext surv covariate covariateNext      fec      stage  stageNext offspringNext
1 5.299204 5.864362    1         0             0 0.000000 continuous continuous         <NA>
2 5.510951 5.167714    0         1             0 6.345835 continuous continuous       sexual
3 4.279321 2.626327    0         1             0 3.379862 continuous continuous         <NA>
4 5.026918 7.419591    1         1             0 0.000000 continuous continuous       sexual
5 5.103107 6.078352    1         1             0 0.000000 continuous continuous         <NA>
6 5.422322 5.951682    1         1             0 8.198216 continuous continuous         <NA>
```

only necessary for models with dependence of offspring size on adult size

Workflow for IPMpack

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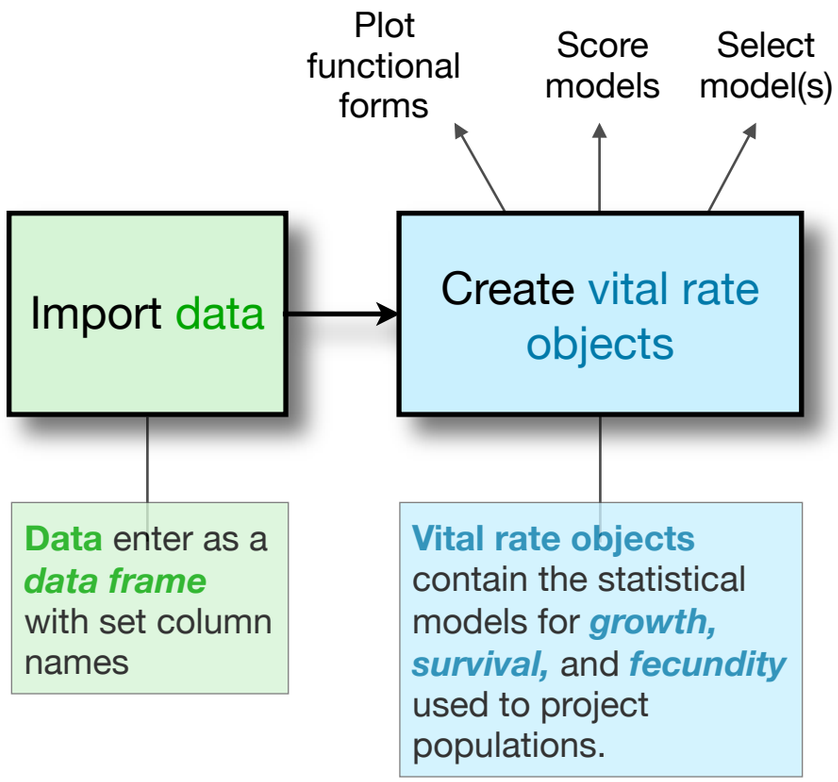

A growth object

```
>
> gr1 <- makeGrowthObj(dataf=dff, Formula=sizeNext~size,regType="constantVar")
> picGrow(dff,gr1)
>
```

data

A growth object

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>
> gr1 <- makeGrowthObj(dataf=dff, Formula=sizeNext~size,regType="constantVar")
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data

regression formula ‘size+size2’, etc.

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handling of variance

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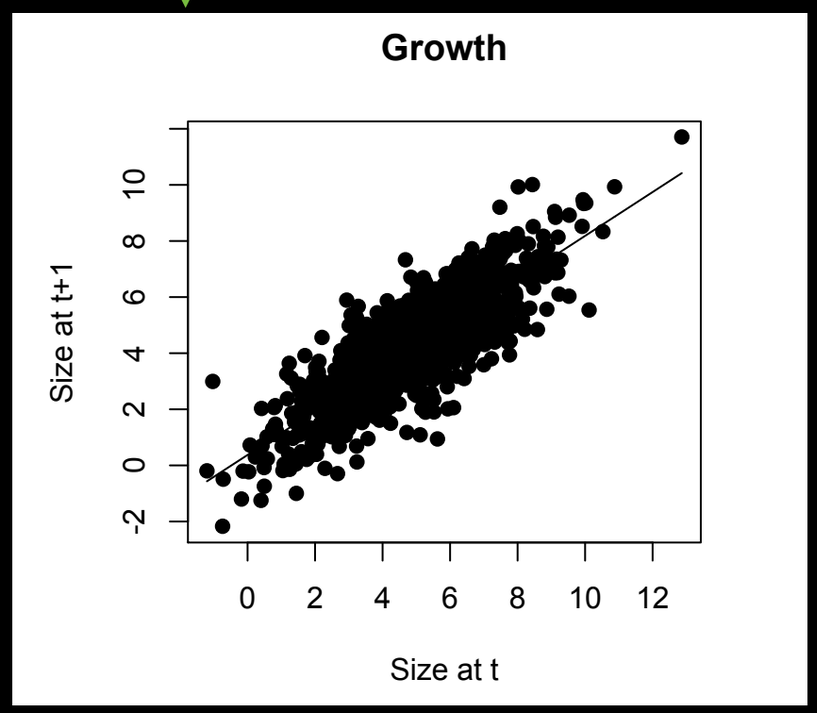

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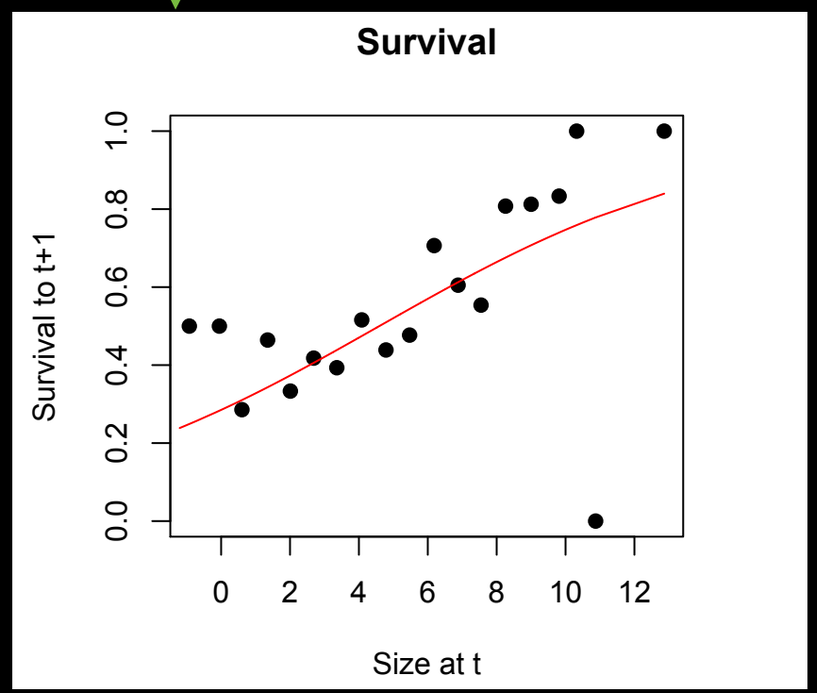

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```

formula, type of distribution (can have several!)

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Transform applied to fertility measure (can be several)

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Transform applied to fertility measure (can be several)

Offspring sizes (NAs means the function will the formula in offspringSizeExplanatoryVariables

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Fraction fecundity for each offspring class

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Link fertility relationships and discrete offspring classes

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Fec by discrete

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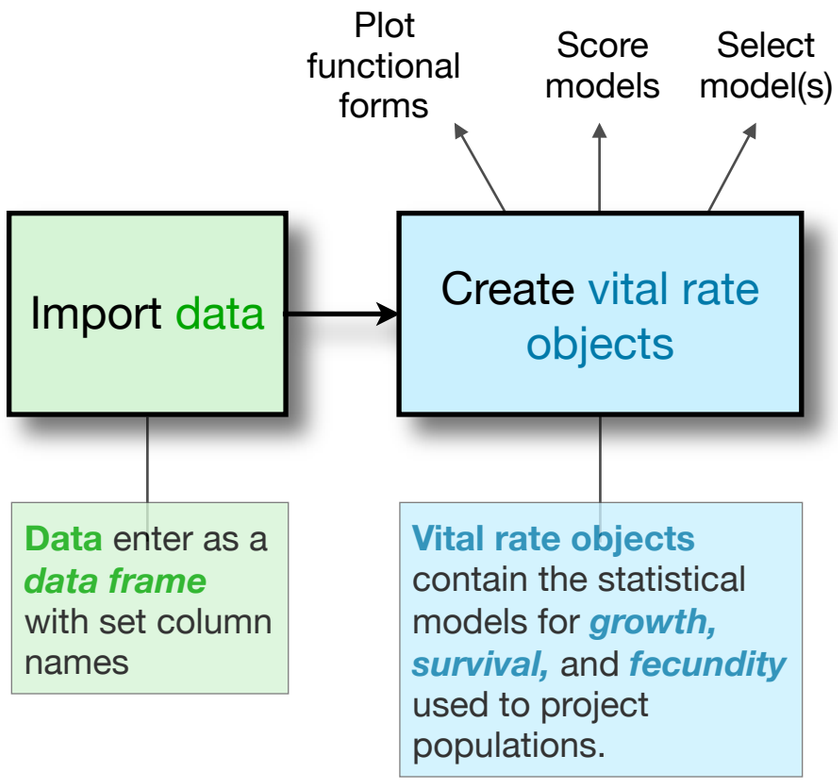
Workflow for IPMpack



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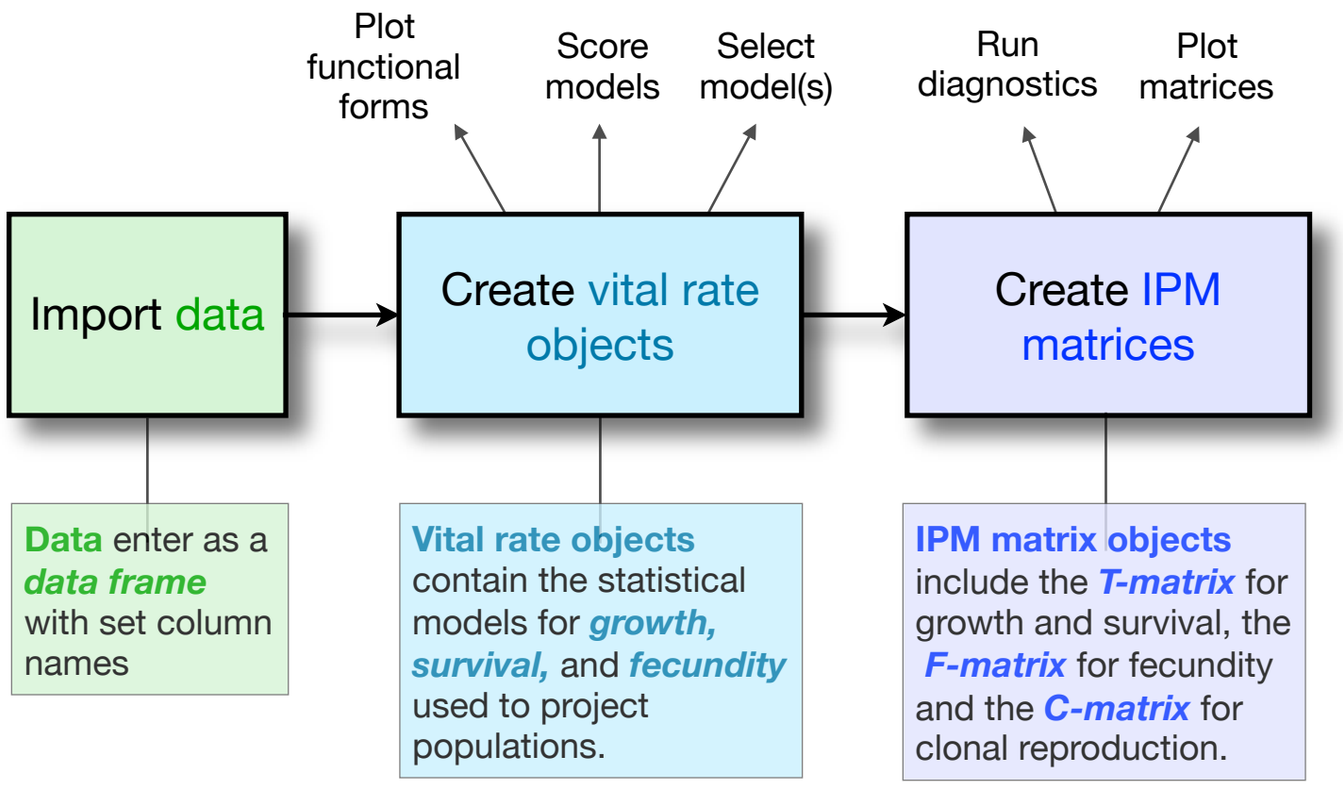
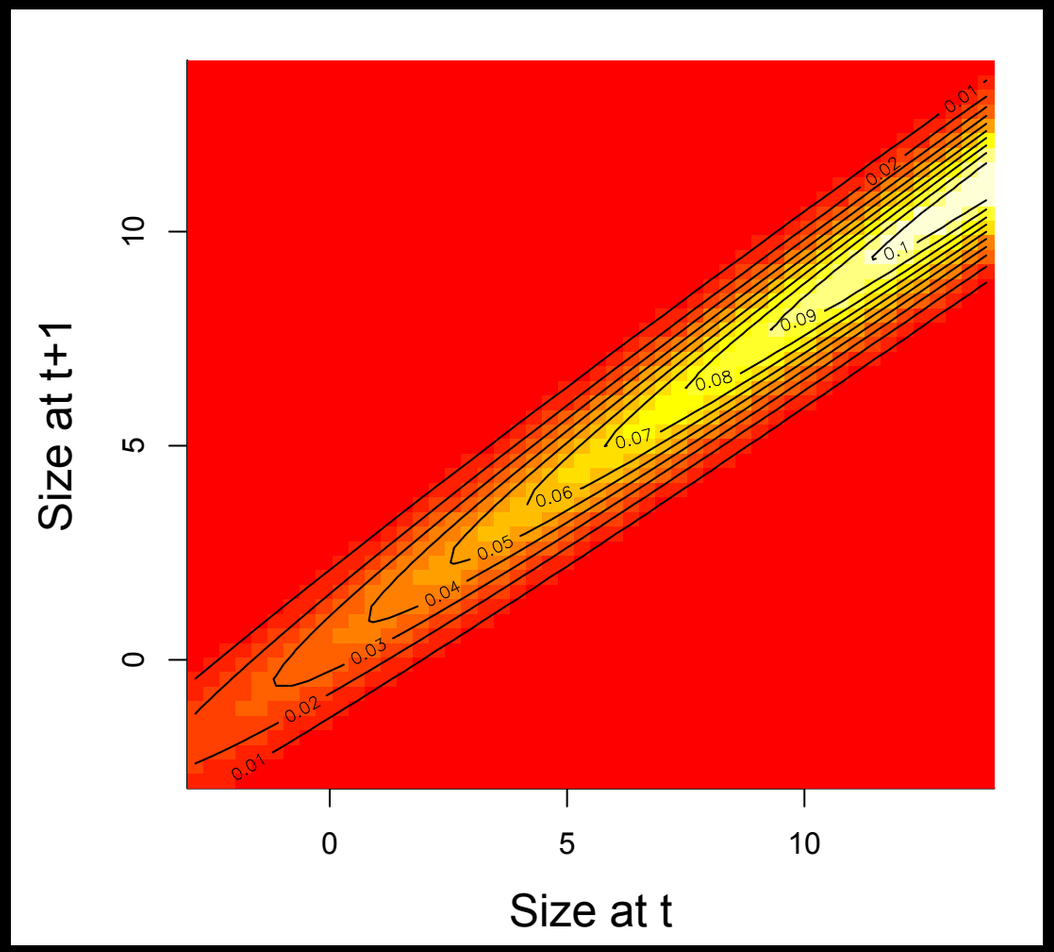
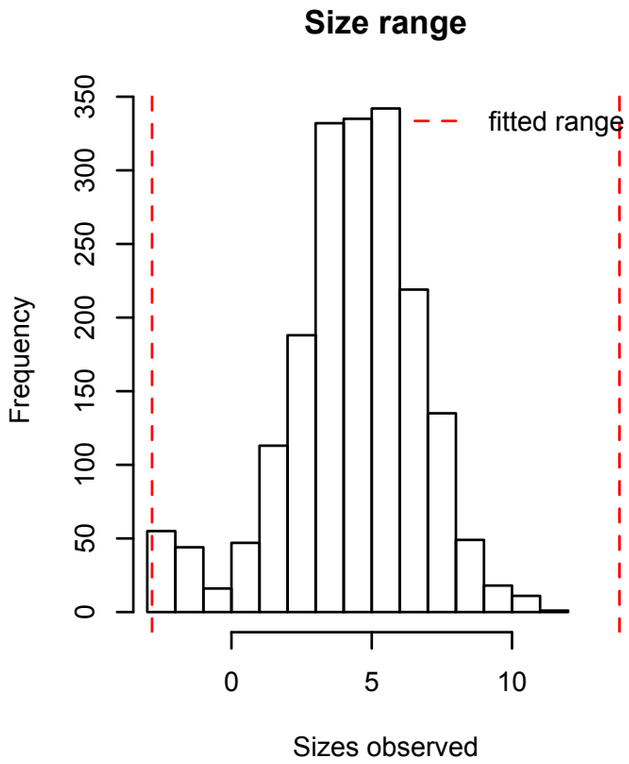


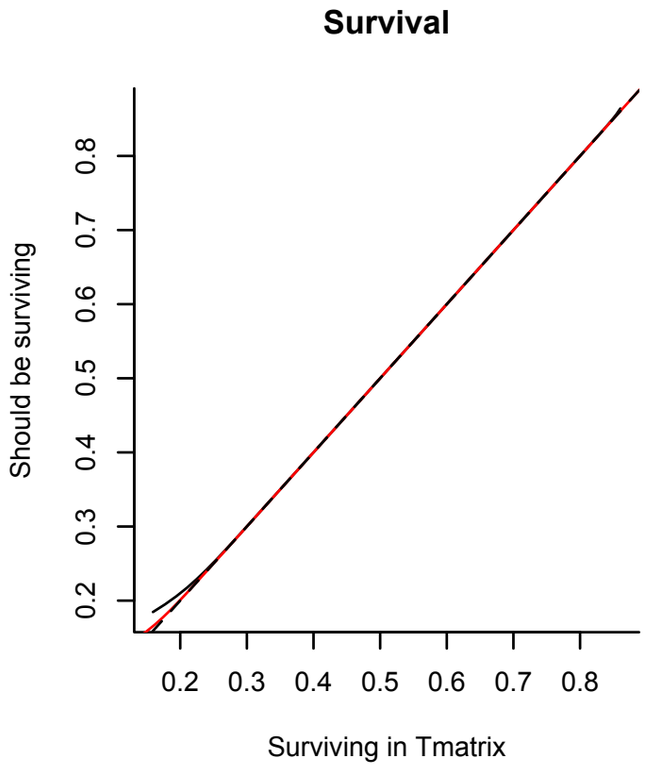
```
>
> Tmat<-createIPMTmatrix(nBigMatrix=50, minSize=-3,maxSize=14,growObj=gr1,survObj=sv1)
>
> image(Tmat@meshpoints,Tmat@meshpoints,t(Tmat),xlab="Size at t", ylab="Size at t+1",cex.lab=1.5)
> contour(Tmat@meshpoints,Tmat@meshpoints,t(Tmat),add=TRUE)
>
```

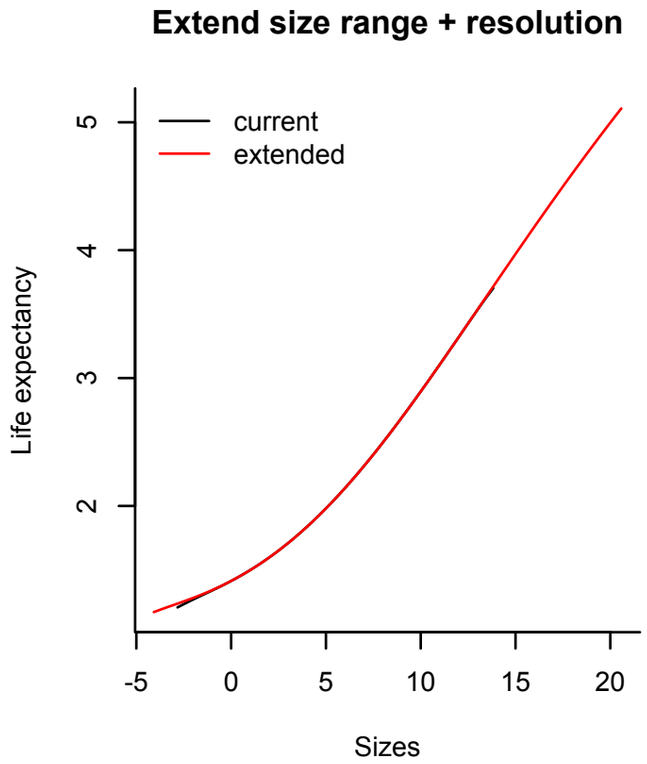


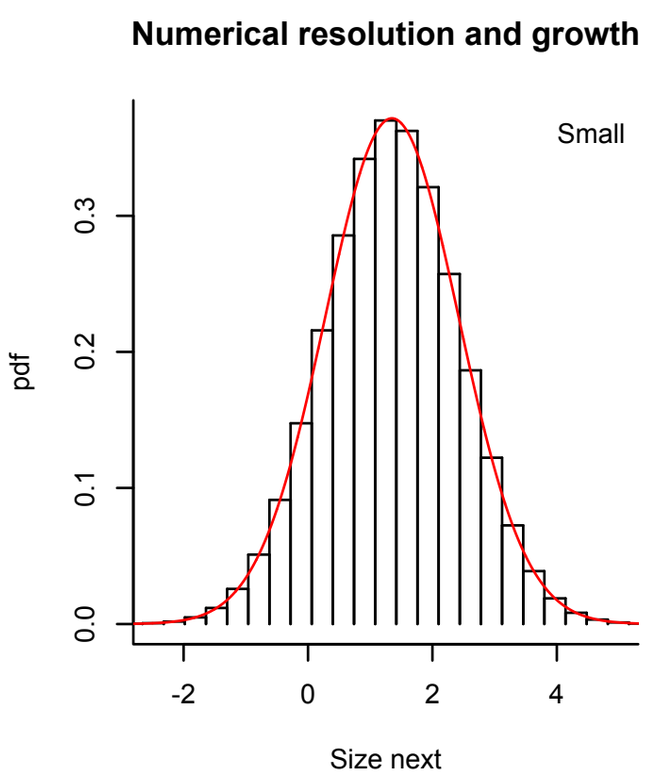

```
>
> diagnosticsTmatrix(Tmatrix=Tmat,growObj=gr1,survObj=sv1,dff=dff)
[1] "Range of Tmatrix is "
[1] 1.304382e-48 1.089820e-01
>
```

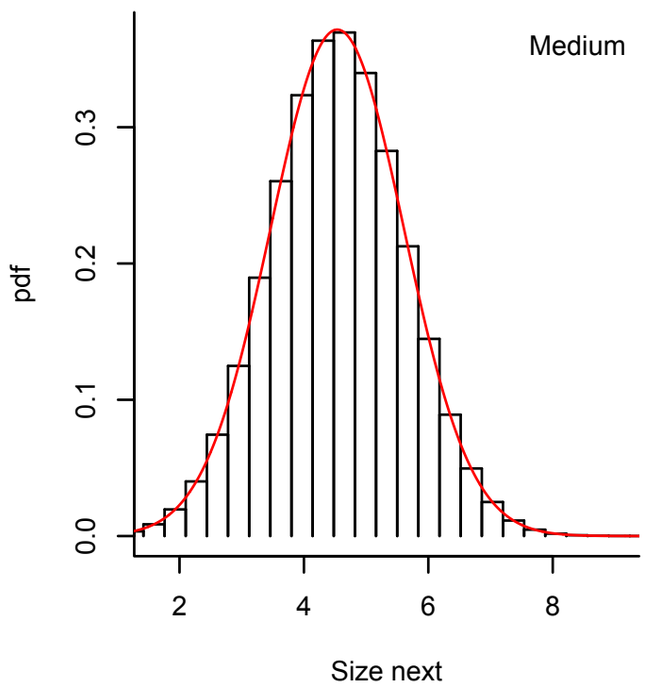
Diagnostics Tmatrix

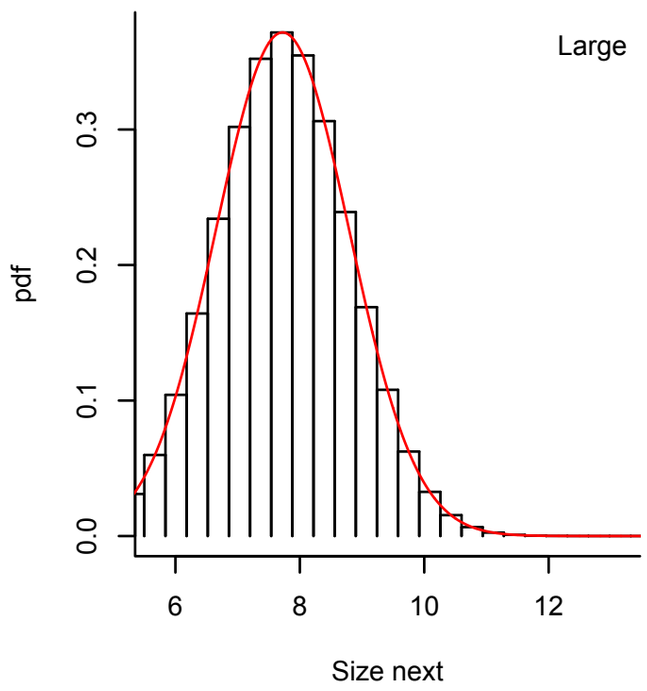












```
>
> Fmat <- createIPMFmatrix(nBigMatrix=50,minSize=-3,maxSize=14,fecObj=fv1)
[1] "Warning: fertility values < 0 exist in matrix, consider transforms. Negative values set to zero"
>
> image(Fmat@meshpoints,Fmat@meshpoints,(t(Fmat)),xlab="Size at t", ylab="Size at t+1",cex.lab=1.5)
> contour(Fmat@meshpoints,Fmat@meshpoints,t(Fmat),add=TRUE)
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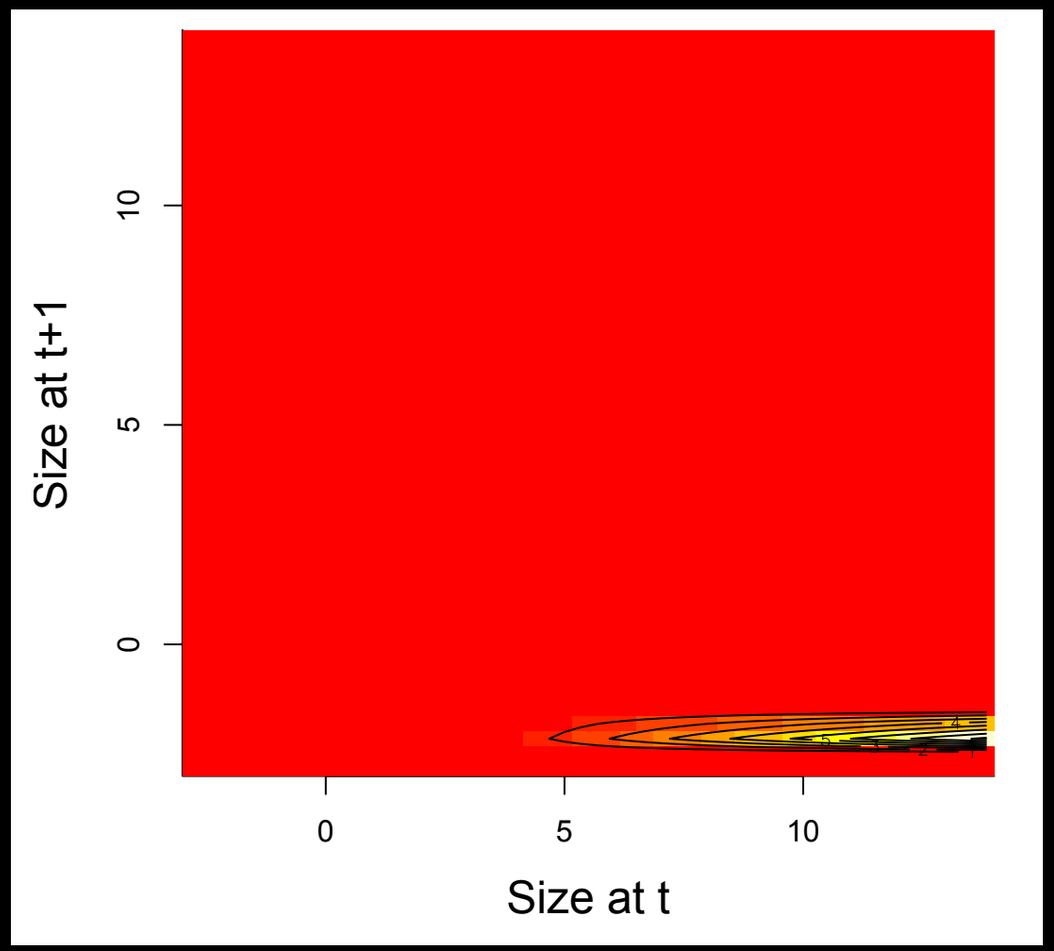


```
>
> IPM <- Tmat + Fmat
>
```

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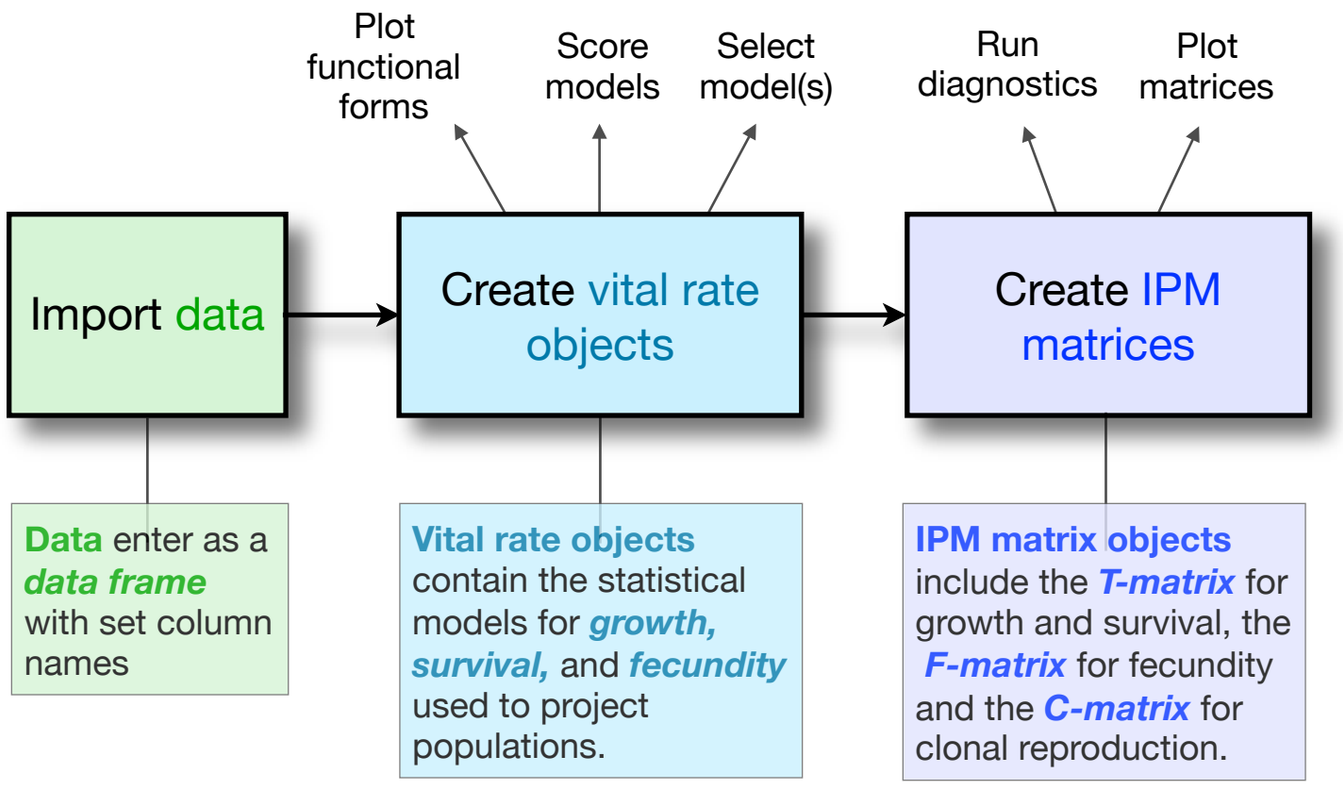

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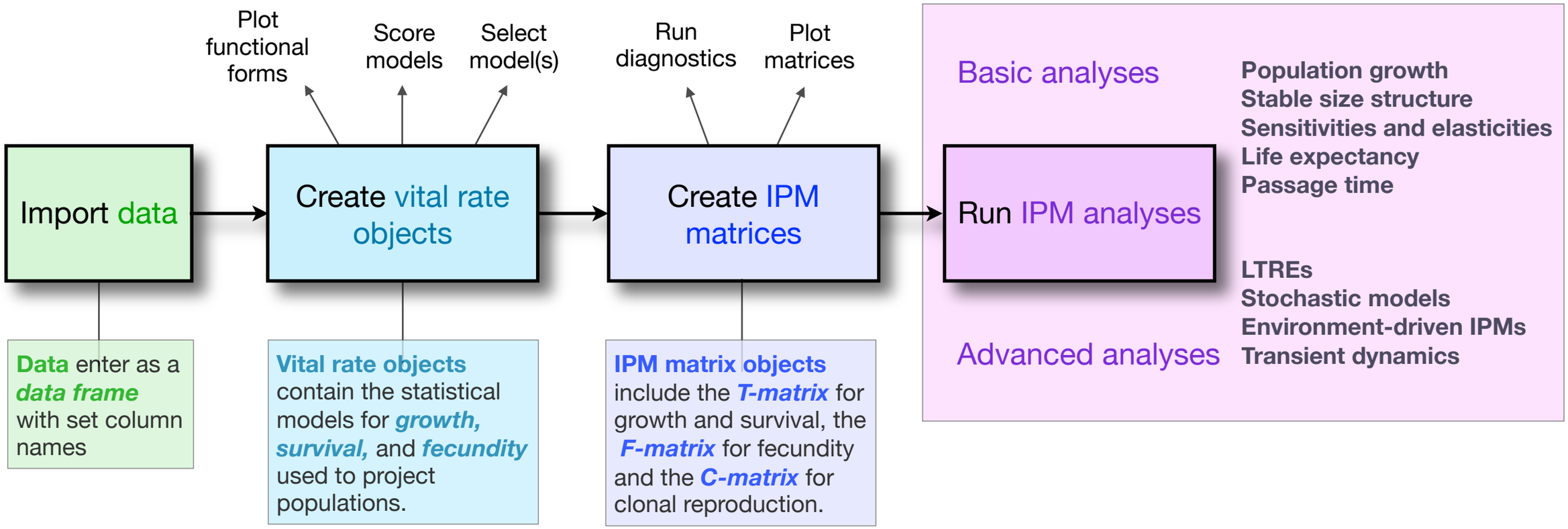
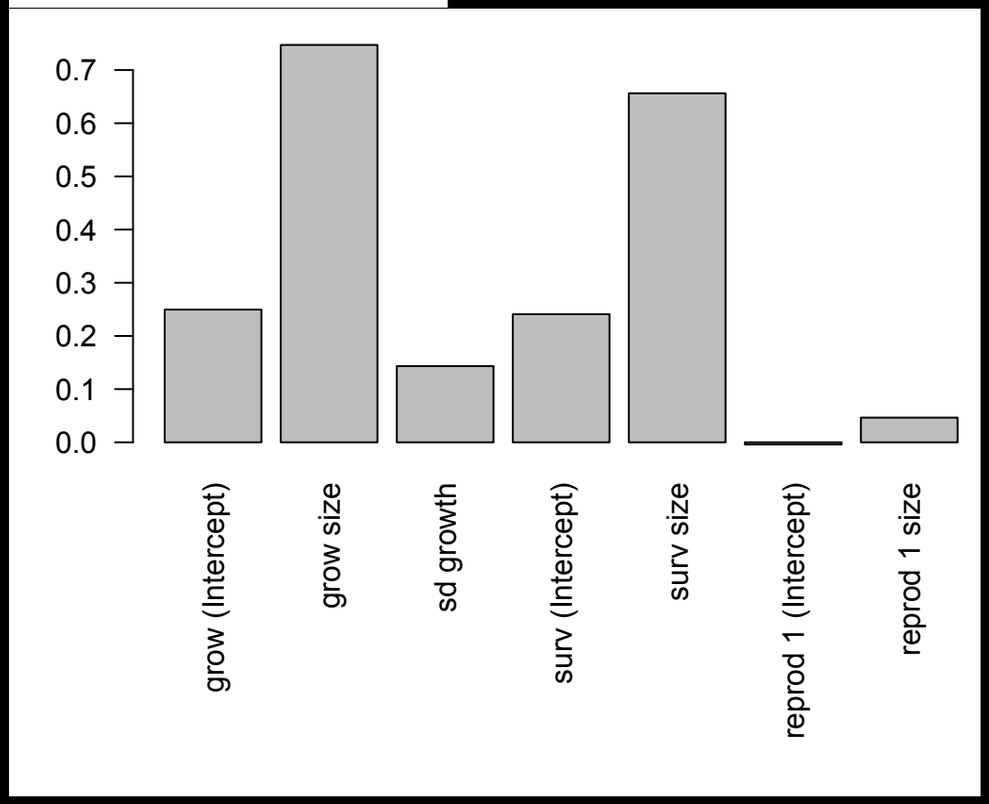


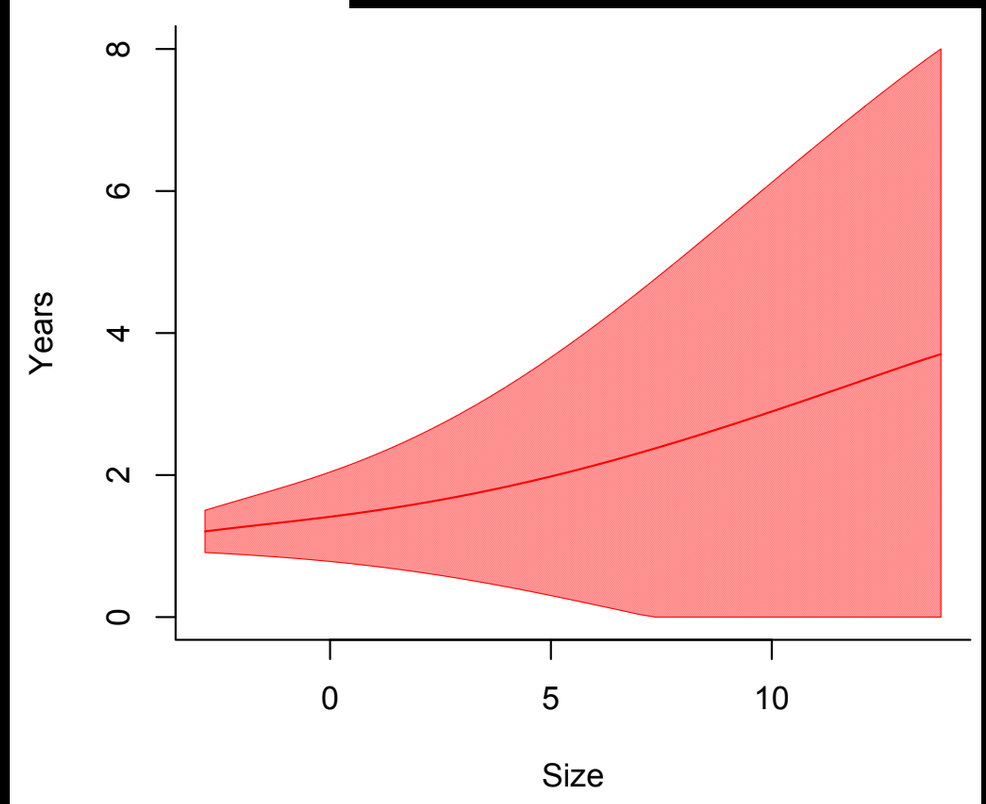
Functions that work only with an IPMpack constructed IPM

Parameter sensitivity



Functions that will work with any matrix

Life expectancy



... and many more....

We want IPMpack to be

- an easy package interface into using IPMs

- NOT a black box. We are trying to design functions so that without knowing all of the code that goes into making the models:
    - assumptions are transparent
    - decisions about what models to use are facilitated
    - implications of different functional forms, etc, are clear

- a handy toolkit of functions even for those who are very comfortable and prefer to make their own IPMs.

Basta





Thank-you!

MAX PLANCK INSTITUTE FOR DEMOGRAPHIC RESEARCH

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Imposing your preferred statistical fit

```
> gr1 <- makeGrowthObj(dff,explanatoryVariables="size")
> gr1
An object of class "growthObj"
Slot "fit":

Call:
lm(formula = Formula, data = dataf)

Coefficients:
(Intercept)         size
     0.3444       0.7957


Slot "sd":
[1] 1.097115
```

build a template

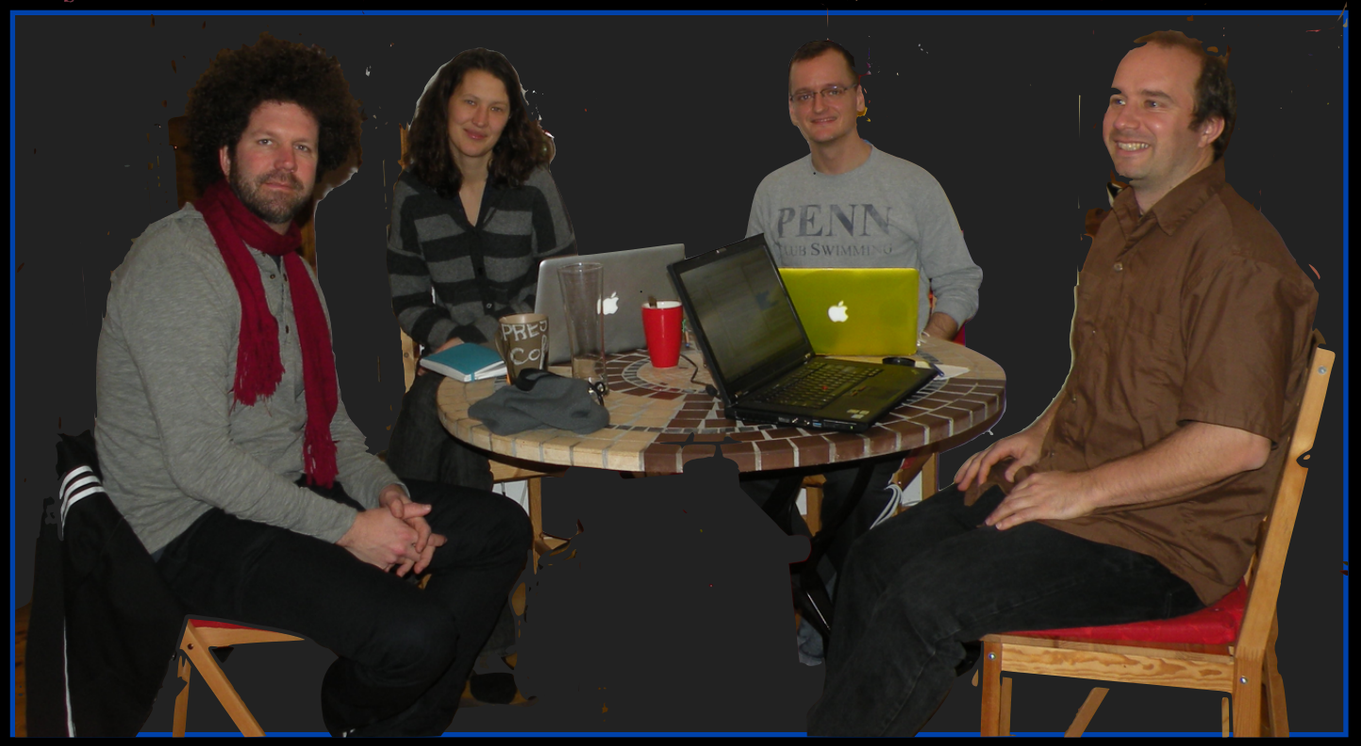
```
> slotNames(gr1)
[1] "fit" "sd"
> gr1@fit$coefficients
(Intercept)        size
  0.3444347   0.7957427
> gr1@sd
[1] 1.097115
>
> gr1@fit$coefficients <- c(1,2)
> gr1@sd <- 3
> gr1
An object of class "growthObj"
Slot "fit":

Call:
lm(formula = Formula, data = dataf)

Coefficients:
[1]  1  2


Slot "sd":
[1] 3
```

over-write the slots with your desired parameters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