Principal component capture-recapture analysis of Snow petrel data

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## Introduction

We illustrate the principal component capture-recapture (P2CR) method for covariates selection in capture-recapture models using data on survival of Snow petrels in Pointe Géologie Archipelago, Terre Adélie, Antarctica. In total, the dataset consists of 604 female histories from 1973 to 2002. The objective is to investigate the effect of climatic conditions on adult survival.

## Explore climatic covariates

First we explore the covariates sea ice extent in summer (SIE.Su), in autumn and winter (SIE.Au and SIE.Wi), in spring (SIE.Sp), annual southern oscillation index (SOI), air temperature in summer (T.Su), in autumn and winter (T.Au and T.Wi) and in spring (T.Sp).

Let us have a look to the correlations between these covariates:

cov <- read.table('cov-petrel.txt',header=T)  
head(cov)

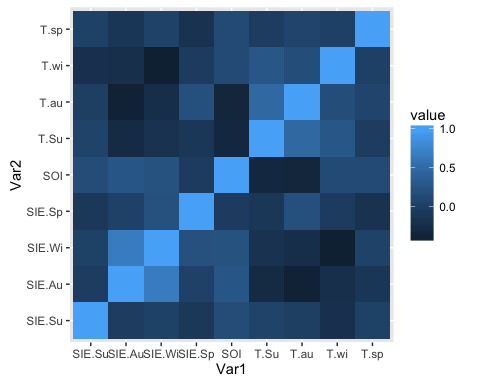
## SIE.Su SIE.Au SIE.Wi SIE.Sp SOI T.Su T.au T.wi  
## 1 0 341 478 348 0.96 -5.233333 -14.98333 -17.01667  
## 2 189 300 600 341 1.33 -4.150000 -15.08333 -17.85000  
## 3 26 270 337 230 0.06 -5.033333 -16.51667 -16.51667  
## 4 81 256 348 337 -1.14 -4.300000 -13.76667 -15.86667  
## 5 22 207 389 437 -0.29 -4.716667 -14.30000 -15.63333  
## 6 111 215 307 437 -0.26 -5.116667 -15.06667 -16.15000  
## T.sp  
## 1 -6.700000  
## 2 -7.250000  
## 3 -7.683333  
## 4 -7.650000  
## 5 -7.916667  
## 6 -6.766667

round(cor(cov),2)

## SIE.Su SIE.Au SIE.Wi SIE.Sp SOI T.Su T.au T.wi T.sp  
## SIE.Su 1.00 -0.05 0.01 -0.10 0.15 0.04 -0.02 -0.21 0.01  
## SIE.Au -0.05 1.00 0.67 0.02 0.26 -0.30 -0.43 -0.23 -0.12  
## SIE.Wi 0.01 0.67 1.00 0.21 0.22 -0.18 -0.24 -0.47 0.04  
## SIE.Sp -0.10 0.02 0.21 1.00 -0.06 -0.11 0.19 -0.06 -0.18  
## SOI 0.15 0.26 0.22 -0.06 1.00 -0.34 -0.37 0.13 0.14  
## T.Su 0.04 -0.30 -0.18 -0.11 -0.34 1.00 0.47 0.27 -0.05  
## T.au -0.02 -0.43 -0.24 0.19 -0.37 0.47 1.00 0.17 0.06  
## T.wi -0.21 -0.23 -0.47 -0.06 0.13 0.27 0.17 1.00 0.00  
## T.sp 0.01 -0.12 0.04 -0.18 0.14 -0.05 0.06 0.00 1.00

Visually, with a heatmap:

library(ggplot2)  
library(reshape2)  
qplot(x=Var1, y=Var2, data=melt(cor(cov)), fill=value, geom="tile")



What are the significant correlations?

library(psych)

##   
## Attaching package: 'psych'

## The following objects are masked from 'package:ggplot2':  
##   
## %+%, alpha

corr.test(cov)

## Call:corr.test(x = cov)  
## Correlation matrix   
## SIE.Su SIE.Au SIE.Wi SIE.Sp SOI T.Su T.au T.wi T.sp  
## SIE.Su 1.00 -0.05 0.01 -0.10 0.15 0.04 -0.02 -0.21 0.01  
## SIE.Au -0.05 1.00 0.67 0.02 0.26 -0.30 -0.43 -0.23 -0.12  
## SIE.Wi 0.01 0.67 1.00 0.21 0.22 -0.18 -0.24 -0.47 0.04  
## SIE.Sp -0.10 0.02 0.21 1.00 -0.06 -0.11 0.19 -0.06 -0.18  
## SOI 0.15 0.26 0.22 -0.06 1.00 -0.34 -0.37 0.13 0.14  
## T.Su 0.04 -0.30 -0.18 -0.11 -0.34 1.00 0.47 0.27 -0.05  
## T.au -0.02 -0.43 -0.24 0.19 -0.37 0.47 1.00 0.17 0.06  
## T.wi -0.21 -0.23 -0.47 -0.06 0.13 0.27 0.17 1.00 0.00  
## T.sp 0.01 -0.12 0.04 -0.18 0.14 -0.05 0.06 0.00 1.00  
## Sample Size   
## [1] 29  
## Probability values (Entries above the diagonal are adjusted for multiple tests.)   
## SIE.Su SIE.Au SIE.Wi SIE.Sp SOI T.Su T.au T.wi T.sp  
## SIE.Su 0.00 1.00 1.00 1.00 1.00 1.00 1.00 1.00 1  
## SIE.Au 0.79 0.00 0.00 1.00 1.00 1.00 0.64 1.00 1  
## SIE.Wi 0.96 0.00 0.00 1.00 1.00 1.00 1.00 0.37 1  
## SIE.Sp 0.59 0.90 0.28 0.00 1.00 1.00 1.00 1.00 1  
## SOI 0.43 0.17 0.25 0.77 0.00 1.00 1.00 1.00 1  
## T.Su 0.83 0.12 0.35 0.56 0.07 0.00 0.33 1.00 1  
## T.au 0.92 0.02 0.20 0.32 0.05 0.01 0.00 1.00 1  
## T.wi 0.28 0.23 0.01 0.76 0.52 0.15 0.37 0.00 1  
## T.sp 0.97 0.53 0.84 0.34 0.47 0.80 0.77 0.99 0  
##   
## To see confidence intervals of the correlations, print with the short=FALSE option

print(corr.test(cov),short=FALSE)

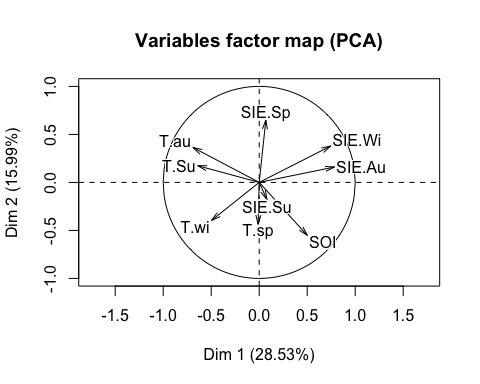
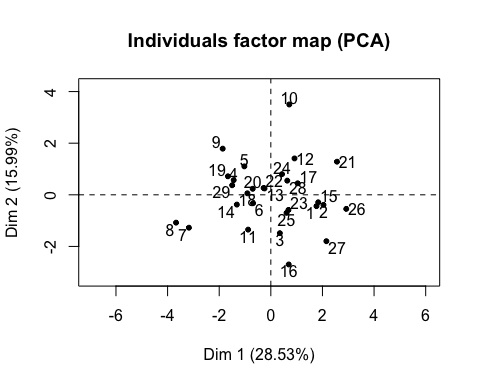
## Call:corr.test(x = cov)  
## Correlation matrix   
## SIE.Su SIE.Au SIE.Wi SIE.Sp SOI T.Su T.au T.wi T.sp  
## SIE.Su 1.00 -0.05 0.01 -0.10 0.15 0.04 -0.02 -0.21 0.01  
## SIE.Au -0.05 1.00 0.67 0.02 0.26 -0.30 -0.43 -0.23 -0.12  
## SIE.Wi 0.01 0.67 1.00 0.21 0.22 -0.18 -0.24 -0.47 0.04  
## SIE.Sp -0.10 0.02 0.21 1.00 -0.06 -0.11 0.19 -0.06 -0.18  
## SOI 0.15 0.26 0.22 -0.06 1.00 -0.34 -0.37 0.13 0.14  
## T.Su 0.04 -0.30 -0.18 -0.11 -0.34 1.00 0.47 0.27 -0.05  
## T.au -0.02 -0.43 -0.24 0.19 -0.37 0.47 1.00 0.17 0.06  
## T.wi -0.21 -0.23 -0.47 -0.06 0.13 0.27 0.17 1.00 0.00  
## T.sp 0.01 -0.12 0.04 -0.18 0.14 -0.05 0.06 0.00 1.00  
## Sample Size   
## [1] 29  
## Probability values (Entries above the diagonal are adjusted for multiple tests.)   
## SIE.Su SIE.Au SIE.Wi SIE.Sp SOI T.Su T.au T.wi T.sp  
## SIE.Su 0.00 1.00 1.00 1.00 1.00 1.00 1.00 1.00 1  
## SIE.Au 0.79 0.00 0.00 1.00 1.00 1.00 0.64 1.00 1  
## SIE.Wi 0.96 0.00 0.00 1.00 1.00 1.00 1.00 0.37 1  
## SIE.Sp 0.59 0.90 0.28 0.00 1.00 1.00 1.00 1.00 1  
## SOI 0.43 0.17 0.25 0.77 0.00 1.00 1.00 1.00 1  
## T.Su 0.83 0.12 0.35 0.56 0.07 0.00 0.33 1.00 1  
## T.au 0.92 0.02 0.20 0.32 0.05 0.01 0.00 1.00 1  
## T.wi 0.28 0.23 0.01 0.76 0.52 0.15 0.37 0.00 1  
## T.sp 0.97 0.53 0.84 0.34 0.47 0.80 0.77 0.99 0  
##   
## To see confidence intervals of the correlations, print with the short=FALSE option  
##   
## Confidence intervals based upon normal theory. To get bootstrapped values, try cor.ci  
## lower r upper p  
## SIE.Su-SIE.A -0.41 -0.05 0.32 0.79  
## SIE.Su-SIE.W -0.36 0.01 0.38 0.96  
## SIE.Su-SIE.Sp -0.45 -0.10 0.27 0.59  
## SIE.Su-SOI -0.23 0.15 0.49 0.43  
## SIE.Su-T.Su -0.33 0.04 0.40 0.83  
## SIE.Su-T.au -0.38 -0.02 0.35 0.92  
## SIE.Su-T.wi -0.53 -0.21 0.17 0.28  
## SIE.Su-T.sp -0.36 0.01 0.37 0.97  
## SIE.A-SIE.W 0.40 0.67 0.83 0.00  
## SIE.A-SIE.Sp -0.35 0.02 0.39 0.90  
## SIE.A-SOI -0.12 0.26 0.57 0.17  
## SIE.A-T.Su -0.60 -0.30 0.08 0.12  
## SIE.A-T.au -0.69 -0.43 -0.08 0.02  
## SIE.A-T.wi -0.55 -0.23 0.15 0.23  
## SIE.A-T.sp -0.47 -0.12 0.26 0.53  
## SIE.W-SIE.Sp -0.17 0.21 0.53 0.28  
## SIE.W-SOI -0.16 0.22 0.54 0.25  
## SIE.W-T.Su -0.51 -0.18 0.20 0.35  
## SIE.W-T.au -0.56 -0.24 0.13 0.20  
## SIE.W-T.wi -0.71 -0.47 -0.12 0.01  
## SIE.W-T.sp -0.33 0.04 0.40 0.84  
## SIE.Sp-SOI -0.41 -0.06 0.32 0.77  
## SIE.Sp-T.Su -0.46 -0.11 0.26 0.56  
## SIE.Sp-T.au -0.19 0.19 0.52 0.32  
## SIE.Sp-T.wi -0.42 -0.06 0.31 0.76  
## SIE.Sp-T.sp -0.52 -0.18 0.20 0.34  
## SOI-T.Su -0.63 -0.34 0.03 0.07  
## SOI-T.au -0.65 -0.37 0.00 0.05  
## SOI-T.wi -0.25 0.13 0.47 0.52  
## SOI-T.sp -0.24 0.14 0.48 0.47  
## T.Su-T.au 0.13 0.47 0.72 0.01  
## T.Su-T.wi -0.10 0.27 0.58 0.15  
## T.Su-T.sp -0.41 -0.05 0.32 0.80  
## T.au-T.wi -0.21 0.17 0.51 0.37  
## T.au-T.sp -0.32 0.06 0.41 0.77  
## T.wi-T.sp -0.37 0.00 0.37 0.99

Seems like sea ice extent in autumn and winter are positively correlated, while sea ice extent in autumn and temperature in autumn are negatively correlated.

## PCA on covariates

Let's perform a PCA on this set of covariates:

library(FactoMineR)  
res.pca = PCA(cov,scale.unit=T,graph=T,ncp=9)



Find the covariates associated to each principal component:

dimdesc(res.pca,axes = 1:9)

## $Dim.1  
## $Dim.1$quanti  
## correlation p.value  
## SIE.Au 0.7846343 4.703772e-07  
## SIE.Wi 0.7444495 3.650675e-06  
## SOI 0.5012694 5.604172e-03  
## T.wi -0.4966878 6.129402e-03  
## T.Su -0.6409107 1.798385e-04  
## T.au -0.6912833 3.291814e-05  
##   
##   
## $Dim.2  
## $Dim.2$quanti  
## correlation p.value  
## SIE.Sp 0.6505897 0.000132906  
## SIE.Wi 0.3787178 0.042773054  
## T.wi -0.3960426 0.033438570  
## T.sp -0.4367718 0.017836263  
## SOI -0.5519112 0.001910053  
##   
##   
## $Dim.3  
## $Dim.3$quanti  
## correlation p.value  
## SIE.Su 0.7413696 4.205825e-06  
## T.wi -0.5808892 9.527347e-04  
##   
##   
## $Dim.4  
## $Dim.4$quanti  
## correlation p.value  
## T.sp 0.8228262 4.300265e-08  
## SIE.Su -0.3946619 3.411627e-02  
##   
##   
## $Dim.5  
## $Dim.5$quanti  
## correlation p.value  
## SIE.Sp 0.6329789 0.0002286769  
## SOI 0.4046400 0.0294590693  
## SIE.Su 0.4020185 0.0306294870  
##   
##   
## $Dim.6  
## $Dim.6$quanti  
## correlation p.value  
## T.Su 0.5642562 0.001431237  
## T.wi 0.3861381 0.038548955  
##   
##   
## $Dim.8  
## NULL

#plot(res.pca)

Percentage of variance explained:

res.pca$eig[,3]

## [1] 28.53227 44.52647 57.72122 68.86126 79.32825 89.27306 93.70949  
## [8] 97.95676 100.00000

Re-project each covariate on each principal component:

pcs = res.pca$ind$coord  
round(pcs,2)

## Dim.1 Dim.2 Dim.3 Dim.4 Dim.5 Dim.6 Dim.7 Dim.8 Dim.9  
## 1 1.77 -0.44 -0.78 1.45 -0.08 0.12 -0.97 -0.13 0.85  
## 2 2.04 -0.39 2.70 -0.78 1.49 1.99 -0.44 -0.63 -0.21  
## 3 0.35 -1.49 -0.46 -1.19 -1.33 -1.04 -0.78 -0.45 0.16  
## 4 -1.44 0.57 0.48 -0.86 -0.07 -0.20 -0.01 0.59 -0.01  
## 5 -1.03 1.10 -1.26 -0.40 1.18 -0.56 -0.37 -0.76 -0.33  
## 6 -0.69 -0.33 0.59 0.08 2.17 -0.99 1.00 -0.10 0.37  
## 7 -3.17 -1.28 -0.08 0.21 0.39 0.83 0.91 -0.79 -0.37  
## 8 -3.67 -1.08 -1.54 0.46 1.39 0.75 -0.45 0.80 0.20  
## 9 -1.87 1.79 0.56 2.40 0.67 -1.92 -0.76 -0.42 -0.51  
## 10 0.72 3.50 0.01 -1.05 0.25 0.99 -0.45 0.57 0.30  
## 11 -0.88 -1.35 1.83 -1.38 0.28 0.08 0.51 -0.52 0.43  
## 12 0.92 1.41 -1.34 0.60 0.12 0.57 0.57 -1.13 0.63  
## 13 -0.24 0.25 -0.19 0.61 -2.19 1.61 -0.49 -1.09 -0.63  
## 14 -1.32 -0.38 1.73 0.04 -1.37 -0.51 0.10 0.65 -0.05  
## 15 1.84 -0.29 0.57 0.29 1.08 0.43 -0.21 0.27 0.32  
## 16 0.69 -2.70 -0.83 -0.01 -0.08 -1.06 0.02 0.14 0.20  
## 17 1.04 0.45 -0.63 0.50 0.31 0.52 0.94 0.61 0.12  
## 18 -0.91 0.06 1.18 1.48 -1.31 1.58 0.28 1.16 0.03  
## 19 -1.66 0.72 -0.74 -2.07 -1.05 -0.19 -0.27 0.38 0.33  
## 20 -0.70 0.23 -0.57 -0.99 -1.25 -0.31 0.93 -0.87 -0.01  
## 21 2.56 1.28 -0.60 -0.26 -0.47 -1.17 1.54 0.61 -0.63  
## 22 -0.28 0.27 0.13 -1.18 0.92 -0.31 -0.72 0.59 -1.06  
## 23 0.68 -0.59 -1.73 1.23 0.13 1.37 0.41 -0.03 -0.33  
## 24 0.43 0.80 1.79 1.19 -0.77 -1.32 0.27 -0.05 0.56  
## 25 0.61 -0.70 1.29 0.93 -0.25 -0.66 -0.18 -0.29 -0.39  
## 26 2.92 -0.55 -0.47 -0.47 0.15 -0.83 -0.75 -0.23 -0.15  
## 27 2.15 -1.80 -0.93 0.19 -0.11 0.10 -0.05 0.95 -0.38  
## 28 0.64 0.55 -0.39 -0.99 0.36 0.24 0.05 -0.17 0.05  
## 29 -1.50 0.37 -0.33 -0.03 -0.52 -0.12 -0.61 0.33 0.52

## Model fitting

We're gonna fit various capture-recapture models to the petrel data. We use [RMark](http://www.phidot.org/software/mark/docs/book/pdf/app_3.pdf) because everything can be done in R, and it's cool for reproducible research. But other pieces of software could be used too, like e.g. E-SURGE.

First, let's read in the data:

library(RMark)

## This is RMark 2.2.0

petrel=convert.inp("females\_petrel")  
#petrel$ch

Before fitting capture-recapture models to the data, we check whether the standard Cormack-Jolly-Seber model is fitting the data well. We use the R package R2ucare.

library(R2ucare)  
petrel.ch <- unlist(strsplit(petrel$ch, ""))  
nocc <- nchar(petrel$ch[1])  
petrel.ch <- matrix(as.numeric(petrel.ch), ncol = nocc, byrow = TRUE)  
freq = petrel$freq  
test3sr\_petrel = test3sr(petrel.ch, freq)  
test3sm\_petrel = test3sm(petrel.ch, freq)  
test2ct\_petrel = test2ct(petrel.ch, freq)  
test2cl\_petrel = test2cl(petrel.ch, freq)  
# display results:  
test3sr\_petrel

## $test3sr  
## stat df p\_val sign\_test   
## 29.095 27.000 0.356 0.903   
##   
## $details  
## component stat p\_val signed\_test test\_perf  
## 1 2 0.001 0.975 -0.032 Chi-square  
## 2 3 0.249 0.618 -0.499 Fisher  
## 3 4 0.213 0.644 0.462 Chi-square  
## 4 5 0 1 0 Fisher  
## 5 6 4.174 0.041 -2.043 Chi-square  
## 6 7 0 1 0 Fisher  
## 7 8 0 1 0 Fisher  
## 8 9 0 0 0 None  
## 9 10 1.13 0.288 -1.063 Chi-square  
## 10 11 0 1 0 Fisher  
## 11 12 1.766 0.184 -1.329 Fisher  
## 12 13 1.19 0.275 1.091 Fisher  
## 13 14 0 1 0 Fisher  
## 14 15 1.224 0.269 1.106 Fisher  
## 15 16 2.696 0.101 -1.642 Chi-square  
## 16 17 0 1 0 Fisher  
## 17 18 0 1 0 Fisher  
## 18 19 3.695 0.055 1.922 Fisher  
## 19 20 0 1 0 Fisher  
## 20 21 1.885 0.17 1.373 Fisher  
## 21 22 0.296 0.586 0.544 Fisher  
## 22 23 0 0.984 0 Chi-square  
## 23 24 0 1 0 Fisher  
## 24 25 6.514 0.011 2.552 Fisher  
## 25 26 0.749 0.387 0.865 Chi-square  
## 26 27 0.102 0.749 -0.319 Chi-square  
## 27 28 0 1 0 Fisher  
## 28 29 3.211 0.073 1.792 Fisher

test3sm\_petrel

## $test3sm  
## stat df p\_val   
## 39.260 31.000 0.147   
##   
## $details  
## component stat df p\_val test\_perf  
## 1 2 0.756 1 0.384 Chi-square  
## 2 3 4.883 1 0.027 Chi-square  
## 3 4 0.172 2 0.918 Chi-square  
## 4 5 0 1 1 Fisher  
## 5 6 1.022 1 0.312 Chi-square  
## 6 7 0.748 1 0.387 Chi-square  
## 7 8 0 1 1 Fisher  
## 8 9 0.294 1 0.588 Fisher  
## 9 10 0.939 1 0.333 Chi-square  
## 10 11 2.88 3 0.411 Chi-square  
## 11 12 1.709 1 0.191 Chi-square  
## 12 13 0.19 1 0.663 Chi-square  
## 13 14 0 1 1 Fisher  
## 14 15 5.705 1 0.017 Fisher  
## 15 16 14.009 2 0.001 Chi-square  
## 16 17 0.309 1 0.578 Chi-square  
## 17 18 0.305 1 0.581 Chi-square  
## 18 19 0 1 1 Fisher  
## 19 20 1.337 1 0.248 Chi-square  
## 20 21 0.547 1 0.46 Chi-square  
## 21 22 0 1 1 Fisher  
## 22 23 0 1 1 Fisher  
## 23 24 1.867 1 0.172 Chi-square  
## 24 25 0.657 1 0.417 Fisher  
## 25 26 0.456 1 0.5 Chi-square  
## 26 27 0.212 1 0.645 Chi-square  
## 27 28 0.263 1 0.608 Fisher  
## 28 29 0 0 0 None

test2ct\_petrel

## $test2ct  
## stat df p\_val sign\_test   
## 103.115 27.000 0.000 -8.441   
##   
## $details  
## component dof stat p\_val signed\_test test\_perf  
## 1 2 1 0.013 0.908 0.114 Chi-square  
## 2 3 1 8.1 0.004 -2.846 Fisher  
## 3 4 1 2.599 0.107 -1.612 Chi-square  
## 4 5 1 1.207 0.272 -1.099 Chi-square  
## 5 6 1 1.162 0.281 -1.078 Chi-square  
## 6 7 1 0.499 0.48 -0.706 Chi-square  
## 7 8 1 0.958 0.328 -0.979 Chi-square  
## 8 9 1 0.977 0.323 -0.988 Chi-square  
## 9 10 1 6.397 0.011 -2.529 Chi-square  
## 10 11 1 2.674 0.102 -1.635 Chi-square  
## 11 12 1 8.56 0.003 -2.926 Chi-square  
## 12 13 1 0.056 0.814 -0.237 Chi-square  
## 13 14 1 0.015 0.903 0.122 Chi-square  
## 14 15 1 5.736 0.017 -2.395 Chi-square  
## 15 16 1 5.291 0.021 -2.3 Chi-square  
## 16 17 1 2.057 0.152 -1.434 Chi-square  
## 17 18 1 10.988 0.001 -3.315 Chi-square  
## 18 19 1 7.809 0.005 -2.794 Chi-square  
## 19 20 1 0.149 0.699 -0.386 Chi-square  
## 20 21 1 5.228 0.022 -2.286 Chi-square  
## 21 22 1 9.259 0.002 -3.043 Chi-square  
## 22 23 1 3.826 0.05 -1.956 Chi-square  
## 23 24 1 9.147 0.002 -3.024 Chi-square  
## 24 25 1 0 1 0 Chi-square  
## 25 26 1 6.442 0.011 -2.538 Chi-square  
## 26 27 1 0 0.984 0 Chi-square  
## 27 28 1 3.966 0.046 -1.991 Chi-square

test2cl\_petrel

## $test2cl  
## stat df p\_val   
## 49.741 42.000 0.192   
##   
## $details  
## component dof stat p\_val test\_perf  
## 1 2 1 0 1 Fisher  
## 2 3 1 1.077 0.299 Fisher  
## 3 4 1 1.42 0.233 Chi-square  
## 4 5 1 0.033 0.855 Chi-square  
## 5 6 3 0.246 0.97 Chi-square  
## 6 7 3 0.955 0.812 Chi-square  
## 7 8 2 0.906 0.636 Chi-square  
## 8 9 1 0.101 0.75 Chi-square  
## 9 10 1 0.808 0.369 Chi-square  
## 10 11 3 8.064 0.045 Chi-square  
## 11 12 2 0.545 0.761 Chi-square  
## 12 13 2 0.973 0.615 Chi-square  
## 13 14 1 1.709 0.191 Chi-square  
## 14 15 2 1.416 0.493 Chi-square  
## 15 16 3 7.218 0.065 Chi-square  
## 16 17 3 9.25 0.026 Chi-square  
## 17 18 2 3.995 0.136 Chi-square  
## 18 19 2 4.387 0.112 Chi-square  
## 19 20 1 0.402 0.526 Chi-square  
## 20 21 1 0.545 0.46 Chi-square  
## 21 22 1 0.683 0.408 Chi-square  
## 22 23 1 1.155 0.283 Chi-square  
## 23 24 1 2.093 0.148 Fisher  
## 24 25 1 0.229 0.633 Chi-square  
## 25 26 1 1.319 0.251 Chi-square  
## 26 27 1 0.212 0.645 Chi-square

It sounds like there is a strong trap-dependence effect. Let's deal with it and create an individual time-varying covariate for trap-dependence (see appendix C of the Gentle introduction to Mark):

petrel.ch <- unlist(strsplit(petrel$ch, ""))  
nocc <- nchar(petrel$ch[1])  
petrel.td <- matrix(as.numeric(petrel.ch), ncol = nocc, byrow = TRUE)  
petrel.td <- petrel.td[, 1:(nocc - 1)]  
petrel.td <- as.data.frame(petrel.td)  
begin.time <- 1974  
names(petrel.td) <- paste('td', (begin.time + 1):(begin.time + nocc - 1), sep = "")  
#head(petrel.td) # dim 430 x 29  
dim(petrel.td)

## [1] 430 29

petrel <- cbind(petrel, petrel.td)  
#head(petrel)

Now process the data:

petrel.processed=process.data(petrel, model="CJS", begin.time=1974)

Create the default design matrix:

design.p=list(time.varying=c('td')) #td  
design.parameters <- list(p=design.p)  
petrel.ddl <- make.design.data(petrel.processed,parameters=design.parameters)

Standardize the covariates:

# standardize  
moy = apply(cov,2,mean)  
prec = apply(cov,2,sd)  
moymat = matrix(rep(moy,nrow(cov)),ncol=ncol(cov),byrow=T)  
precmat = matrix(rep(prec,nrow(cov)),ncol=ncol(cov),byrow=T)  
covstar = (cov - moymat)/precmat  
#apply(covstar,2,mean)  
#apply(covstar,2,sd)  
cov = covstar

Add raw covariates to the design matrix:

petrel.ddl$Phi$x1=0  
petrel.ddl$Phi$x2=0  
petrel.ddl$Phi$x3=0  
petrel.ddl$Phi$x4=0  
petrel.ddl$Phi$x5=0  
petrel.ddl$Phi$x6=0  
petrel.ddl$Phi$x7=0  
petrel.ddl$Phi$x8=0  
petrel.ddl$Phi$x9=0  
ind=1  
for (i in 1974:2002){  
 petrel.ddl$Phi$x1[petrel.ddl$Phi$time==i]=cov[ind,1]  
 petrel.ddl$Phi$x2[petrel.ddl$Phi$time==i]=cov[ind,2]  
 petrel.ddl$Phi$x3[petrel.ddl$Phi$time==i]=cov[ind,3]  
 petrel.ddl$Phi$x4[petrel.ddl$Phi$time==i]=cov[ind,4]  
 petrel.ddl$Phi$x5[petrel.ddl$Phi$time==i]=cov[ind,5]  
 petrel.ddl$Phi$x6[petrel.ddl$Phi$time==i]=cov[ind,6]  
 petrel.ddl$Phi$x7[petrel.ddl$Phi$time==i]=cov[ind,7]  
 petrel.ddl$Phi$x8[petrel.ddl$Phi$time==i]=cov[ind,8]  
 petrel.ddl$Phi$x9[petrel.ddl$Phi$time==i]=cov[ind,9]  
 ind=ind+1  
}

Specify the effects on survival and detection probabilities:

# for survival probabilities  
Phidot=list(formula=~1) # constant  
Phitime=list(formula=~time) # time  
PhiCov=list(formula=~x1+x2+x3+x4+x5+x6+x7+x8+x9) # all covariates  
# Define range of models for detection probabilities  
pdot=list(formula=~td) # constant, with trap-dependence  
ptime=list(formula=~time+td) # additive effect of time and trap-dependence (no interaction because of severe identifiability issues Gimenez et al. 2003)

Fit models:

# phi,p  
phip = mark(petrel.processed,petrel.ddl,model.parameters=list(Phi=Phidot,p=pdot),output = FALSE,delete=T)  
# phit,p  
phitp = mark(petrel.processed,petrel.ddl,model.parameters=list(Phi=Phitime,p=pdot),output = FALSE,delete=T)  
# phi,pt  
phipt = mark(petrel.processed,petrel.ddl,model.parameters=list(Phi=Phidot,p=ptime),output = FALSE,delete=T)  
# phit,pt  
phitpt = mark(petrel.processed,petrel.ddl,model.parameters=list(Phi=Phitime,p=ptime),output = FALSE,delete=T)  
# phi(cov),pt  
phixpt = mark(petrel.processed,petrel.ddl,model.parameters=list(Phi=PhiCov,p=ptime),output = FALSE,delete=T)  
# phi(cov),p  
phixp = mark(petrel.processed,petrel.ddl,model.parameters=list(Phi=PhiCov,p=pdot),output = FALSE,delete=T)

Compare models

collect.models()

## model npar  
## 4 Phi(~time)p(~time + td) 59  
## 6 Phi(~x1 + x2 + x3 + x4 + x5 + x6 + x7 + x8 + x9)p(~time + td) 40  
## 2 Phi(~1)p(~time + td) 31  
## 3 Phi(~time)p(~td) 31  
## 5 Phi(~x1 + x2 + x3 + x4 + x5 + x6 + x7 + x8 + x9)p(~td) 12  
## 1 Phi(~1)p(~td) 3  
## AICc DeltaAICc weight Deviance  
## 4 6535.214 0.00000 8.255973e-01 6414.843  
## 6 6538.323 3.10948 1.744027e-01 6457.232  
## 2 6580.016 44.80247 1.541825e-10 6517.358  
## 3 7035.196 499.98207 0.000000e+00 6972.538  
## 5 7065.792 530.57806 0.000000e+00 7041.689  
## 1 7141.081 605.86722 0.000000e+00 7135.073

Clearly, there is time variation in the detection process. Now, let's have a look to the estimates of the covariate regression parameters:

phixpt$results$beta

## estimate se lcl ucl  
## Phi:(Intercept) 3.0215025 0.1266475 2.7732735 3.2697315  
## Phi:x1 -0.0214575 0.1238100 -0.2641250 0.2212100  
## Phi:x2 0.5045044 0.2437935 0.0266692 0.9823397  
## Phi:x3 -0.5050213 0.2135690 -0.9236166 -0.0864259  
## Phi:x4 -0.1875460 0.1633837 -0.5077780 0.1326860  
## Phi:x5 -0.3384230 0.1285892 -0.5904579 -0.0863881  
## Phi:x6 0.0366726 0.1194038 -0.1973588 0.2707040  
## Phi:x7 0.4200924 0.2218795 -0.0147914 0.8549763  
## Phi:x8 -0.5388492 0.1450617 -0.8231701 -0.2545282  
## Phi:x9 -0.1858334 0.1744053 -0.5276678 0.1560010  
## p:(Intercept) -0.2761772 0.3517370 -0.9655816 0.4132273  
## p:time1976 1.4052782 0.5014516 0.4224332 2.3881233  
## p:time1977 1.1938900 0.4353436 0.3406165 2.0471635  
## p:time1978 -1.3621145 0.3973423 -2.1409053 -0.5833236  
## p:time1979 0.8850791 0.4069705 0.0874170 1.6827413  
## p:time1980 -1.3972660 0.4108535 -2.2025390 -0.5919930  
## p:time1981 -0.8393465 0.4093094 -1.6415930 -0.0371000  
## p:time1982 -1.4862916 0.4314322 -2.3318988 -0.6406844  
## p:time1983 1.0600325 0.4127526 0.2510374 1.8690276  
## p:time1984 0.4538240 0.3939147 -0.3182488 1.2258967  
## p:time1985 -1.0119331 0.3845208 -1.7655940 -0.2582723  
## p:time1986 0.0048123 0.3854654 -0.7506998 0.7603245  
## p:time1987 -1.0459933 0.3889402 -1.8083161 -0.2836704  
## p:time1988 0.5125532 0.3873106 -0.2465757 1.2716820  
## p:time1989 1.1524405 0.4015803 0.3653431 1.9395379  
## p:time1990 -0.3716929 0.3781745 -1.1129150 0.3695292  
## p:time1991 0.6520397 0.3843860 -0.1013568 1.4054362  
## p:time1992 0.6618721 0.3825593 -0.0879441 1.4116884  
## p:time1993 0.6817004 0.3839203 -0.0707834 1.4341842  
## p:time1994 0.0531793 0.3752936 -0.6823961 0.7887547  
## p:time1995 0.7756355 0.3815203 0.0278558 1.5234152  
## p:time1996 1.6025645 0.4090705 0.8007862 2.4043428  
## p:time1997 1.4892937 0.4097446 0.6861942 2.2923933  
## p:time1998 0.4982421 0.3782740 -0.2431750 1.2396591  
## p:time1999 1.4753069 0.4081101 0.6754110 2.2752027  
## p:time2000 0.5117622 0.3839862 -0.2408508 1.2643753  
## p:time2001 -0.1193446 0.3820091 -0.8680824 0.6293931  
## p:time2002 -0.0080104 0.3828684 -0.7584325 0.7424118  
## p:time2003 0.2303002 0.3862412 -0.5267326 0.9873330  
## p:td 0.7281677 0.0827991 0.5658815 0.8904538

Remember, from our preliminary exploration step above, we know that covariates 2 and 3 are highly positively correlated. However by inspecting the estimates here, these covariates seem to have an opposite effect on survival!

## P2CR analysis

In this section, we show how to perform a P2CR analysis. First, we amend the design matrix we built before, and add the coordinates of the raw covariates on the principal components:

petrel.ddl$Phi$pc1=0  
petrel.ddl$Phi$pc2=0  
petrel.ddl$Phi$pc3=0  
petrel.ddl$Phi$pc4=0  
petrel.ddl$Phi$pc5=0  
petrel.ddl$Phi$pc6=0  
petrel.ddl$Phi$pc7=0  
petrel.ddl$Phi$pc8=0  
petrel.ddl$Phi$pc9=0  
ind=1  
for (i in 1974:2002){  
 petrel.ddl$Phi$pc1[petrel.ddl$Phi$time==i]=pcs[ind,1]  
 petrel.ddl$Phi$pc2[petrel.ddl$Phi$time==i]=pcs[ind,2]  
 petrel.ddl$Phi$pc3[petrel.ddl$Phi$time==i]=pcs[ind,3]  
 petrel.ddl$Phi$pc4[petrel.ddl$Phi$time==i]=pcs[ind,4]  
 petrel.ddl$Phi$pc5[petrel.ddl$Phi$time==i]=pcs[ind,5]  
 petrel.ddl$Phi$pc6[petrel.ddl$Phi$time==i]=pcs[ind,6]  
 petrel.ddl$Phi$pc7[petrel.ddl$Phi$time==i]=pcs[ind,7]  
 petrel.ddl$Phi$pc8[petrel.ddl$Phi$time==i]=pcs[ind,8]  
 petrel.ddl$Phi$pc9[petrel.ddl$Phi$time==i]=pcs[ind,9]  
 ind=ind+1  
}

In the first step of the P2CR analysis, we consider each PC separately:

Phipc1=list(formula=~pc1)  
Phipc2=list(formula=~pc2)  
Phipc3=list(formula=~pc3)  
Phipc4=list(formula=~pc4)  
Phipc5=list(formula=~pc5)  
Phipc6=list(formula=~pc6)  
Phipc7=list(formula=~pc7)  
Phipc8=list(formula=~pc8)  
Phipc9=list(formula=~pc9)  
phipc1 = mark(petrel.processed,petrel.ddl,model.parameters=list(Phi=Phipc1,p=ptime),output = FALSE,delete=T)  
phipc2 = mark(petrel.processed,petrel.ddl,model.parameters=list(Phi=Phipc2,p=ptime),output = FALSE,delete=T)  
phipc3 = mark(petrel.processed,petrel.ddl,model.parameters=list(Phi=Phipc3,p=ptime),output = FALSE,delete=T)  
phipc4 = mark(petrel.processed,petrel.ddl,model.parameters=list(Phi=Phipc4,p=ptime),output = FALSE,delete=T)  
phipc5 = mark(petrel.processed,petrel.ddl,model.parameters=list(Phi=Phipc5,p=ptime),output = FALSE,delete=T)  
phipc6 = mark(petrel.processed,petrel.ddl,model.parameters=list(Phi=Phipc6,p=ptime),output = FALSE,delete=T)  
phipc7 = mark(petrel.processed,petrel.ddl,model.parameters=list(Phi=Phipc7,p=ptime),output = FALSE,delete=T)  
phipc8 = mark(petrel.processed,petrel.ddl,model.parameters=list(Phi=Phipc8,p=ptime),output = FALSE,delete=T)  
phipc9 = mark(petrel.processed,petrel.ddl,model.parameters=list(Phi=Phipc9,p=ptime),output = FALSE,delete=T)

We now use ANODEV to to test the significance of these PCs:

# get info on model with time-dependent survival  
devtime = phitpt$results$lnl  
npartime = phitpt$results$npar  
  
# get info on model with constant survival  
devct = phipt$results$lnl  
nparct = phipt$results$npar  
  
# test each PC:  
stat = rep(NA,9)  
df1 = rep(NA,9)  
df2 = rep(NA,9)  
for (i in 1:9){  
 name = paste('phipc',i,sep="")  
 devco = get(name)$results$lnl  
 nparco = get(name)$results$npar  
 num = (devct - devco)/(nparco-nparct)  
 den = (devco - devtime)/(npartime-nparco)   
 stat[i] <- num/den  
 df1[i] <- nparco-nparct  
 df2[i] <- npartime-nparco  
}  
# calculate p-value  
pval = 1-pf(stat,df1,df2)  
pval

## [1] 0.50516673 0.16519536 0.01154679 0.09421164 0.09162907 0.13028550  
## [7] 0.71524153 0.58159214 0.38469323

We can reject the null hypothesis that PC3 has no effect on survival.

In step 2 of the P2CR, we keep PC3 and test the significance of the other PCs:

Phipc1=list(formula=~pc1+pc3)  
Phipc2=list(formula=~pc2+pc3)  
Phipc3=list(formula=~pc4+pc3)  
Phipc4=list(formula=~pc5+pc3)  
Phipc5=list(formula=~pc6+pc3)  
Phipc6=list(formula=~pc7+pc3)  
Phipc7=list(formula=~pc8+pc3)  
Phipc8=list(formula=~pc9+pc3)  
phipc11 = mark(petrel.processed,petrel.ddl,model.parameters=list(Phi=Phipc1,p=ptime),output = FALSE,delete=T)  
phipc21 = mark(petrel.processed,petrel.ddl,model.parameters=list(Phi=Phipc2,p=ptime),output = FALSE,delete=T)  
phipc31 = mark(petrel.processed,petrel.ddl,model.parameters=list(Phi=Phipc3,p=ptime),output = FALSE,delete=T)  
phipc41 = mark(petrel.processed,petrel.ddl,model.parameters=list(Phi=Phipc4,p=ptime),output = FALSE,delete=T)  
phipc51 = mark(petrel.processed,petrel.ddl,model.parameters=list(Phi=Phipc5,p=ptime),output = FALSE,delete=T)  
phipc61 = mark(petrel.processed,petrel.ddl,model.parameters=list(Phi=Phipc6,p=ptime),output = FALSE,delete=T)  
phipc71 = mark(petrel.processed,petrel.ddl,model.parameters=list(Phi=Phipc7,p=ptime),output = FALSE,delete=T)  
phipc81 = mark(petrel.processed,petrel.ddl,model.parameters=list(Phi=Phipc8,p=ptime),output = FALSE,delete=T)

stat = rep(NA,8)  
df1 = rep(NA,8)  
df2 = rep(NA,8)  
for (i in 1:8){  
 name = paste('phipc',3,sep="")  
 devct = get(name)$results$lnl  
 nparct = get(name)$results$npar  
 namex = paste('phipc',paste(i,'1',sep=""),sep="")  
 devco = get(namex)$results$lnl  
 nparco = get(namex)$results$npar  
 num = (devct - devco)/(nparco-nparct)  
 den = (devco - devtime)/(npartime-nparco)   
 stat[i] <- num/den  
 df1[i] <- nparco-nparct  
 df2[i] <- npartime-nparco  
  
}  
  
pval = 1-pf(stat,df1,df2)  
pval

## [1] 0.73721042 0.09856576 0.04088822 0.12464467 0.07255703 0.60381779  
## [7] 0.93642783 0.40284581

Now PC4 is significant according the ANODEV (remember that PC3 was removed from the list).

In step 3 of the P2CR analysis, we reiterate the process, that is we test the significance of the other PCs in presence of PC3 and PC4:

Phipc1=list(formula=~pc1+pc3+pc4)  
Phipc2=list(formula=~pc2+pc3+pc4)  
Phipc3=list(formula=~pc5+pc3+pc4)  
Phipc4=list(formula=~pc6+pc3+pc4)  
Phipc5=list(formula=~pc7+pc3+pc4)  
Phipc6=list(formula=~pc8+pc3+pc4)  
Phipc7=list(formula=~pc9+pc3+pc4)  
phipc12 = mark(petrel.processed,petrel.ddl,model.parameters=list(Phi=Phipc1,p=ptime),output = FALSE,delete=T)  
phipc22 = mark(petrel.processed,petrel.ddl,model.parameters=list(Phi=Phipc2,p=ptime),output = FALSE,delete=T)  
phipc32 = mark(petrel.processed,petrel.ddl,model.parameters=list(Phi=Phipc3,p=ptime),output = FALSE,delete=T)  
phipc42 = mark(petrel.processed,petrel.ddl,model.parameters=list(Phi=Phipc4,p=ptime),output = FALSE,delete=T)  
phipc52 = mark(petrel.processed,petrel.ddl,model.parameters=list(Phi=Phipc5,p=ptime),output = FALSE,delete=T)  
phipc62 = mark(petrel.processed,petrel.ddl,model.parameters=list(Phi=Phipc6,p=ptime),output = FALSE,delete=T)  
phipc72 = mark(petrel.processed,petrel.ddl,model.parameters=list(Phi=Phipc7,p=ptime),output = FALSE,delete=T)

What does the ANODEV tell us?

stat = rep(NA,7)  
df1 = rep(NA,7)  
df2 = rep(NA,7)  
for (i in 1:7){  
 name = paste('phipc',31,sep="")  
 devct = get(name)$results$lnl  
 nparct = get(name)$results$npar  
 namex = paste('phipc',paste(i,'2',sep=""),sep="")  
 devco = get(namex)$results$lnl  
 nparco = get(namex)$results$npar  
 num = (devct - devco)/(nparco-nparct)  
 den = (devco - devtime)/(npartime-nparco)   
 stat[i] <- num/den  
 df1[i] <- nparco-nparct  
 df2[i] <- npartime-nparco  
  
}  
  
pval = 1-pf(stat,df1,df2)  
pval

## [1] 0.7872699 0.1827054 0.2505976 0.4662657 0.6318687 0.9624121 0.2682514

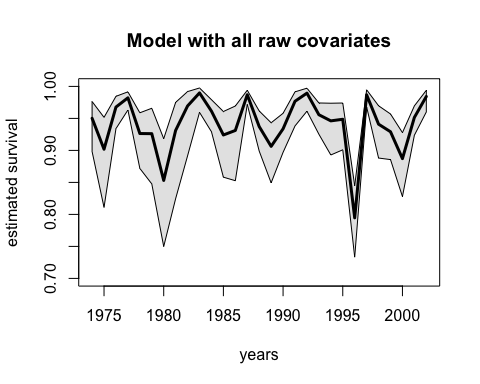
No more significant PC, the algorithm stops here.

## Post-process results

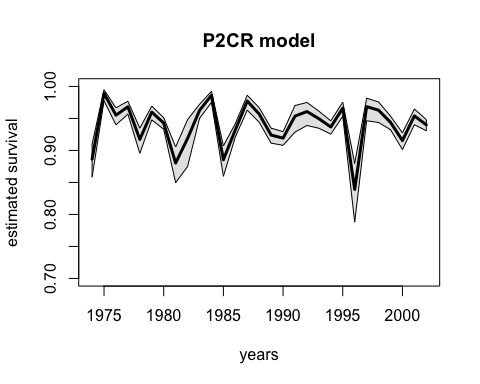
We will make two plots, one with time-varying survival estimates, and another oneto illustrate the relationship between survival and the selected PCs.

First, a figure displaying the time variation in survival according to a model with all raw covariates and the PC2R model:

#phit\_mle <- phitpt$results$real[1:29,]  
phicov\_mle <- phixpt$results$real[1:29,]  
phipca\_mle <- phipc31$results$real[1:29,]  
# Make a 6x6 inch image at 300dpi  
#ppi <- 300  
#png("time\_survival\_allcov.png", width=6\*ppi, height=6\*ppi, res=ppi)  
plot(1974:2002,phicov\_mle[,1],lwd=3,col='black',type='n',ylim=c(0.7,1),xlab='years',ylab='estimated survival',main='Model with all raw covariates')  
polygon(x=c(1974:2002, rev(1974:2002)),y=c(phicov\_mle[,3], rev(phicov\_mle[,4])),col='grey90')  
lines(1974:2002,phicov\_mle[,1],lwd=3,col='black')



#dev.off()  
#png("time\_survival\_p2cr.png", width=6\*ppi, height=6\*ppi, res=ppi)  
plot(1974:2002,phipca\_mle[,1],lwd=3,col='black',type='n',ylim=c(0.7,1),xlab='years',ylab='estimated survival',main='P2CR model')  
polygon(x=c(1974:2002, rev(1974:2002)),y=c(phipca\_mle[,3], rev(phipca\_mle[,4])),col='grey90')  
lines(1974:2002,phipca\_mle[,1],lwd=3,col='black')



#dev.off()

Second, a figure displaying the relationship between survival and the PCs selected by the P2CR analysis.

Get the coefficient estimates for each PC and the intercept:

phipc31$results$beta[1:3,]

## estimate se lcl ucl  
## Phi:(Intercept) 2.9065532 0.0930352 2.7242042 3.0889022  
## Phi:pc4 -0.3179574 0.0937601 -0.5017273 -0.1341876  
## Phi:pc3 0.4987766 0.1117003 0.2798439 0.7177093

Get confidence intervals using the delta-method:

library(msm)  
PC3 = pcs[,3]  
PC4 = pcs[,4]  
phi\_SE3 = matrix(0, nrow = 29, ncol = 1)  
estmean3 <- c(2.9065503,0.4987728)  
estvar3 <- diag(c(0.0930351,0.1117004)^2)  
phi\_SE4 = matrix(0, nrow = 29, ncol = 1)  
estmean4 <- c(2.9065503,-0.3179579)  
estvar4 <- diag(c(0.0930351,0.0937603)^2)  
for (i in 1:29){  
 temp3 <- PC3[i]  
 temp4 <- PC4[i]  
 phi\_SE3[i,] <- deltamethod(~ x1+x2\*temp3, estmean3, estvar3)  
 phi\_SE4[i,] <- deltamethod(~ x1+x2\*temp4, estmean4, estvar4)  
}  
  
ilogitphi3 <- estmean3[1] + estmean3[2] \* PC3  
ilogitphi3lb <- ilogitphi3 - 1.96 \* as.vector(phi\_SE3)  
ilogitphi3ub <- ilogitphi3 + 1.96 \* as.vector(phi\_SE3)  
phi3lb <- 1/(1+exp(-(ilogitphi3lb)))  
phi3ub <- 1/(1+exp(-(ilogitphi3ub)))  
phi3 <- 1/(1+exp(-(ilogitphi3)))  
  
ilogitphi4 <- estmean4[1] + estmean4[2] \* PC4  
ilogitphi4lb <- ilogitphi4 - 1.96 \* as.vector(phi\_SE4)  
ilogitphi4ub <- ilogitphi4 + 1.96 \* as.vector(phi\_SE4)  
phi4lb <- 1/(1+exp(-(ilogitphi4lb)))  
phi4ub <- 1/(1+exp(-(ilogitphi4ub)))  
phi4 <- 1/(1+exp(-(ilogitphi4)))

Before plotting the survival as a function of the PC values, we need to find out about the raw covariates that were used to build these PCs:

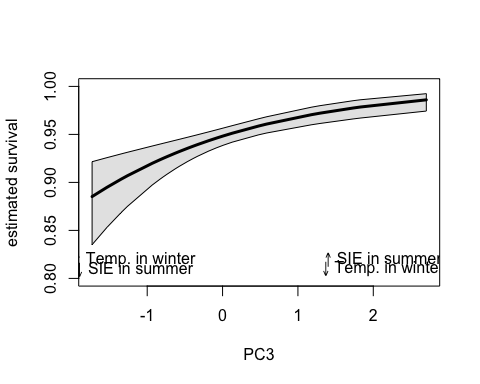
dimdesc(res.pca,axes = c(3:4))

## $Dim.3  
## $Dim.3$quanti  
## correlation p.value  
## SIE.Su 0.7413696 4.205825e-06  
## T.wi -0.5808892 9.527347e-04  
##   
##   
## $Dim.4  
## $Dim.4$quanti  
## correlation p.value  
## T.sp 0.8228262 4.300265e-08  
## SIE.Su -0.3946619 3.411627e-02

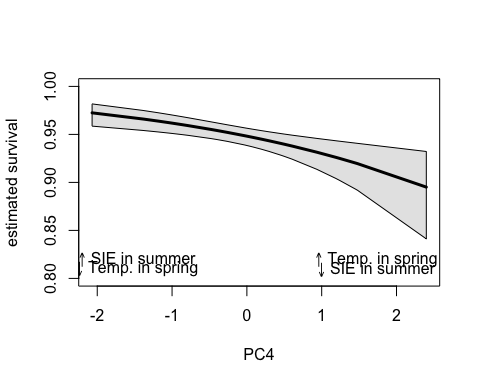
High (resp. low) values of PC3 mean high (resp. low) values of SIE in summer and low (resp. high) values of temperature in winter. High (resp. low) values of PC4 mean high (resp. low) values of temperature in spring and low (resp. high) values of SIE in summer.

Now we can plot the survival - PC relationships, and add the interpretation of the PCs:

# Make a 6x6 inch image at 300dpi  
#ppi <- 300  
#png("pc3\_survival.png", width=6\*ppi, height=6\*ppi, res=ppi)  
ord<-order(PC3)  
plot(PC3[ord],phi3[ord],lwd=3,col='black',type='n',xlab='PC3',ylab='estimated survival',main='',ylim=c(0.8,1))  
polygon(x=c(PC3[ord], rev(PC3[ord])),y=c(phi3lb[ord], rev(phi3ub[ord])),col='grey90')  
lines(PC3[ord],phi3[ord],lwd=3,col='black')  
text(-1.2,0.82,expression('' %up% 'Temp. in winter'),cex=1)  
text(-1.2,0.81,expression('' %down% 'SIE in summer'),cex=1)  
text(2.1,0.82,expression('' %up% 'SIE in summer'),cex=1)  
text(2.1,0.81,expression('' %down% 'Temp. in winter'),cex=1)



ord<-order(PC4)  
#dev.off()  
#png("pc4\_survival.png", width=6\*ppi, height=6\*ppi, res=ppi)  
plot(PC4[ord],phi4[ord],lwd=3,col='black',type='n',xlab='PC4',ylab='estimated survival',main='',ylim=c(0.8,1))  
polygon(x=c(PC4[ord], rev(PC4[ord])),y=c(phi4lb[ord], rev(phi4ub[ord])),col='grey90')  
lines(PC4[ord],phi4[ord],lwd=3,col='black')  
text(-1.5,0.82,expression('' %up% 'SIE in summer'),cex=1)  
text(-1.5,0.81,expression('' %down% 'Temp. in spring'),cex=1)  
text(1.7,0.82,expression('' %up% 'Temp. in spring'),cex=1)  
text(1.7,0.81,expression('' %down% 'SIE in summer'),cex=1)



#dev.off()