Supplementary material for 'Dealing with many correlated covariates in capture-recapture models' by Gimenez and Barbraud.

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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).

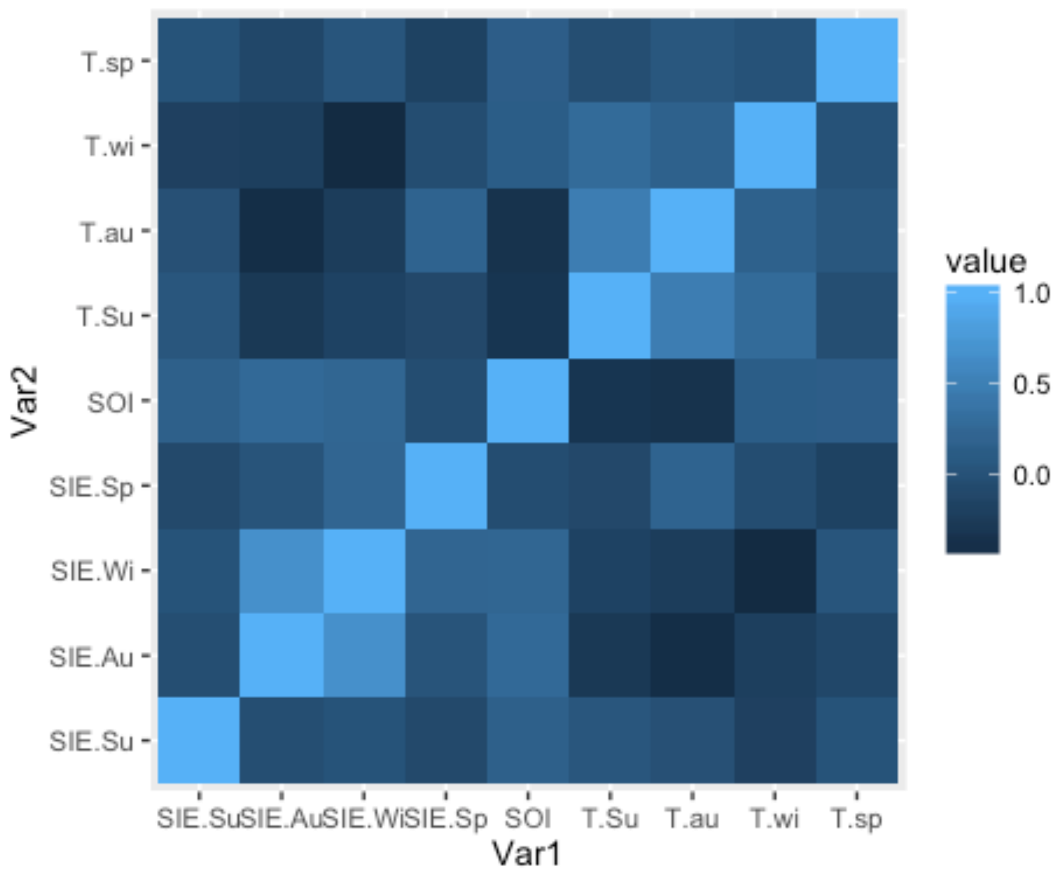
Let us have a look to the correlations between these covariates:

```
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
```

```r
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
```

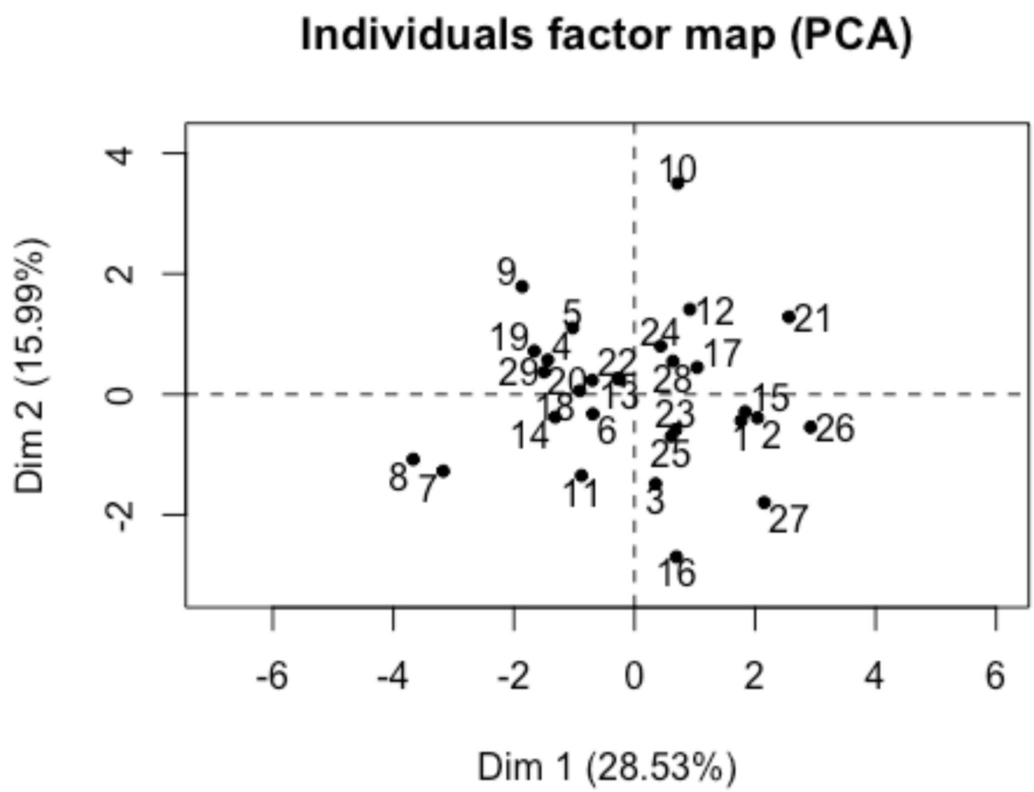
```
## T.au-T.sp     -0.32  0.06  0.41 0.77
## T.wi-T.sp     -0.37  0.00  0.37 0.99
```

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.

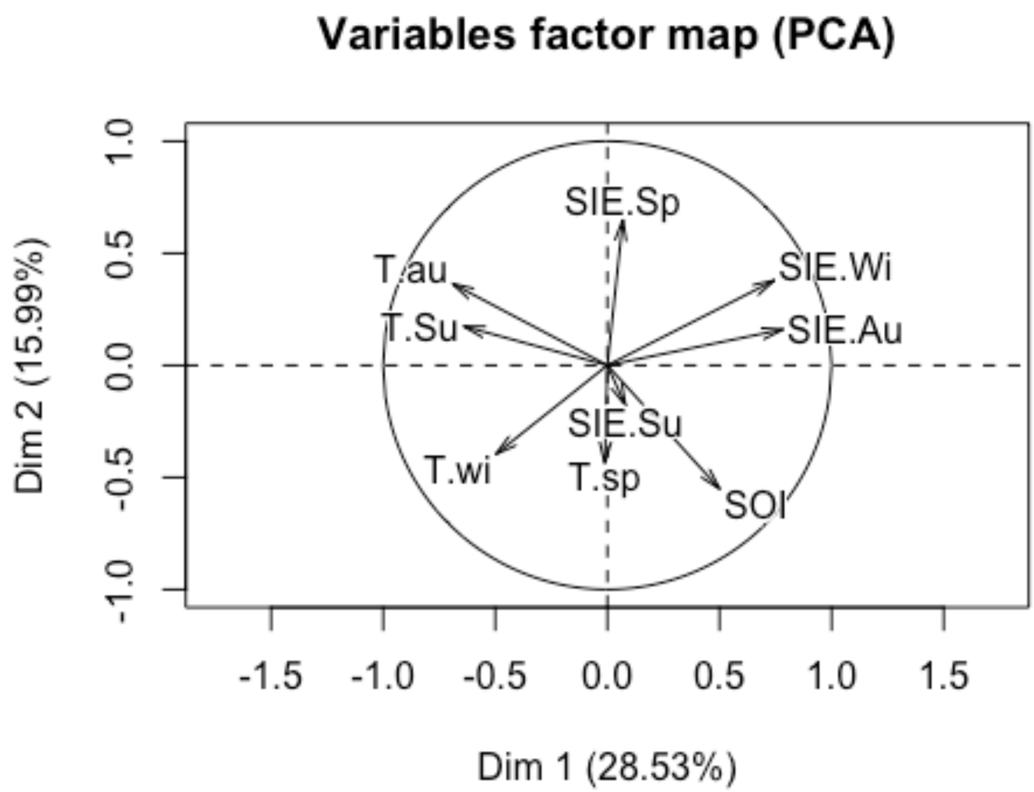
PCA on covariates

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

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



Individuals factor map (PCA)
Dim 1 (28.53%)
Dim 2 (15.99%)
-6
-4
-2
0
2
4
6
10
9
5
12
21
19
4
24
17
29
20
22
28
13
15
18
23
26
14
6
1
2
25
8
7
11
3
27
16



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
```

The loadings:

```
res.pca$var$cor
```

```
##              Dim.1      Dim.2      Dim.3       Dim.4       Dim.5
## SIE.Su  0.08057735 -0.1786150  0.7413696 -0.39466187  0.40201850
## SIE.Au  0.78463426  0.1601660 -0.1358873 -0.02360527 -0.28475060
## SIE.Wi  0.74444946  0.3787178  0.1390330  0.26085759 -0.10566944
## SIE.Sp  0.06940453  0.6505897 -0.2874635  0.14838490  0.63297890
## SOI     0.50126942 -0.5519112 -0.1726551  0.02166076  0.40463998
```

```
## T.Su   -0.64091072  0.1741091  0.1976988 -0.02932482 -0.29134793
## T.au   -0.69128327  0.3642634  0.1570772  0.27691731  0.17674456
## T.wi   -0.49668781 -0.3960426 -0.5808892 -0.03417841  0.08316850
## T.sp   -0.01138968 -0.4367718  0.2940550  0.82282616  0.02694411
##              Dim.6       Dim.7       Dim.8       Dim.9
## SIE.Su  0.20439145  0.16833601  0.15205046 -0.03696014
## SIE.Au  0.32726859  0.07959270  0.31757770  0.21046404
## SIE.Wi  0.33851943 -0.03721296 -0.08556715 -0.28376578
## SIE.Sp  0.00660304  0.22829056 -0.08806289  0.08176243
## SOI     0.34355549 -0.29450675 -0.19246270  0.09112650
## T.Su    0.56425618  0.10752351 -0.30114518  0.11600140
## T.au    0.20978102 -0.36666032  0.27977904  0.01097100
## T.wi    0.38613805  0.19899778  0.18999768 -0.16165470
## T.sp   -0.04458262  0.19690112  0.03311646  0.05485501
```

Re-project each covariate on each principal component:

```r
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 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.

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)
geese = read_inp("females_petrel.inp")
petrel.ch = geese$encounter_histories
freq = geese$sample_size
test3sr(petrel.ch, freq)
```

```
## $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
```

```r
test3sm(petrel.ch, freq)

## $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.ch, freq)

## $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.ch, freq)
```

```
## $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
```

```
overall_CJS(petrel.ch, freq)
```

```
##                             chi2 degree_of_freedom p_value
## Gof test for CJS model: 221.211               127       0
```

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):

```
# let's read in the data:
library(RMark)
```

```
## This is RMark 2.2.0
```

```
petrel=convert.inp("females_petrel")
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),out
put = FALSE,delete=T)
# phit,p
phitp =
```

```r
mark(petrel.processed,petrel.ddl,model.parameters=list(Phi=Phitime,p=pdot),ou
tput = FALSE,delete=T)
# phi,pt
phipt =
mark(petrel.processed,petrel.ddl,model.parameters=list(Phi=Phidot,p=ptime),ou
tput = FALSE,delete=T)
# phit,pt
phitpt =
mark(petrel.processed,petrel.ddl,model.parameters=list(Phi=Phitime,p=ptime),o
utput = FALSE,delete=T)
```

Compare models

```r
collect.models()

##                          model npar     AICc DeltaAICc       weight Deviance
## 4 Phi(~time)p(~time + td)   59 6535.213   0.00000 1.000000e+00 6414.843
## 2    Phi(~1)p(~time + td)   31 6580.016  44.80257 1.867433e-10 6517.358
## 3        Phi(~time)p(~td)   31 7035.196 499.98207 0.000000e+00 6972.538
## 1           Phi(~1)p(~td)    3 7141.081 605.86732 0.000000e+00 7135.073
```

Clearly, there is time variation in the detection process. Also, it's worth investigating further time variation in survival.

Now, let's fit a model with all covariates:

```r
phixpt =
mark(petrel.processed,petrel.ddl,model.parameters=list(Phi=PhiCov,p=ptime),ou
tput = FALSE,delete=T)
```

And have a look to the parameter estimates:

```r
phixpt$results$beta

##                     estimate        se        lcl        ucl
## Phi:(Intercept)  3.0215060 0.1266494  2.7732732  3.2697387
## Phi:x1          -0.0214620 0.1238117 -0.2641330  0.2212090
## Phi:x2           0.5045047 0.2437983  0.0266601  0.9823493
## Phi:x3          -0.5050284 0.2135734 -0.9236323 -0.0864245
## Phi:x4          -0.1875423 0.1633858 -0.5077786  0.1326939
## Phi:x5          -0.3384231 0.1285901 -0.5904597 -0.0863865
## Phi:x6           0.0366714 0.1194053 -0.1973630  0.2707058
## Phi:x7           0.4200922 0.2218835 -0.0147995  0.8549838
## Phi:x8          -0.5388505 0.1450639 -0.8231758 -0.2545252
## Phi:x9          -0.1858380 0.1744092 -0.5276800  0.1560040
## p:(Intercept)   -0.2762016 0.3517732 -0.9656772  0.4132739
## p:time1976       1.4053160 0.5014804  0.4224145  2.3882176
## p:time1977       1.1939140 0.4353712  0.3405864  2.0472416
## p:time1978      -1.3620914 0.3973730 -2.1409425 -0.5832403
## p:time1979       0.8851054 0.4070028  0.0873800  1.6828308
## p:time1980      -1.3972451 0.4108840 -2.2025777 -0.5919125
## p:time1981      -0.8393193 0.4093394 -1.6416245 -0.0370140
```

```
## p:time1982      -1.4862613 0.4314627 -2.3319283 -0.6405944
## p:time1983       1.0600652 0.4127852  0.2510062  1.8691243
## p:time1984       0.4538497 0.3939467 -0.3182859  1.2259853
## p:time1985      -1.0119075 0.3845536 -1.7656325 -0.2581824
## p:time1986       0.0048380 0.3854982 -0.7507385  0.7604144
## p:time1987      -1.0459663 0.3889723 -1.8083521 -0.2835805
## p:time1988       0.5125816 0.3873434 -0.2466114  1.2717746
## p:time1989       1.1524630 0.4016116  0.3653043  1.9396217
## p:time1990      -0.3716715 0.3782079 -1.1129590  0.3696161
## p:time1991       0.6520627 0.3844183 -0.1013973  1.4055227
## p:time1992       0.6618918 0.3825929 -0.0879902  1.4117739
## p:time1993       0.6817241 0.3839534 -0.0708246  1.4342728
## p:time1994       0.0532029 0.3753291 -0.6824423  0.7888480
## p:time1995       0.7756565 0.3815531  0.0278125  1.5235005
## p:time1996       1.6025804 0.4091014  0.8007416  2.4044192
## p:time1997       1.4893106 0.4097755  0.6861506  2.2924706
## p:time1998       0.4982627 0.3783074 -0.2432197  1.2397452
## p:time1999       1.4753226 0.4081407  0.6753668  2.2752784
## p:time2000       0.5117819 0.3840192 -0.2408957  1.2644595
## p:time2001      -0.1193226 0.3820433 -0.8681275  0.6294823
## p:time2002      -0.0079864 0.3829045 -0.7584793  0.7425064
## p:time2003       0.2303222 0.3862746 -0.5267761  0.9874204
## p:td             0.7281693 0.0827992  0.5658830  0.8904557
```

The covariates are in that order: SIE.Su (x1), SIE.Au (x2), SIE.Wi (x3), SIE.Sp (x4), SOI (x5), T.Su (x6), T.au (x7), T.wi (x8) and T.sp (x9). 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),ou
tput = FALSE,delete=T)
phipc2 =
mark(petrel.processed,petrel.ddl,model.parameters=list(Phi=Phipc2,p=ptime),ou
tput = FALSE,delete=T)
phipc3 =
mark(petrel.processed,petrel.ddl,model.parameters=list(Phi=Phipc3,p=ptime),ou
tput = FALSE,delete=T)
phipc4 =
mark(petrel.processed,petrel.ddl,model.parameters=list(Phi=Phipc4,p=ptime),ou
tput = FALSE,delete=T)
phipc5 =
mark(petrel.processed,petrel.ddl,model.parameters=list(Phi=Phipc5,p=ptime),ou
tput = FALSE,delete=T)
phipc6 =
mark(petrel.processed,petrel.ddl,model.parameters=list(Phi=Phipc6,p=ptime),ou
tput = FALSE,delete=T)
phipc7 =
mark(petrel.processed,petrel.ddl,model.parameters=list(Phi=Phipc7,p=ptime),ou
tput = FALSE,delete=T)
phipc8 =
mark(petrel.processed,petrel.ddl,model.parameters=list(Phi=Phipc8,p=ptime),ou
tput = FALSE,delete=T)
phipc9 =
mark(petrel.processed,petrel.ddl,model.parameters=list(Phi=Phipc9,p=ptime),ou
tput = 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)
stat

## [1] 0.4561618 2.0348053 7.3439558 3.0089184 3.0594652 2.4351876 0.1359247
## [8] 0.3111153 0.7808127

df1

## [1] 1 1 1 1 1 1 1 1 1

df2

## [1] 27 27 27 27 27 27 27 27 27

pval

## [1] 0.50516694 0.16519557 0.01154684 0.09421181 0.09162924 0.13028569
## [7] 0.71524166 0.58159232 0.38469346
```

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),ou
tput = FALSE,delete=T)
phipc21 =
mark(petrel.processed,petrel.ddl,model.parameters=list(Phi=Phipc2,p=ptime),ou
tput = FALSE,delete=T)
phipc31 =
mark(petrel.processed,petrel.ddl,model.parameters=list(Phi=Phipc3,p=ptime),ou
tput = FALSE,delete=T)
phipc41 =
mark(petrel.processed,petrel.ddl,model.parameters=list(Phi=Phipc4,p=ptime),ou
tput = FALSE,delete=T)
phipc51 =
mark(petrel.processed,petrel.ddl,model.parameters=list(Phi=Phipc5,p=ptime),ou
tput = FALSE,delete=T)
phipc61 =
mark(petrel.processed,petrel.ddl,model.parameters=list(Phi=Phipc6,p=ptime),ou
tput = FALSE,delete=T)
phipc71 =
mark(petrel.processed,petrel.ddl,model.parameters=list(Phi=Phipc7,p=ptime),ou
tput = FALSE,delete=T)
phipc81 =
mark(petrel.processed,petrel.ddl,model.parameters=list(Phi=Phipc8,p=ptime),ou
tput = 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)
stat

## [1] 0.115032061 2.935263243 4.629627302 2.517956493 3.502807470
0.275952354
## [7] 0.006486012 0.723243675

df1
```

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

df2

## [1] 26 26 26 26 26 26 26 26

pval

## [1] 0.73721058 0.09856598 0.04088835 0.12464492 0.07255722 0.60381802
## [7] 0.93642787 0.40284611
```

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),ou
tput = FALSE,delete=T)
phipc22 =
mark(petrel.processed,petrel.ddl,model.parameters=list(Phi=Phipc2,p=ptime),ou
tput = FALSE,delete=T)
phipc32 =
mark(petrel.processed,petrel.ddl,model.parameters=list(Phi=Phipc3,p=ptime),ou
tput = FALSE,delete=T)
phipc42 =
mark(petrel.processed,petrel.ddl,model.parameters=list(Phi=Phipc4,p=ptime),ou
tput = FALSE,delete=T)
phipc52 =
mark(petrel.processed,petrel.ddl,model.parameters=list(Phi=Phipc5,p=ptime),ou
tput = FALSE,delete=T)
phipc62 =
mark(petrel.processed,petrel.ddl,model.parameters=list(Phi=Phipc6,p=ptime),ou
tput = FALSE,delete=T)
phipc72 =
mark(petrel.processed,petrel.ddl,model.parameters=list(Phi=Phipc7,p=ptime),ou
tput = 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)
stat

## [1] 0.074403780 1.878326793 1.383423294 0.547418815 0.235266864
0.002265893
## [7] 1.282105461

df1

## [1] 1 1 1 1 1 1 1

df2

## [1] 25 25 25 25 25 25 25

pval

## [1] 0.7872701 0.1827058 0.2505979 0.4662660 0.6318690 0.9624122 0.2682518
```

No more significant PC, the algorithm stops here.

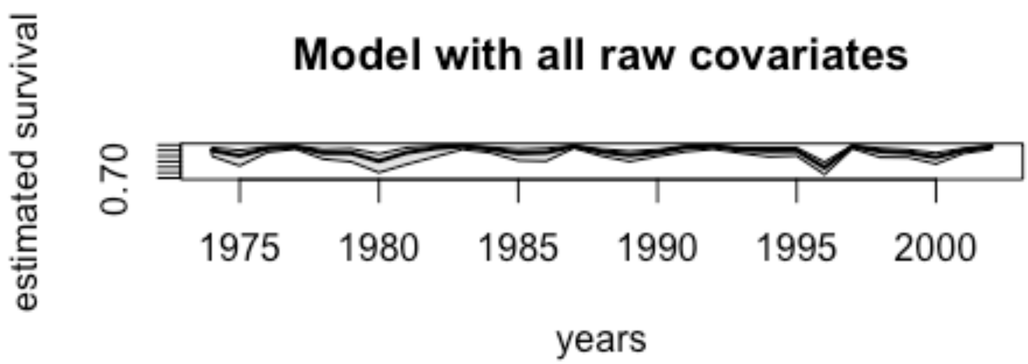
Post-process results

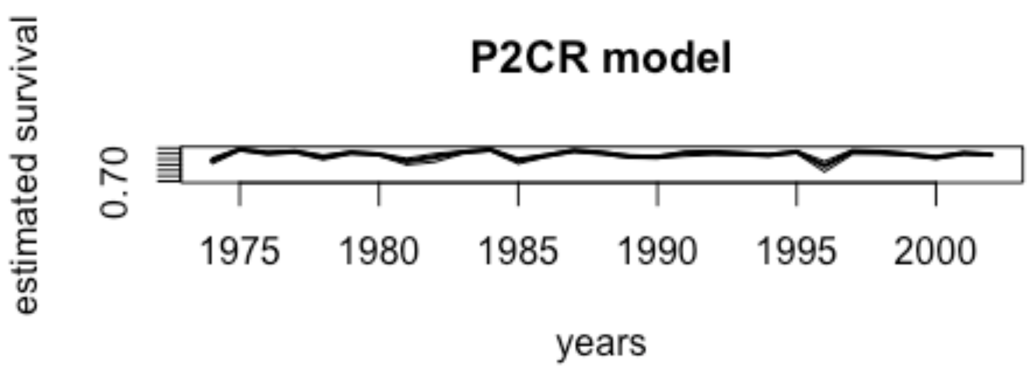
We will make two plots, one with time-varying survival estimates, and another oneto illustrate the relationship between survival and the selected PCs.

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)
par(mfrow=c(2,1))
plot(1974:2002,phicov_mle[,1],lwd=2,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=2,col='black')
#dev.off()
#png("time_survival_p2cr.png", width=6*ppi, height=6*ppi, res=ppi)
plot(1974:2002,phipca_mle[,1],lwd=2,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=2,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)  2.9065522 0.0930351  2.7242034  3.0889011
## Phi:pc4         -0.3179564 0.0937600 -0.5017259 -0.1341868
## Phi:pc3          0.4987761 0.1117003  0.2798436  0.7177086
```

Get estimates of recapture probabilities:

```
# recapture given no recapture before
lp1=phipc31$results$beta$estimate[4] + phipc31$results$beta$estimate[5:32]
p1 = 1/(1+exp(-lp1))
p1

##  [1] 0.6849746 0.6950760 0.1598929 0.6532750 0.1491627 0.2186214 0.1380855
##  [8] 0.6799233 0.5559293 0.2101191 0.4365717 0.2081893 0.5650886 0.7013967
## [15] 0.3322997 0.5843022 0.5899870 0.6135584 0.4454385 0.6270107 0.7892102
## [22] 0.7614159 0.5662430 0.7626795 0.5415127 0.3768231 0.4066767 0.4896963

# recapture given recapture before
lp2=phipc31$results$beta$estimate[4]+phipc31$results$beta$estimate[5:32]+phip
c31$results$beta$estimate[33]
p2 = 1/(1+exp(-lp2))
p2

##  [1] 0.8225429 0.8293322 0.2886228 0.8006576 0.2720513 0.3736066 0.2545787
##  [8] 0.8191149 0.7274257 0.3618683 0.6228953 0.3591785 0.7347356 0.8335364
## [15] 0.5147810 0.7497732 0.7541472 0.7719294 0.6313063 0.7818290 0.8886588
## [22] 0.8718483 0.7356503 0.8726249 0.7157297 0.5631334 0.5936855 0.6716644

# get min/max for p1 with SEs
ind.min = which.min(p1) # index min p1
ind.max = which.max(p1) # index max p1
varlp1 = phipc31$results$beta$se[4]^2 + phipc31$results$beta$se[5:32]^2 # var
of p1 on logit scale
lp1mi = lp1[ind.min]
varlp1mi = varlp1[ind.min]
library(msm)
sep1mi = deltamethod(~ 1/(1+exp(-x1)), lp1mi, varlp1mi)
min(p1)

## [1] 0.1380855

sep1mi

## [1] 0.06613978

lp1ma = lp1[ind.max]
varlp1ma = varlp1[ind.max]
sep1ma = deltamethod(~ 1/(1+exp(-x1)), lp1ma, varlp1ma)
max(p1)

## [1] 0.7892102

sep1ma

## [1] 0.08957517

# get min/max for p2 with SEs
ind.min = which.min(p2) # index min p2
```

```
ind.max = which.max(p2) # index max p2
varlp2 = phipc31$results$beta$se[4]^2 + phipc31$results$beta$se[5:32]^2 +
phipc31$results$beta$estimate[33]^2# var of p2 on logit scale
lp2mi = lp2[ind.min]
varlp2mi = varlp2[ind.min]
sep2mi = deltamethod(~ 1/(1+exp(-x1)), lp2mi, varlp2mi)
min(p2)

## [1] 0.2545787

sep2mi

## [1] 0.1781984

lp2ma = lp2[ind.max]
varlp2ma = varlp2[ind.max]
sep2ma = deltamethod(~ 1/(1+exp(-x1)), lp2ma, varlp2ma)
max(p2)

## [1] 0.8886588

sep2ma

## [1] 0.0919113
```

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)))
```

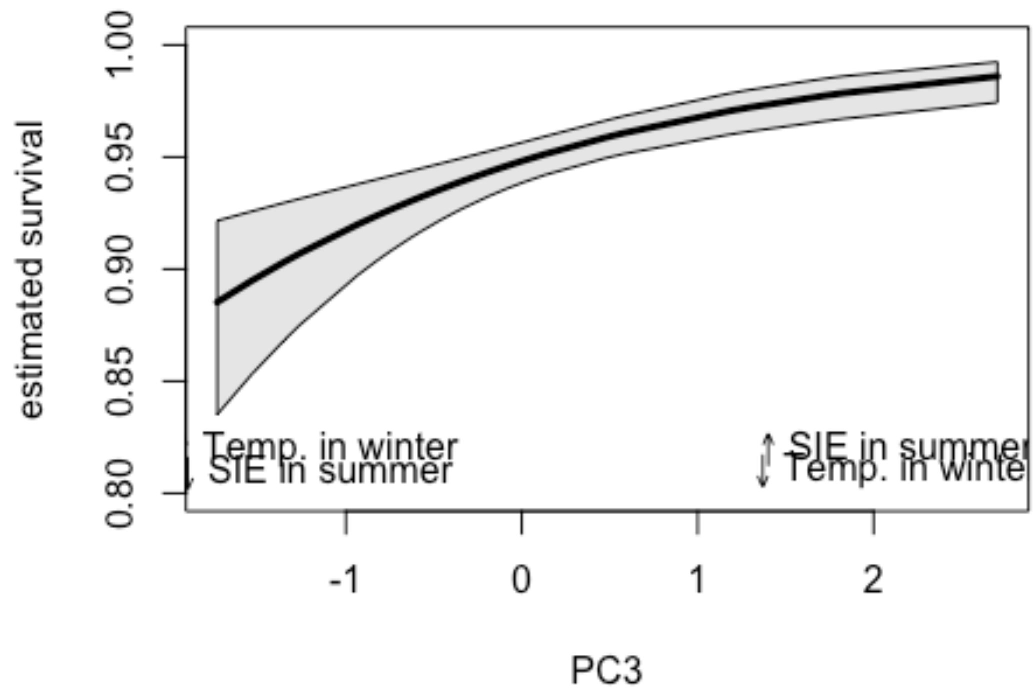
Before plotting the survival as a function of the PC values, we need to find out about the raw covariates that were used to build these PCs:

```
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
```

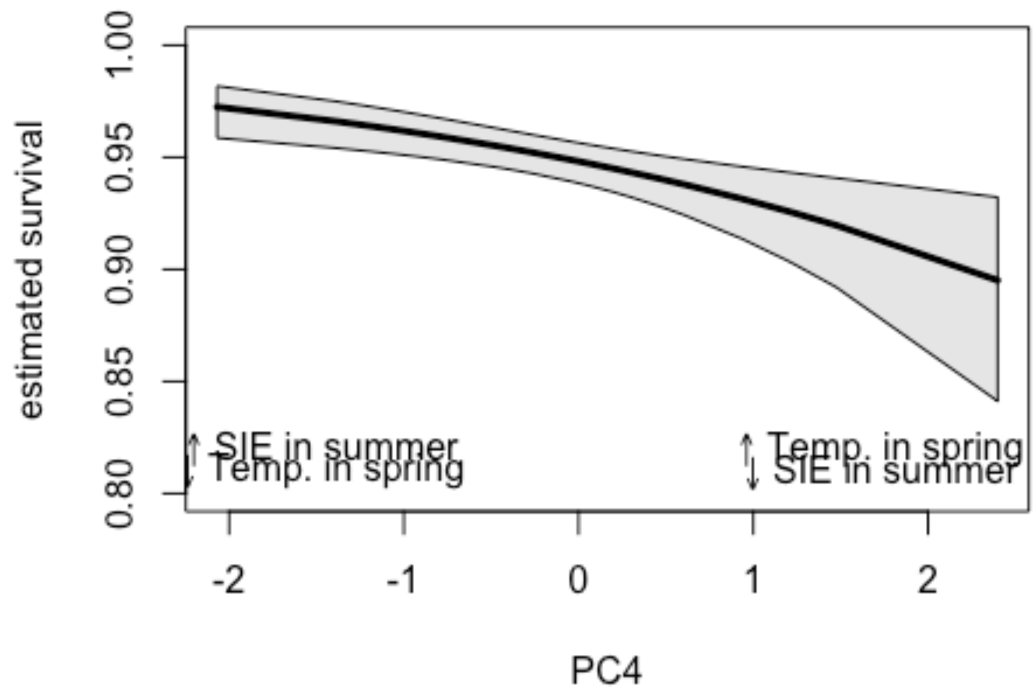
High (resp. low) values of PC3 mean high (resp. low) values of SIE in summer and low (resp. high) values of temperature in winter. High (resp. low) values of PC4 mean high (resp. low) values of temperature in spring and low (resp. high) values of SIE in summer.

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)
```



estimated survival
1.00
0.95
0.90
0.85
0.80
↑ SIE in summer
↓ Temp. in spring
↑ Temp. in spring
↓ SIE in summer
-2
-1
0
1
2
PC4


```
#dev.off()
```