Analysis of Directional Data

Brett Presnell

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Examples

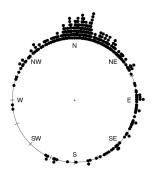
Wish to analyze data in which response is a "direction":

- 2d directional data are called circular data
- 3d directional data are called spherical data
- not all "directional" data are directions in the usual sense
- "directional" data may also arise in higher dimensions

Wind Directions

- Recorded at Col de la Roa, Italian Alps
- ▶ n = 310 (first 40 listed below)
- ▶ Radians, clockwise from north
- Source: Agostinelli (CSDA 2007); also R package circular

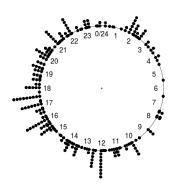
6.23	1.03	0.15	0.72	2.20
0.46	0.63	1.45	0.37	1.95
0.08	0.15	0.33	0.09	0.09
6.23	0.05	6.14	6.28	6.17
6.24	6.02	6.14	6.25	0.01
5.38	5.30	5.63	0.77	1.34
6.14	0.22	6.23	2.33	3.61
0.49	6.12	0.01	0.00	0.46



Arrival Times at an ICU

- ▶ 24-hour clock times (format hrs.mins)
- ▶ n = 254 (first 32 listed below)
- ► Source: Cox & Lewis (1966); also Fisher (1993) and R package circular

11.00	17.00	23.15	10.00
12.00	8.45	16.00	10.00
15.30	20.20	4.00	12.00
2.20	12.00	5.30	7.30
12.00	16.00	16.00	1.30
11.05	16.00	19.00	17.45
20.20	21.00	12.00	12.00
18.00	22.00	22.00	22.05



Primate Vertebrae

- Orientation of left superior facet of last lumbar vertebra in humans, gorillas, and chimpanzees
- Source: Keifer (2005 UF Anthropology MA Thesis)

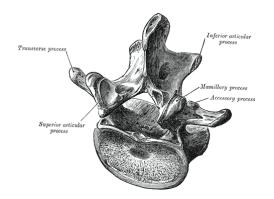


Figure : Human lumbar vertebra with right superior facet labelled as superior articulate process.

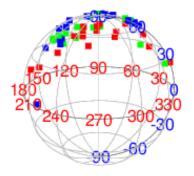


Figure: Orientation of left superior facets for samples of 18 chimpanzees (red), 16 gorillas (green) and 19 humans (blue).

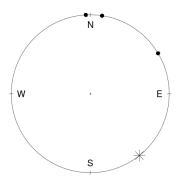
Butterfly Migrations

- Direction of travel observed for 2649 migrating butterflies in Florida
- Source: Thomas J Walker, University of Florida, Dept of Entomology and Nematology
- Other variables:
 - site: 23 locations in Florida
 - observer: Thomas Walker (tw) or James J. Whitesell (jw)
 - species: cloudless sulphur (cs), gulf fritillary (gf), long-tailed skipper (lt)
 - distance to coast (km)
 - date and time of observation
 - percentage of sky free of clouds
 - quality of sunlight: (b)right, (h)aze, (o)bstructed, (p)artly obstructed
 - presence/absence and direction (N, NE, E, SE, S, SW, W, NW) of wind
 - temperature



Why is the Analysis of Directional Data Different?

- ► First three observations from the wind directions data: 6.23, 1.03, 0.15
- ▶ The mean of these three numbers is 2.47
- ► What do you think?



Graphical Display of Circular Data (in R)

Have already seen simple dot plots for circular data, e.g., for the wind data:

```
windc <- circular(wind, type="angles", units="radians",</pre>
 1
                       template="geographics")
2
    require("circular")
3
    par(mar=c(0,0,0,0)+0.1, oma=c(0,0,0,0)+0.1)
    plot(windc, cex=1.5, axes=FALSE,
5
          bin=360, stack=TRUE, sep=0.035, shrink=1.3)
6
    axis.circular(at=circular(seq(0, (7/4)*pi, pi/4),
7
                       template="geographics"),
8
                   labels=c("N","NE","E","SE","S","SW","W","NW"),
9
                   cex=1.4)
10
    ticks.circular(circular(seq(0, (15/8)*pi, pi/8)),
11
                    zero=pi/2, rotation="clock",
12
                    tcl=0.075)
13
```

and for the ICU data:

```
## Note that pch=17 does not work properly here.
par(mar=c(0,0,0,0)+0.1, oma=c(0,0,0,0)+0.1)
plot(fisherB1c, cex=1.5, axes=TRUE,
bin=360, stack=TRUE, sep=0.035, shrink=1.3)
```

and one more

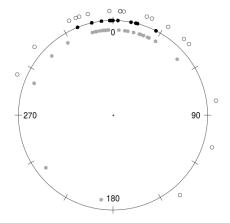


Figure : Walking directions of long-legged desert ants under three different experimental conditions:

```
par(mar=c(0,0,0,0)+0.1, oma=c(0,0,0,0)+0.1)
1
    plot(fisherB10c$set1, units="degrees", zero=pi/2,
3
         rotation="clock", pch=16, cex=1.5)
    ticks.circular(circular(seq(0, (11/6)*pi, pi/6)),
4
                    zero=pi/2, rotation="clock", tcl=0.075)
5
    points(fisherB10c$set2, zero=pi/2,
6
           rotation="clock", pch=16, col="darkgrey",
           next.points=-0.1, cex=1.5)
8
    points(fisherB10c$set3, zero=pi/2,
9
           rotation="clock", pch=1,
10
           next.points=0.1, cex=1.5)
```

11

Circular Histograms

► Circular histograms exist (see Fisher and Mardia and Jupp) but is there a ready-made function in R?

Rose Diagrams

- Invented by Florence Nightingale (elected first female member of the Royals Statistical Society in 1859; honorary member of ASA)
- Nightingale's rose in R (see also this post and the R graph catalog)
- ▶ Note that radii of segments are proportional to *square root* of the frequencies (counts), so that areas are proportional to frequencies. Is this the right thing to do?
- ► Rose diagrams suffer from the same problems as histograms. The impression conveyed may depend strongly on:
 - the binwidth of the cells
 - the choice of starting point for the bins

Adding a Rose Diagram to the Plot of Wind Directions

```
rose.diag(windc, bins=16, col="darkgrey",
cex=1.5, prop=1.35, add=TRUE)
```

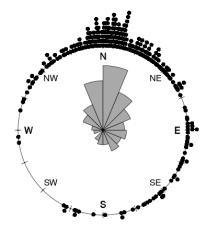
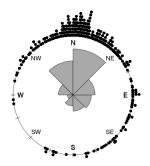
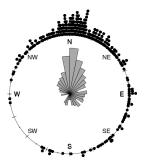


Figure: Wind direction data with rose diagram with segment areas are proportional to counts (segment radii are proportional to square roots of counts).

Changing the Binwidth





Changing the Radii

▶ I think that the default "radii proportional to counts" is generally best, but this is not always obvious. The scale certainly makes a big difference however.

```
rose.diag(windc, bins=16, col="darkgrey",
radii.scale="linear",
cex=1.5, prop=2.4, add=TRUE)
```

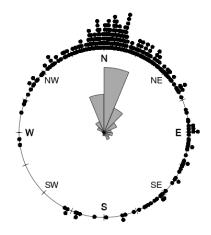


Figure: Wind direction data with rose diagram (segment radii proportional to counts).

Kernel Density Estimates

```
lines(density.circular(windc, bw=40), lwd=2, lty=1)
```

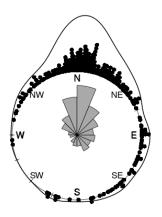


Figure : Wind direction data with rose diagram and kernel density estimate.

Spherical Data

▶ Are there any canned routines for plotting spherical data in R?

Mean Direction and Mean Resultant Length

First three observations from the wind directions data:

- resultant (sum of direction vectors): (0.952, 2.5)
- mean vector: $(\bar{x}, \bar{y}) = (0.317, 0.833)$
- ▶ resultant length (Euclidean norm of resultant): R = 2.675
- mean resultant length: $\bar{R} = 0.892$
- mean direction: $(\bar{x}, \bar{y})/\bar{R} = (0.356, 0.934)$
- $ightharpoonup ilde{ heta} = 0.364$

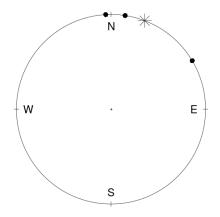


Figure : First three observations from the wind directions data and their sample mean direction.

Generating Random Points on the Sphere

- ▶ Wish to generate a random "direction" in d-dimensions; i.e., an observation from the uniform distribution in the d-1 sphere.
- ▶ Usual way: let $X \sim N_d(0, I)$ and return U = X/||X||.
- An alternative rejection sampler:
 - ► Repeat until ||X|| <= 1
 - Let X be uniformly distributed on the cube [-1,1]^d
 - Return U = X/||X||
- What is the acceptance rate for the rejection sampler:
 - ▶ Volume of the d-1 sphere is $\pi^{d/2}/\Gamma(d/2+1)$
 - ▶ Volume of [-1,1]^d is 2^d
 - Acceptance rate is $(\pi^{1/2}/2)^d/\Gamma(d/2+1)$
 - Curse of dimensionality

dimension 2 3 4 5 6 7 8 9 10 accept rate (%) 79 52 31 16 8 4 2 1 0

```
runifSphere <- function(n, dimension, method=c("norm", "cube", "slownorm")) {</pre>
 1
         method <- match.arg(method)</pre>
 2
 3
         if (method=="norm") {
              u <- matrix(rnorm(n*dimension), ncol=dimension)</pre>
              u \leftarrow sweep(u, 1, sqrt(apply(u*u, 1, sum)), "/")
 5
         } else if (method=="slownorm") {
              u <- matrix(nrow=n, ncol=dimension)
              for (i in 1:n) {
 8
                  x <- rnorm(dimension)
9
                  xnorm <- sqrt(sum(x^2))</pre>
10
                  u[i,] <- x/xnorm
11
12
13
         } else {
14
              u <- matrix(nrow=n, ncol=dimension)</pre>
              for (i in 1:n) {
15
                  x <- runif(dimension, -1, 1)
16
                  xnorm <- sqrt(sum(x^2))</pre>
17
                  while (xnorm > 1) {
18
                       x <- runif(dimension, -1, 1)
19
20
                       xnorm <- sqrt(sum(x^2))</pre>
                   }
21
22
                  u[i,] <- x/xnorm
23
24
25
26
```

Easy fix for Borel's paradox in 3-d

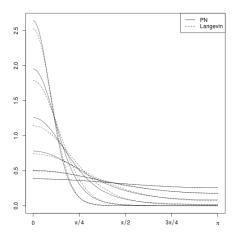
Take longitude $\phi \sim U(0, 2\pi)$ independent of latitude $\theta = \arcsin(2U-1), \ U \sim U(0,1).$

Comparison of Projected Normal and Langevin Distributions

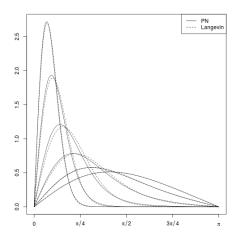
One way that we might compare the (μ,κ) and $(\gamma\mu,I)$ distributions by choosing κ and γ to give the same mean resultant lengths and comparing the densities of the cosine of the angle θ between U and μ .

Of course matching mean resultant lengths is not necessarily the best way to compare these families of distributions.

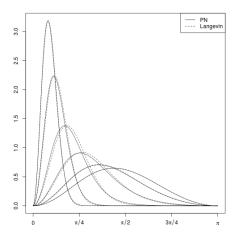
d=2



d = 3



d = 4



Gould's Model

A.k.a., the barber pole model.

Gould's Model: Likelihood

Calculate the (profile) log-likelihood for Gould (1969 Biometrics) model for simple (single predictor) regression with an intercept. For fixed "slope" β , this function "profiles out" (maximizes over) the "intercept" term and optionally the concentration parameter κ .

```
loglklhd.gould <- function(beta, theta, x, do.kappa=FALSE) {</pre>
1
         res <- sapply(beta,
                        function(b, th, x) {
3
                            sqrt(sum(cos(th - b*x))^2
4
                                  + sum(sin(th - b*x))^2)
5
6
                        },
                        th=theta, x=x)
7
         if (do.kappa) {
8
             n <- length(theta)
             kappa <- sapply(res/n, imrlLvMF, dimen=2)</pre>
10
             res <- n*log(constLvMF(kappa, dimen=2)) + kappa*res
11
         }
12
13
         res
14
```

Gould's Model with Equally Spaced X

```
alpha <- 0
    beta <- 1
2
    kappa = 2.5
3
    x < - seq(-1, 1, length=10)
4
    mu <- as.circular((alpha + beta*x) %% (2*pi))</pre>
5
    theta <- as.circular(mu + rvonmises(length(mu), mu=0, kappa=kappa))
6
    period <- 2*pi/(min(diff(sort(x)))) # Useful only for lattice x</pre>
7
    nperiods <- 1
8
    curve(loglklhd.gould(beta, theta, x, do.kappa), xname="beta",
9
           xlim=beta + nperiods*period*c(-1.125,1.125), n=nperiods*200,
10
          xlab=expression(beta),
11
           ylab="Log-Likelihood")
12
    abline(v = beta + ((-nperiods):nperiods)*period, lty=3) # for lattice x
13
```

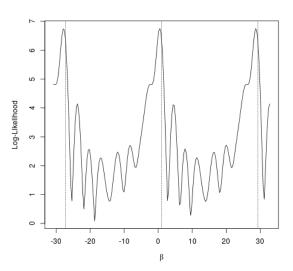


Figure : Gould's model log-likelihood with n=10 equally-spaced x's; κ not profiled out.

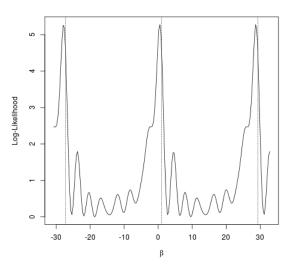


Figure : Gould's model log-likelihood with n=10 equally-spaced x's; κ profiled out.

Gould's Model with Random X: Data Generation

```
1 alpha <- 0
2 beta <- 1
3 kappa = 2.5
4 x <- rnorm(10)
5 mu <- as.circular((alpha + beta*x) %% (2*pi))
6 theta <- as.circular(mu + rvonmises(length(mu), mu=0, kappa=kappa))</pre>
```

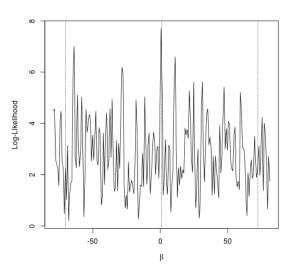


Figure : Gould's model log-likelihood with n=10 random normal x's; κ not profiled out.

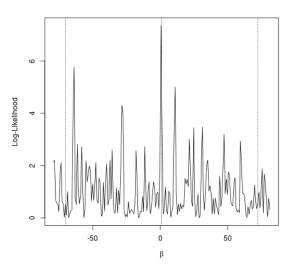


Figure : Gould's model log-likelihood with n=10 random normal x's; κ profiled out.

Fisher-Lee Model: Likelihood

Calculate the (profile) log-likelihood for the Fisher-Lee (1992) Biometrics) model. For fixed "slope" β , this function "profiles out" (maximizes over) the "intercept" term and optionally the concentration parameter κ . Computing this with biggish matrix multiplies instead of using apply() or looping.

```
loglklhdFisherLee <- function(beta, theta, X, do.kappa=FALSE) {</pre>
         n <- length(theta)</pre>
         nbeta <- dim(beta)[2]
3
         if (\dim(X)[1] != n) {
             stop("Number of rows of X must equal length of theta.")
         }
         if (dim(beta)[1] != dim(X)[2]) {
             stop("Number of rows of beta must equal number of columns of X")
8
         }
         dev <- theta - 2*atan(X %*% beta)
10
         res <- sqrt(apply(cos(dev), 2, sum)^2
11
                      + apply(sin(dev), 2, sum)^2)
12
         if (do.kappa) {
13
             kappa <- sapply(res/n, imrlLvMF, dimen=2)</pre>
14
             res <- n*log(constLvMF(kappa, dimen=2)) + kappa*res
15
16
17
         res
18
```

Fisher-Lee Model with Random X: Data Generation

```
1 alpha <- 0
2 beta <- 1
3 kappa = 2.5
4 x <- rnorm(10)
5 mu <- as.circular(alpha + 2*atan(beta*x))
6 theta <- as.circular(mu + rvonmises(length(mu), mu=0, kappa=kappa))</pre>
```

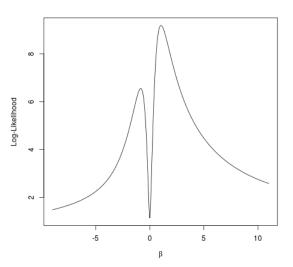


Figure : Fisher-Lee model log-likelihood with n=10 random normal x's; κ not profiled out.

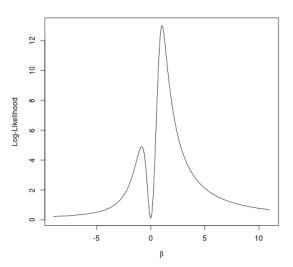


Figure : Fisher-Lee model log-likelihood with n=10 random normal x's; κ profiled out.

Blue Periwinkles

```
periwinkles <- read.table(datafile("periwinkle.txt"), header=TRUE)</pre>
```

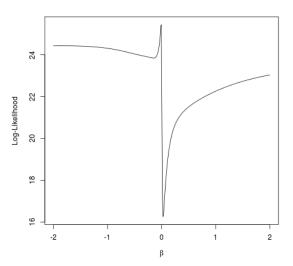


Figure : Fisher-Lee model log-likelihood for periwinkle data; κ not profiled out.

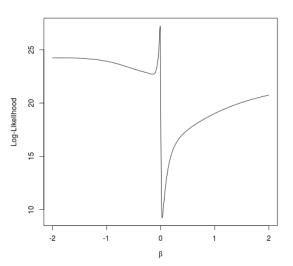


Figure : Fisher-Lee model log-likelihood for periwinkle data; κ profiled out.

Fisher-Lee Model with Two Predictors

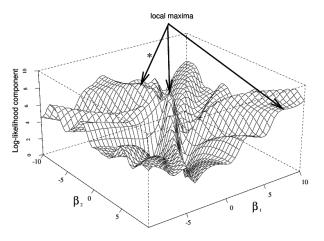


Figure : Fisher-Lee profile log-likelihood for a simulated data set with n = 10, κ = 1.0, β_1 = 0.1, and β_2 = 0.1. The global maximum is indicated by an asterisk.