广义线性地统计模型及其应用

黄湘云

目录

1 研究意义

广义线性混合模型具有广泛的应用，冈比亚的疟疾流行度分析，城市的重金属污染分析

2   论文综述

主要参考书籍 Diggle and Ribeiro Jr (2007) 和 Blangiardo and Cameletti (2015)，广义线性地统计模型在疟疾流行度分析中的应用 Diggle and Giorgi (2016) 及基于似然方法的软件实现 Ribeiro Jr and Diggle (2016)、Christensen and Ribeiro Jr (2002) 和 Giorgi and Diggle (2016) ，广义线性混合效应模型 Bates et al. (2015) 和非线性混合模型 Pinheiro et al. (2016) 在空间数据分析中的应用，集成嵌套拉普拉斯近似方法 (INLA) Havard Rue and Chopin (2009) 及软件实现 Finn Lindgren (2015) 。

3   探索性分析

3.1   某城市重金属污染分析

导入数据

```
> cumcm2011A <- readRDS("data/cumcm2011A.RDS")
> str(cumcm2011A)
```

```
'data.frame':    319 obs. of  12 variables:
 $ x   : num  74 1373 1321 0 1049 ...
 $ y   : num  781 731 1791 1787 2127 ...
 $ z   : num  5 11 28 4 12 6 15 7 22 7 ...
 $ area: num  4 4 4 2 4 2 4 2 4 4 ...
 $ As  : num  7.84 5.93 4.9 6.56 6.35 ...
 $ Cd  : num  154 146 439 224 525 ...
 $ Cr  : num  44.3 45 29.1 40.1 59.4 ...
 $ Cu  : num  20.6 22.5 64.6 25.2 117.5 ...
 $ Hg  : num  266 86 109 950 800 1040 121 13500 16000 63 ...
 $ Ni  : num  18.2 17.2 10.6 15.4 20.2 28.2 17.8 41.7 25.8 21.7 ...
 $ Pb  : num  35.4 36.2 74.3 32.3 170 ...
 $ Zn  : num  72.3 94.6 218.4 117.3 726 ...
```

```
> head(cumcm2011A)
```

	x	y	z	area	As	Cd	Cr	Cu	Hg	Ni	Pb	Zn
1	74	781	5	4	7.84	153.8	44.31	20.56	266	18.2	35.38	72.35
2	1373	731	11	4	5.93	146.2	45.05	22.51	86	17.2	36.18	94.59
3	1321	1791	28	4	4.90	439.2	29.07	64.56	109	10.6	74.32	218.37
4	0	1787	4	2	6.56	223.9	40.08	25.17	950	15.4	32.28	117.35

```
5 1049 2127 12    4  6.35  525.2 59.35 117.53  800 20.2 169.96 726.02
6 1647 2728  6    2 14.08 1092.9 67.96 308.61 1040 28.2 434.80 966.73
```

加载必要的 **R** 包，设置字体

```r
> library(RColorBrewer)
> library(viridis)
> library(sysfonts)
> library(showtext)
> font.add("AdobeKaitiStd",regular="C:/Windows/Fonts/AdobeKaitiStd-Regular.otf")
> font.add("arial",regular="C:/Windows/Fonts/arial.ttf")
```

```r
> par(mar = c(4, 4, .5, .5),family="arial")
> mba.int <- MBA::mba.surf(cumcm2011A[,1:3],100, 100, extend=TRUE)$xyz.est
> image(mba.int,axes=FALSE, col = viridis(100,begin = 0.2, end = .8))
> contour(mba.int, levels = seq(0, 200, by = 20),add = TRUE, col = "orange")
> axis(1,at=seq(from=0,to=30000,by=2500),labels=seq(from=0,to=30,by=2.5))
> axis(2,at=seq(from=0,to=20000,by=2500),labels=seq(from=0,to=20,by=2.5))
> title(xlab = " 横坐标（千米）",ylab = " 纵坐标（千米）",family="AdobeKaitiStd")
```

```r
> par(mar = c(4, 4, .5, .5))
> with(cumcm2011A,{
+   plot(c(0,30000),c(0,20000),axes=FALSE,type = "n",
+        xlab = " 横坐标（千米）",ylab = " 纵坐标（千米）",family="AdobeKaitiStd")
+   abline(h=seq(from=0,to=20000,by=2500),v=seq(from=0,to=30000,by=2500),
+          lty=2,col="lightgray")
+   points(y ~ x,cex=As/5,
+          col=brewer.pal(5, "Set1")[unclass(area)],pch=16)
+   par(family="AdobeKaitiStd")
+   legend("top",legend = c(" 生活区"," 工业区"," 山区"," 交通区"," 公园绿地区"),
+          col = brewer.pal(5, "Set1"),pch = 16,box.col = "gray",horiz = TRUE)
+   par(family="arial")
+   legend( 0,17500,legend = seq(from=.5,to=2.5,by=.5)*5,border="gray",
+           pt.cex=seq(from=.5,to=2.5,by=.5),pch=16,box.col = "gray")
+   text(2500,17500," 浓度   \n（微克/克）",adj=c(0.7,-0.2),family="AdobeKaitiStd")
+   axis(1,at=seq(from=0,to=30000,by=2500),labels=seq(from=0,to=30,by=2.5),family="arial")
+   axis(2,at=seq(from=0,to=20000,by=2500),labels=seq(from=0,to=20,by=2.5),family="arial")
+ })
```
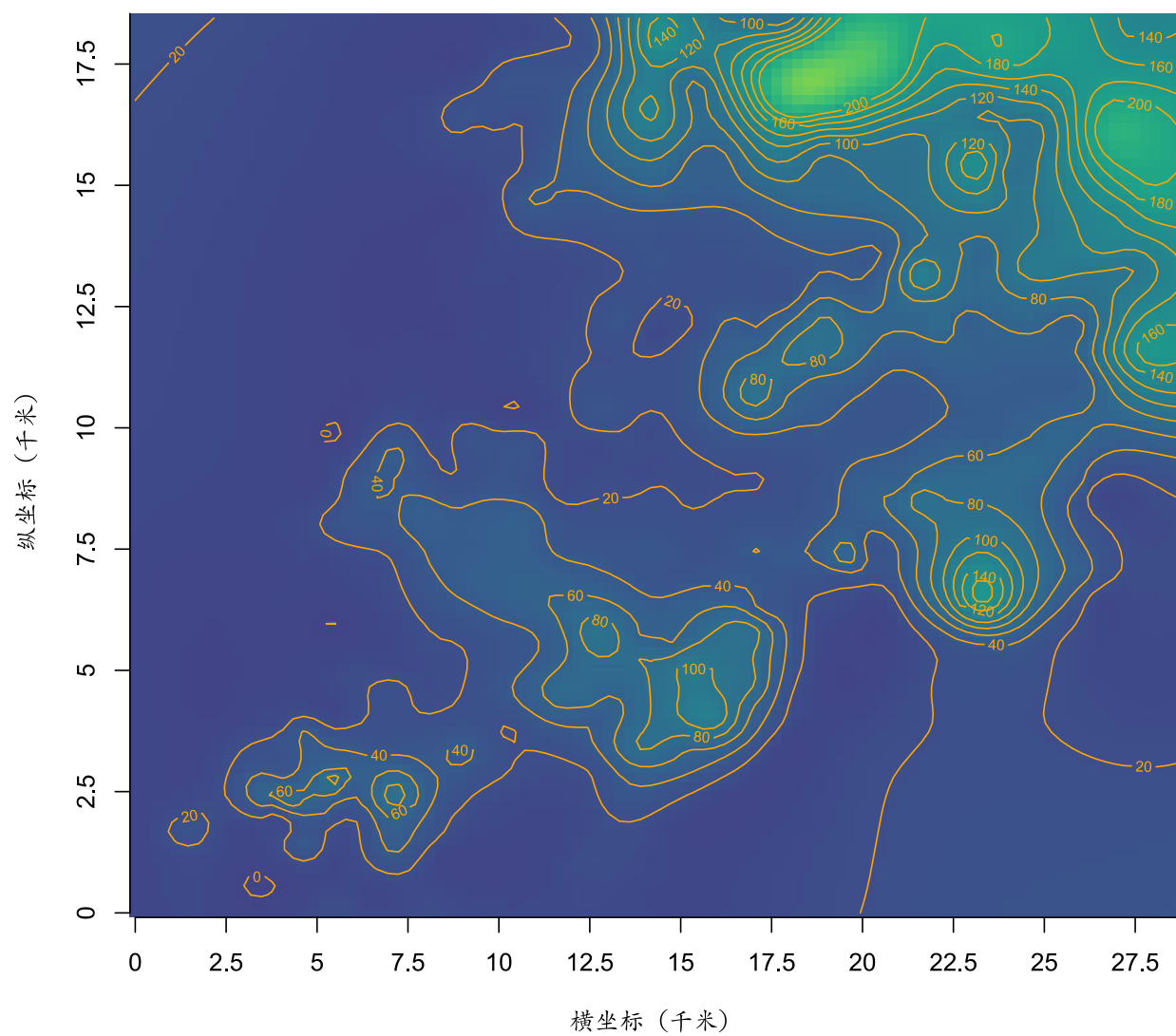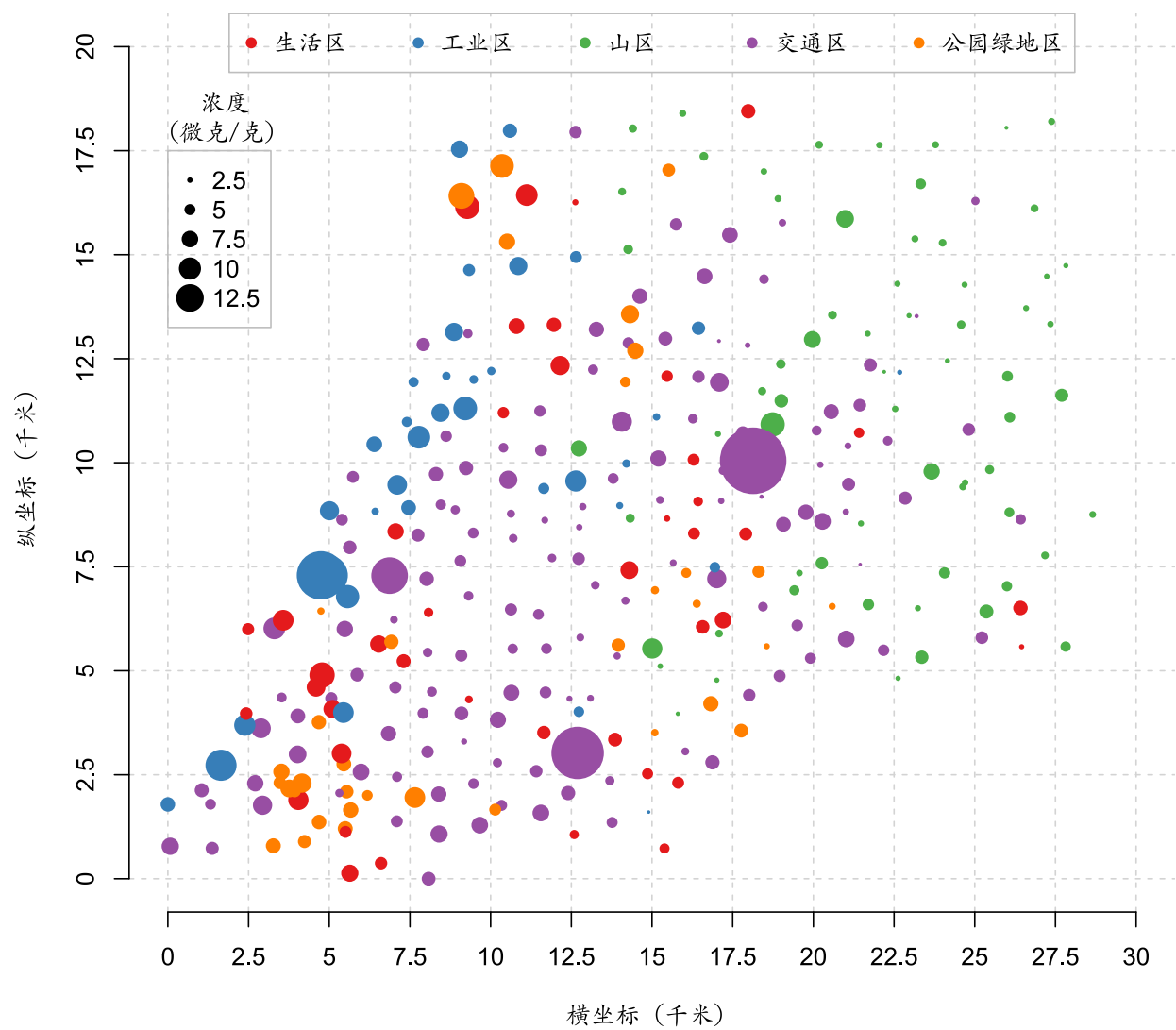
图 1: 城市等高线图

图 2: 金属砷的浓度分布

```
> par(mfrow=c(3,2),mar = c(4, 4, .5, .5))
> with(cumcm2011A,{
+ for(i in seq(5)){
+   plot(c(0,310),c(1,31),axes=FALSE,type = "n",
+        xlab = " 海拔（米）",ylab = " 浓度（微克/克）",family="AdobeKaitiStd")
+   abline(v=seq(from=0,to=320,by=40),h=seq(from=0,to=32,by=4),
+          lty=2,col="lightgray")
+   points(As~z,subset=area == i,col=brewer.pal(5, "Set1")[unclass(area)],pch=16)
+   lines(lowess(subset(cumcm2011A,area == i,select=c(z,As))),col="Black",lwd=2)
+   axis(1,at=seq(from=0,to=320,by=40),family="arial")
+   axis(2,at=seq(from=0,to=32,by=4),family="arial")
+ }
+   plot(c(0,310),c(40,1640),axes=FALSE,type = "n",xlab="",ylab="")
+   par(family="AdobeKaitiStd")
+   legend("center",legend = c(" 生活区"," 工业区"," 山区"," 交通区"," 公园绿地区"),
+          col = brewer.pal(5, "Set1"),pch = 16,box.col = "white",horiz = FALSE)
+ })
```

3.1.1 预测任务

1. 重金属浓度最高的位置（最大值，污染源）
2. 重金属浓度超过给定值的区域（区间估计）
3. 重金属在某个区域的含量（积分）

3.2 冈比亚疟疾流行度分析

3.2.1 调查及数据描述

从冈比亚的 5 个区域，65 个村庄，共采集 2035 个 5 岁以下儿童的血液样本，并记录儿童的年龄，村庄的位置坐标，血液样本中是否含有疟疾寄生虫，儿童是否睡在蚊帐中，是否使用杀虫剂对蚊帐杀虫，村庄附近的绿色植物的绿色度，村庄是否有健康中心。变量如下：

- (x, y) 村庄的坐标
- pos 血样中是否出现疟疾（1 是 0 否）
- age 儿童的年龄（按天计算）
- netuse 儿童是否睡在蚊帐中（1 是 0 否）
- treated 蚊帐是否杀虫（1 是 0 否）
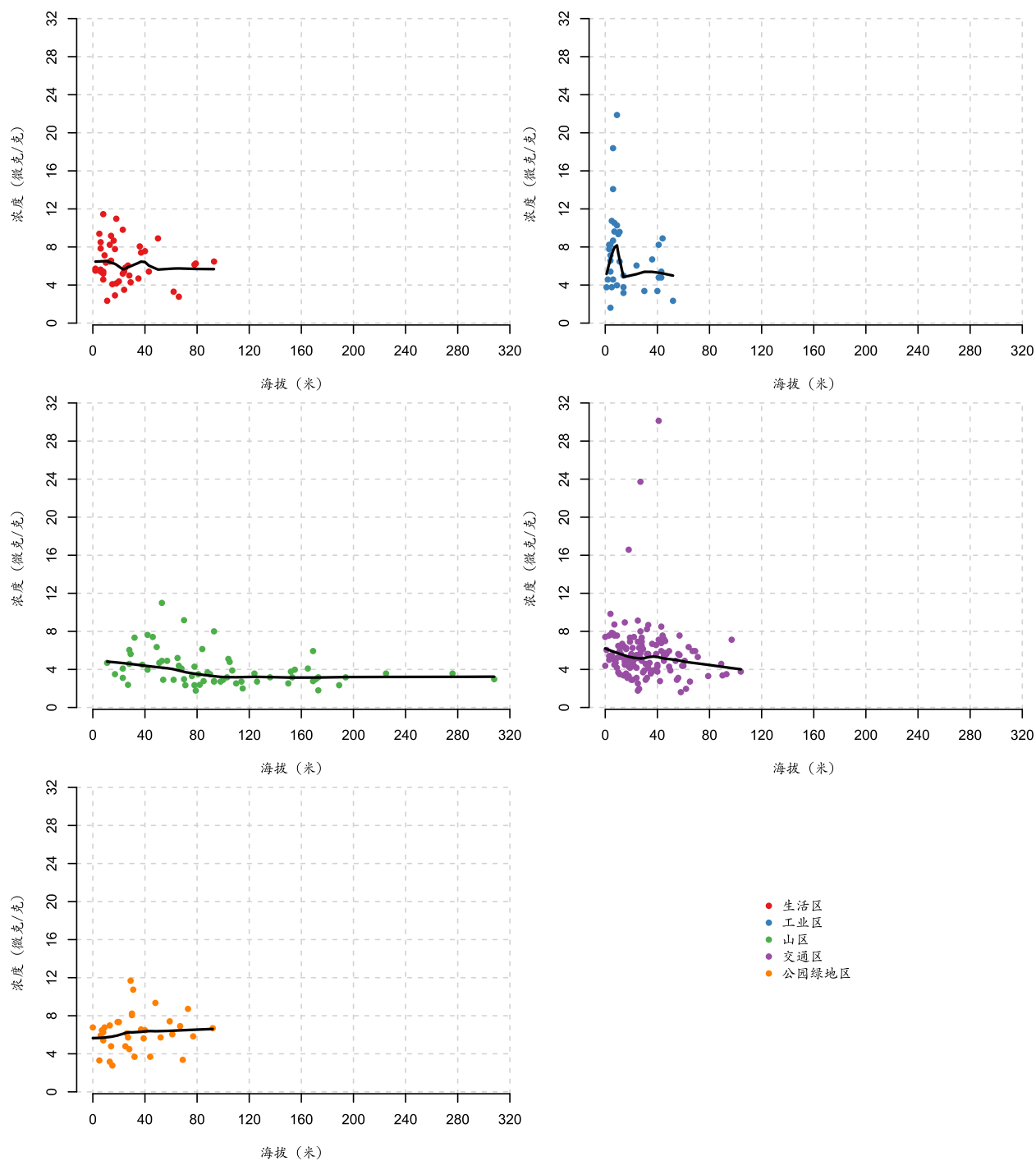- green 村庄附近的绿色植物的绿色度（卫星测得）
- phc 村庄是否有健康中心（1 是 0 否）

图 3: 金属砷的浓度与城市功能区、海拔的关系

3.2.2 数据分析

```
> library(geoR)
> data(gambia,package="geoR")
> str(gambia)

'data.frame':    2035 obs. of  8 variables:
 $ x       : num  349631 349631 349631 349631 349631 ...
 $ y       : num  1458055 1458055 1458055 1458055 1458055 ...
 $ pos     : num  1 0 0 1 0 1 1 0 0 1 ...
 $ age     : num  1783 404 452 566 598 ...
 $ netuse  : num  0 1 1 1 1 1 1 1 1 0 ...
 $ treated : num  0 0 0 0 0 0 0 0 0 0 ...
 $ green   : num  40.9 40.9 40.9 40.9 40.9 ...
 $ phc     : num  1 1 1 1 1 1 1 1 1 1 ...

> head(gambia)

             x       y pos  age netuse treated green phc
1850 349631.3 1458055   1 1783      0       0 40.85   1
1851 349631.3 1458055   0  404      1       0 40.85   1
1852 349631.3 1458055   0  452      1       0 40.85   1
1853 349631.3 1458055   1  566      1       0 40.85   1
1854 349631.3 1458055   0  598      1       0 40.85   1
1855 349631.3 1458055   1  590      1       0 40.85   1

> gambia.map.col <- function (col="red",pch=3,cex=1,lwd=2)
+ {
+     gb <- gambia.borders/1000
+     gd <- gambia[, 1:2]/1000
+     plot(gb, ty = "l", asp = 1,xlab = " 西-东 （千米）", ylab = " 北-南 （千米）")
+     points(gd, pch = pch, cex = cex,col=col,lwd=lwd)
+     r1b <- gb[gb[, 1] < 420, ]
+     r2b <- gb[gb[, 1] >= 420 & gb[, 1] < 550, ]
+     r3b <- gb[gb[, 1] >= 550, ]
+     r1bn <- zoom.coords(r1b, 1.7, xoff = 30, yoff = -90)
+     lines(r1bn)
```

```
+       r2bn <- zoom.coords(r2b, 1.7, xoff = -20, yoff = 90)
+       lines(r2bn)
+       r3bn <- zoom.coords(r3b, 1.7, xoff = -20, yoff = -90)
+       lines(r3bn)
+       r1d <- gd[gd[, 1] < 420, ]
+       r2d <- gd[gd[, 1] >= 420 & gd[, 1] < 550, ]
+       r3d <- gd[gd[, 1] >= 550, ]
+       r1dn <- zoom.coords(r1d, 1.7, xoff = 20, yoff = -90)
+       r1dn <- zoom.coords(r1d, 1.7, xlim.o = range(r1b[, 1], na.rm = TRUE),
+           ylim.o = range(r1b[, 2], na.rm = TRUE), xoff = 20, yoff = -90)
+       points(r1dn, pch = pch, cex = cex,col=col,lwd=lwd)
+       r2dn <- zoom.coords(r2d, 1.7, xlim.o = range(r2b[, 1], na.rm = TRUE),
+           ylim.o = range(r2b[, 2], na.rm = TRUE), xoff = -20, yoff = 90)
+       points(r2dn, pch = pch, cex = cex,col=col,lwd=lwd)
+       r3dn <- zoom.coords(r3d, 1.7, xlim.o = range(r3b[, 1], na.rm = TRUE),
+           ylim.o = range(r3b[, 2], na.rm = TRUE), xoff = -20, yoff = -90)
+       points(r3dn, pch = pch, cex = cex,col=col,lwd=lwd)
+       rc1n <- rect.coords(r1bn, xzoom = 1.05, lty = 2)
+       rc2n <- rect.coords(r2bn, xzoom = 1.05, lty = 2)
+       rc3n <- rect.coords(r3bn, xzoom = 1.05, lty = 2)
+       text(c(400, 550, 480), c(1340, 1430, 1550), c(" 西部",
+           " 东部", " 中部"), cex = 1.5)
+       return(invisible())
+ }
> par(mar = c(4, 4, .5, .5))
> gambia.map.col(col=brewer.pal(5, "Set1")[1],pch=16,cex=.5,lwd=1)
```

```
> gambia.borders <- readRDS("data/gambia.borders.RDS")
> library(ggplot2)
> ggplot(gambia.borders/1000,aes(x,y)) +
+   geom_point(size=.1)+
+   geom_point(data=gambia/1000,pch=3,aes(x,y),colour="red")+
+   scale_y_continuous(name = " 北-南（千米）")+
+   scale_x_continuous(name = " 西-东（千米）")
```
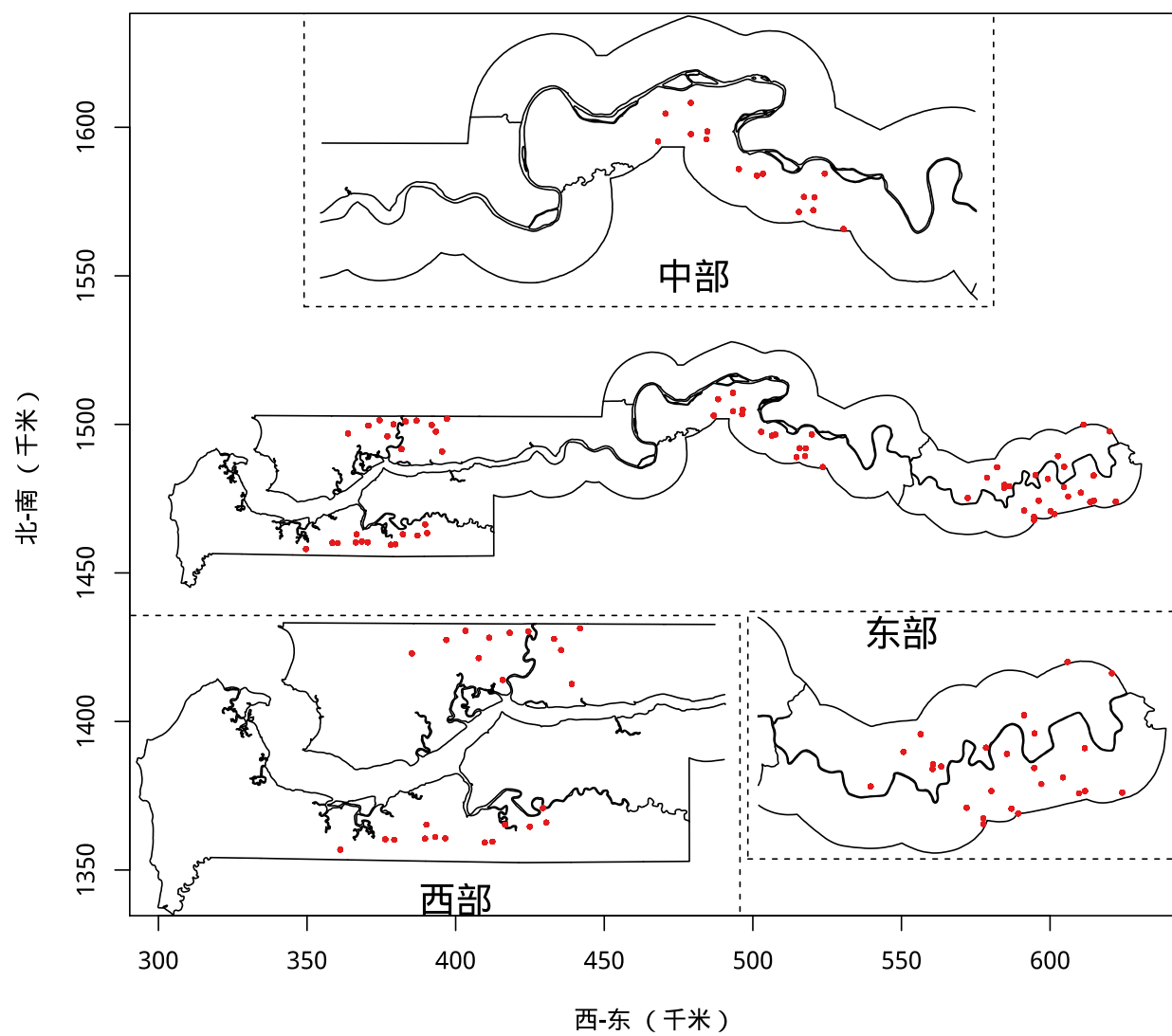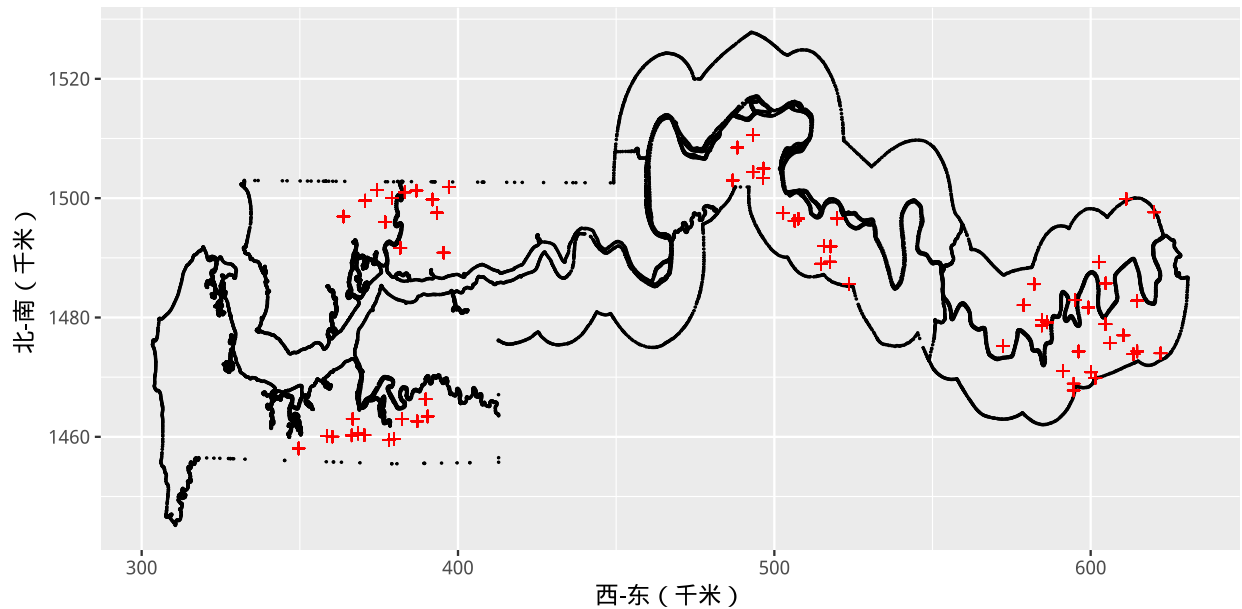
图 4: 采样数据位置

```
> # 有疟疾的儿童年龄分布
> par(mar=c(4,4,.5,.5))
> pos1 <- subset(gambia,pos==1,select=c(pos,age))
> with(pos1,{
+ hist(age,freq = FALSE,plot=TRUE,axes=FALSE,
+   col=rgb(77, 175, 74, 90,  maxColorValue = 255),border="white",
+   xlab=" 年龄（天数）",ylab=" 概率密度 10^(-4)",main="")
+ xlim <- seq(300,1900,by=100)
+ ylim <- seq(0,10,by=1)
+ yylim <- seq(0,10,by=1)/10000
+ axis(1,labels=xlim,at=xlim,las=1) # x 轴
+ axis(2,labels=ylim,at=yylim,las=1) # y 轴
+ lines(density(age),col= brewer.pal(5, "Set1")[3],lwd=2)
+ })
> # 无疟疾的儿童年龄分布
> pos0 <- subset(gambia,pos==0,select=c(pos,age))
> with(pos0,{
+ hist(age,freq = FALSE,plot=TRUE,axes=FALSE,add=TRUE,
+   col=rgb(255, 127, 0, 90,maxColorValue = 255),border="white")
+ lines(density(age),col=brewer.pal(5, "Set1")[5],lwd=2)
+ })
> legend("topright",legend=c(" 有疟疾"," 无疟疾"),
```

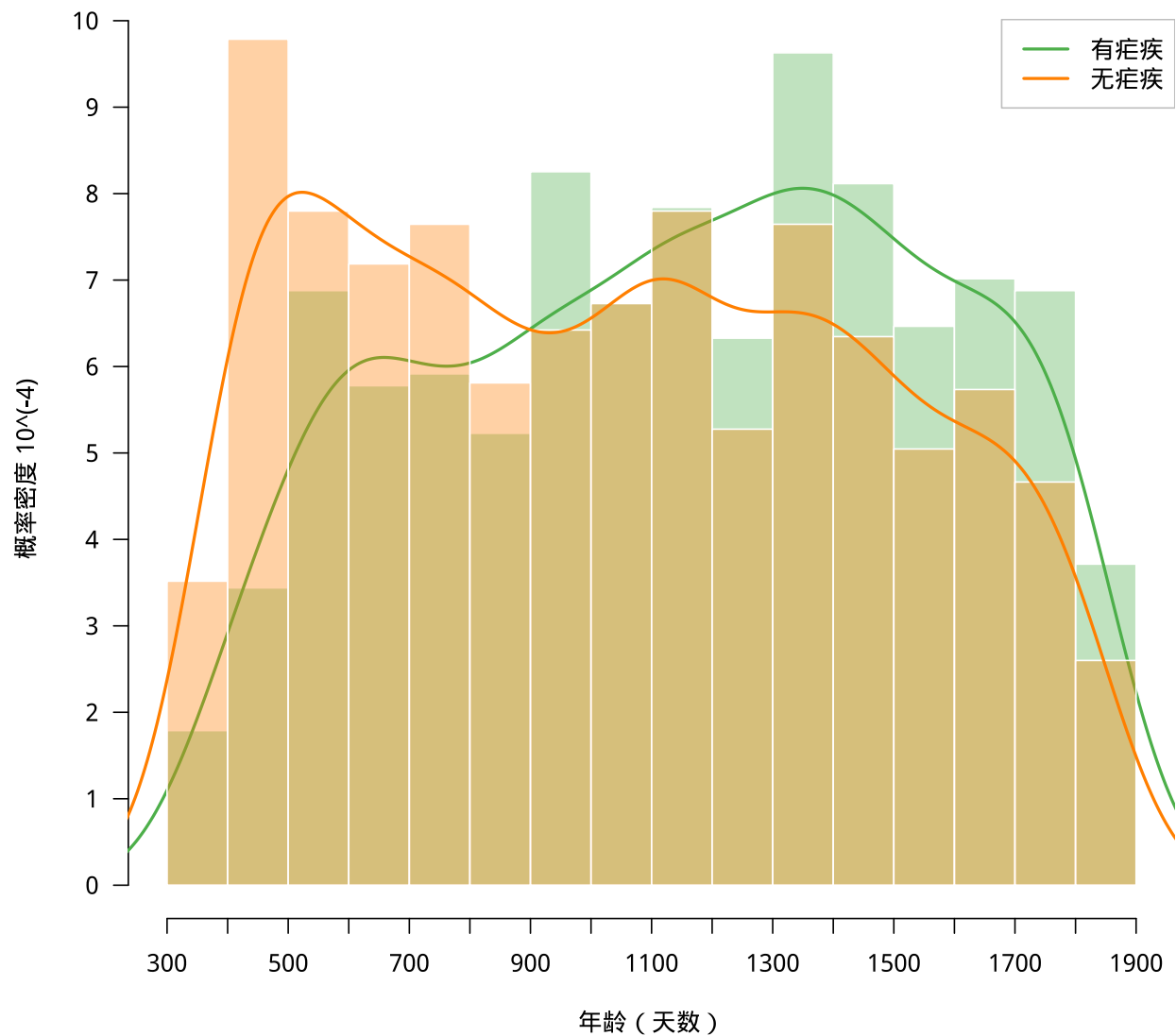图 5: 疟疾与年龄的关系

```
+          col=brewer.pal(5, "Set1")[c(3,5)],lwd=2,box.col = "gray")
```

```
> # 没有使用蚊帐，有疟疾
> dat1<-subset(gambia,netuse==0 & pos==1)
> # 没有使用蚊帐，无疟疾
> dat2<-subset(gambia,netuse==0 & pos==0)
> dat3<-subset(gambia,netuse==1 & pos==1)
> dat4<-subset(gambia,netuse==1 & pos==0)
> # 使用蚊帐但没有杀虫，无疟疾
> dat5<-subset(gambia,netuse==1 & treated==0 & pos==0)
```

```
> # 使用蚊帐但没有杀虫，有疟疾
> dat6<-subset(gambia,netuse==1 & treated==0 & pos==1)
> # 使用蚊帐且有杀虫，无疟疾
> dat7<-subset(gambia,netuse==1 & treated==1 & pos==0)
> # 使用蚊帐且有杀虫，有疟疾
> dat8<-subset(gambia,netuse==1 & treated==1 & pos==1)
>
> op <- par(mfrow=c(1,4),mar=c(4,4,0.5,0.5))
> cols <- viridis(4,begin = 0.2, end = .8,alpha = .5)
> ylim <- seq(from=300,to=1900,by=200)
> xlim <- c(0,1)
> plot(c(-1,2),c(300,1900),xlab="",ylab="",
+     type="n",axes = FALSE, frame.plot=FALSE)
> axis(2,labels=ylim,at=ylim,las=0)
> axis(1,labels=xlim,at=c(0,1),las=1)
> plot(age~factor(pos),at=c(0,1),subset=netuse==0,xlab="net not use",ylab="age",
+         axes = FALSE,col=cols[1], frame.plot=FALSE,add=TRUE,data=gambia)
> points(jitter(dat1$pos, amount = .2),dat1$age,col=cols[1])
> points(jitter(dat2$pos, amount = .2),dat2$age,col=cols[1])
> plot(c(-1,2),c(300,1900),xlab="net use",ylab="",
+     type="n",axes = FALSE, frame.plot=FALSE)
> axis(1,labels=xlim,at=c(0,1),las=1)
> plot(age~factor(pos),at=c(0,1),subset=netuse==1,xlab="net use",ylab="",
+         axes = FALSE,col=cols[2], frame.plot=FALSE,add=TRUE,data=gambia)
> points(jitter(dat3$pos, amount = .2),dat3$age,col=cols[2])
> points(jitter(dat4$pos, amount = .2),dat4$age,col=cols[2])
> plot(c(-1,2),c(300,1900),xlab="not treated",ylab="",
+     type="n",axes = FALSE, frame.plot=FALSE)
> axis(1,labels=xlim,at=c(0,1),las=1)
> plot(age~factor(pos),at=c(0,1),subset=netuse==1 & treated==0,
+     xlab="not treated",ylab="",axes = FALSE,
+     col=cols[3], frame.plot=FALSE,add=TRUE,data=gambia)
> points(jitter(dat5$pos, amount = .2),dat5$age,col=cols[3])
> points(jitter(dat6$pos, amount = .2),dat6$age,col=cols[3])
> plot(c(-1,2),c(300,1900),xlab="treated",ylab="",
+     type="n",axes = FALSE, frame.plot=FALSE)
```

图 6: 疟疾与蚊帐、杀虫的关系

```
> axis(1,labels=xlim,at=c(0,1),las=1)
> plot(age~factor(pos),at=c(0,1),subset=netuse==1 & treated==1,
+     xlab="treated",ylab="",axes = FALSE,col=cols[4],
+     frame.plot=FALSE,add=TRUE,data=gambia)
> points(jitter(dat7$pos, amount = .2),dat7$age,col=cols[4])
> points(jitter(dat8$pos, amount = .2),dat8$age,col=cols[4])
```
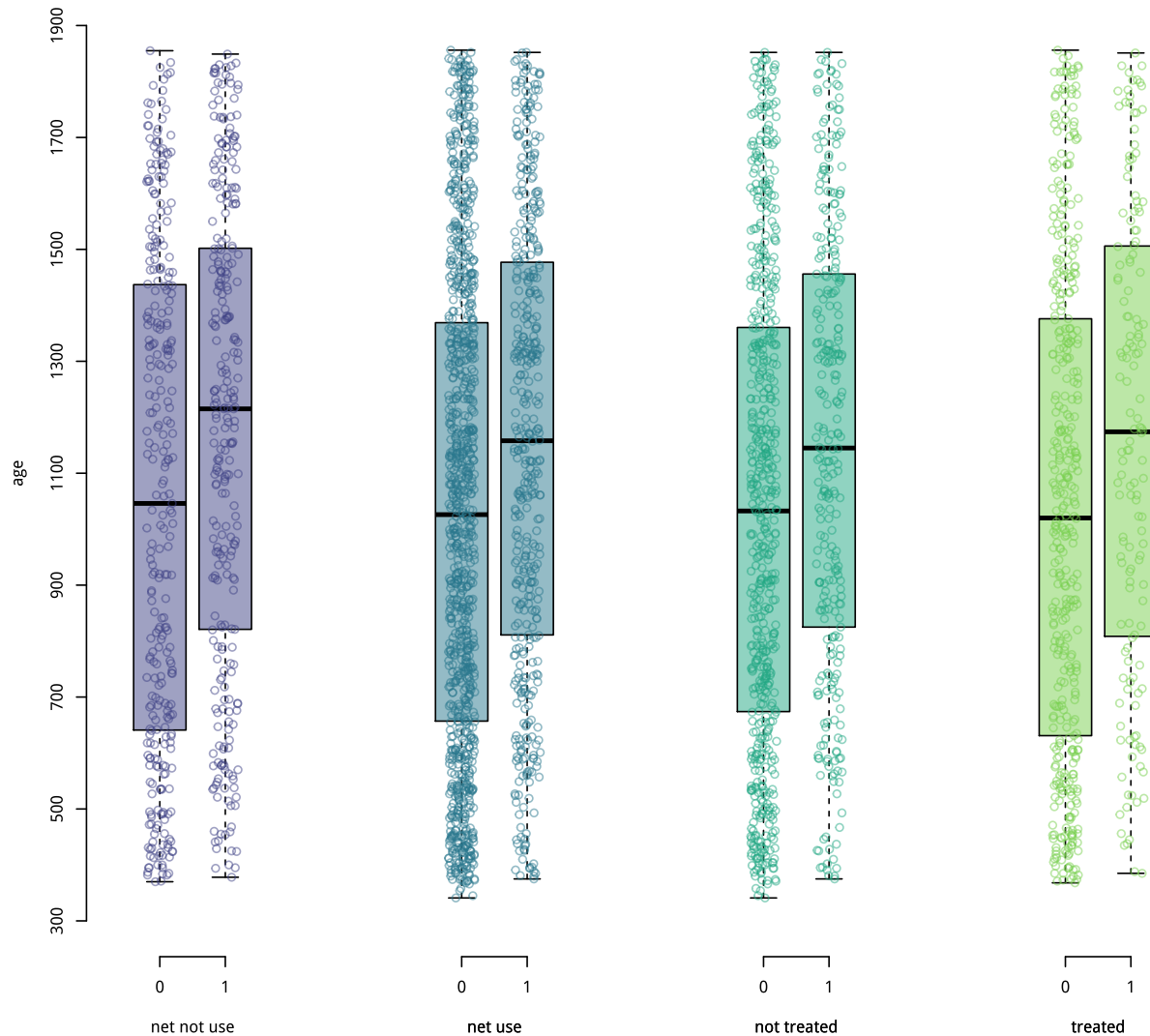
```
> prevalence <- rep(0,65)
> greeness <- rep(0,65)
> health <- rep(0,65)
```

```
> for( i in seq(65)){
+     ii <- unique(gambia$x)[i]
+     dat <- subset(gambia,x==ii)
+     prevalence[i] <- sum(dat$pos)/dim(dat)[1]
+     greeness[i] <- unique(dat$green)
+     health[i] <- unique(dat$phc)
+ }
> par(mar = c(4, 4, .5, .5))
> plot(prevalence~greeness,axes=FALSE,type = "n")
> abline(h=seq(from=0,to=.9,by=.1),v=seq(from=25,to=60,by=5),
+        lty=2,col="lightgray")
> # 绿色 表示有健康中心 橘色 表示没有健康中心
> points(prevalence~greeness,pch=1,lwd=2,cex=1.5,
+        col=ifelse(health,brewer.pal(5, "Set1")[3],brewer.pal(5, "Set1")[5]) )
> axis(1,at=seq(from=30,to=60,by=5))
> axis(2,at=seq(from=0,to=.9,by=.1))
```

3.3 西非 Loa loa 疟疾流行度分析

```
> loaloa <- read.table("data/loaloa.txt",header = FALSE)
> colnames(loaloa) <- c("lon","lat","No_tested","No_pos","ELEV","maxNDVI","stdNDVI")
> str(loaloa)

'data.frame':   197 obs. of  7 variables:
 $ lon      : num  8.04 8 8.91 8.1 8.18 ...
 $ lat      : num  5.74 5.68 5.35 5.92 5.1 ...
 $ No_tested: int  162 167 88 62 167 66 163 83 30 57 ...
 $ No_pos   : int  0 1 5 5 3 3 11 0 4 4 ...
 $ ELEV     : int  108 99 783 104 109 909 503 103 751 268 ...
 $ maxNDVI  : num  0.69 0.74 0.79 0.67 0.85 0.8 0.78 0.69 0.8 0.84 ...
 $ stdNDVI  : num  0.139 0.153 0.165 0.122 0.166 ...

> head(loaloa)

      lon       lat No_tested No_pos ELEV maxNDVI   stdNDVI
1 8.041860 5.736750       162      0  108    0.69 0.1394377
```
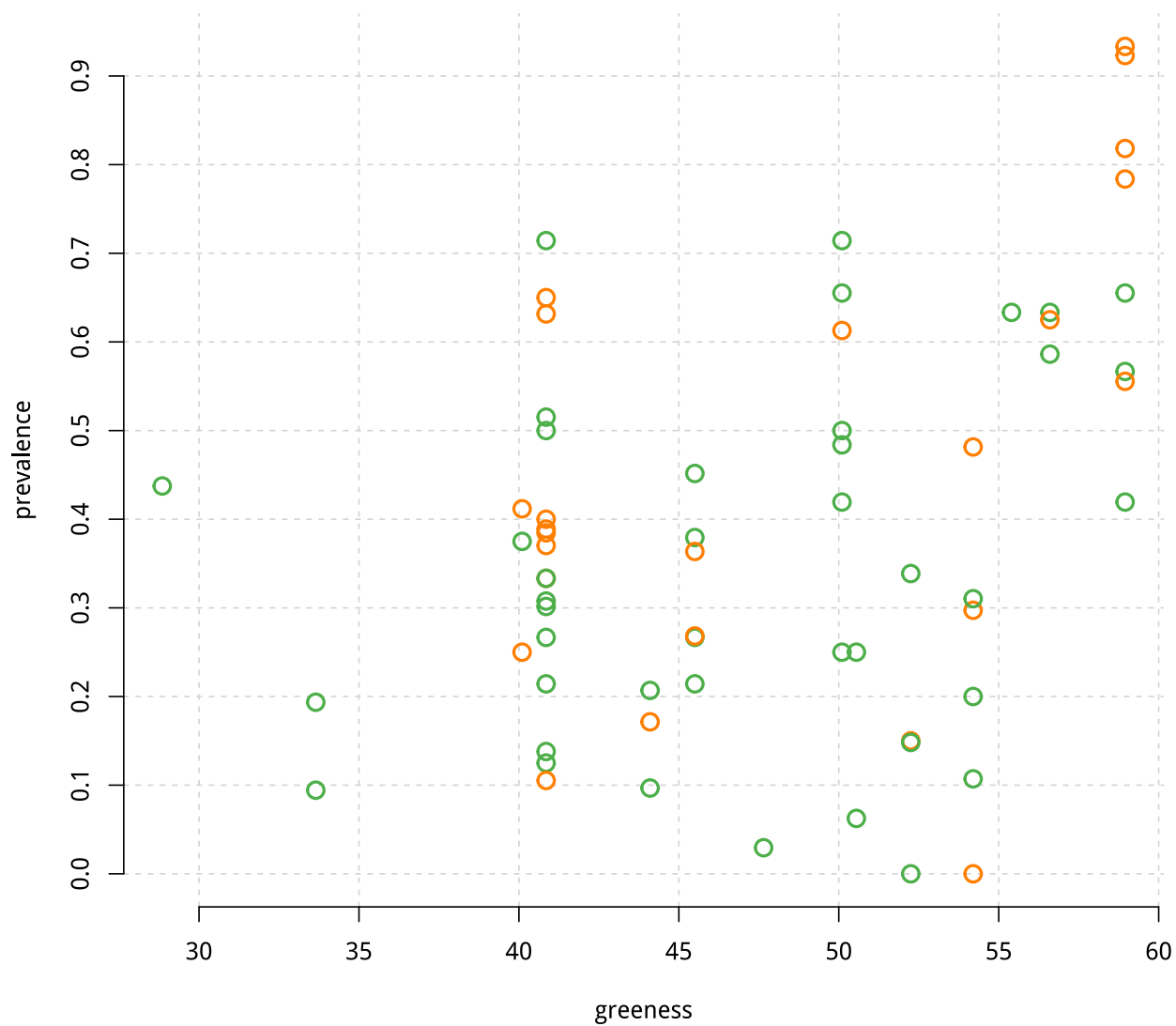
图 7: 疟疾流行度与植被的关系

2 8.004330 5.680280		167	1	99	0.74	0.1529836
3 8.905556 5.347222		88	5	783	0.79	0.1646169
4 8.100720 5.917420		62	5	104	0.67	0.1223972
5 8.182510 5.104540		167	3	109	0.85	0.1656000
6 8.929167 5.355556		66	3	909	0.80	0.1915820

```r
> # plot(lat~lon,data = loaloa,pch=21,
> #      xlab="longitude",ylab = "latitude",
> #      bg="gray50",col="white")
> # plot(lat~lon,data = loaloa,pch=16,col="gray50",
> #      xlab="longitude",ylab = "latitude")
> ggplot(loaloa,aes(x=lon,y=lat))+
+   geom_point(aes(size = ELEV),shape=20)+
+   xlab(" 西-东（度）")+ylab(" 北-南（度）")+
+   labs(size=" 海拔\n（米）")
```
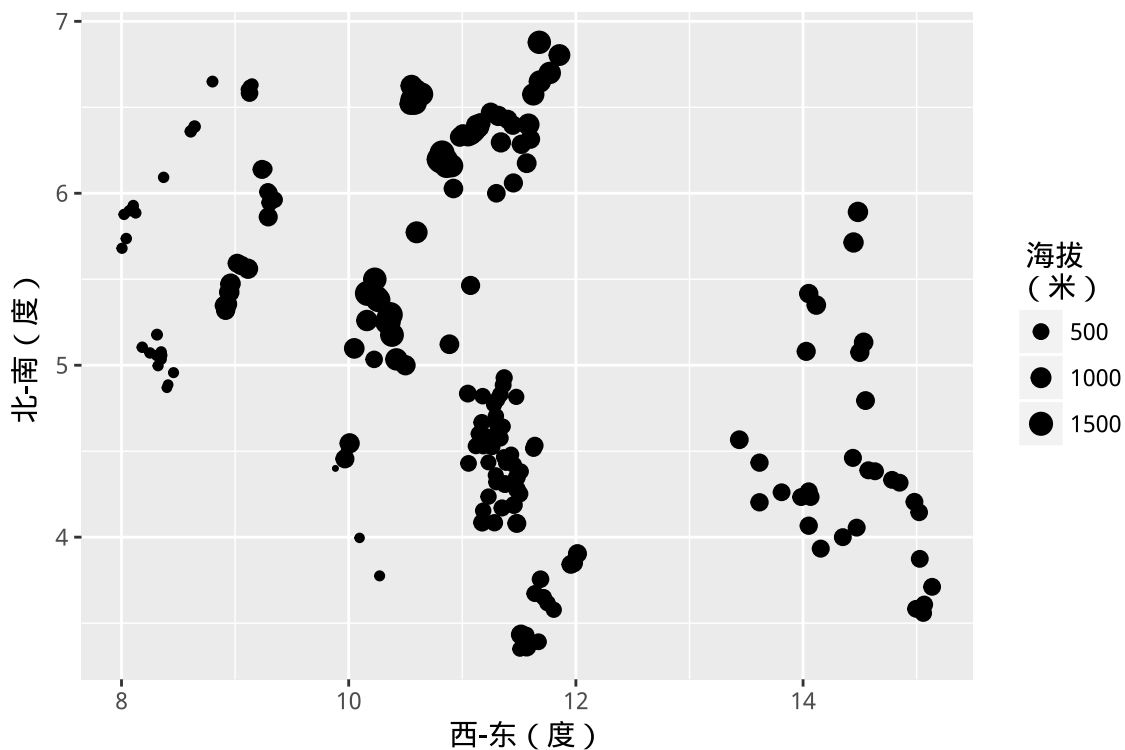


```r
> library(ggplot2)
> library(ggmap)
> map <- get_map(location = c(lon = 11.57022, lat = 5.114),zoom =6)
> ggmap(map, extent='device') +
```

```
+    geom_point(aes(x=lon, y=lat,size=ELEV),alpha=.2, colour="red", data=loaloa)
```
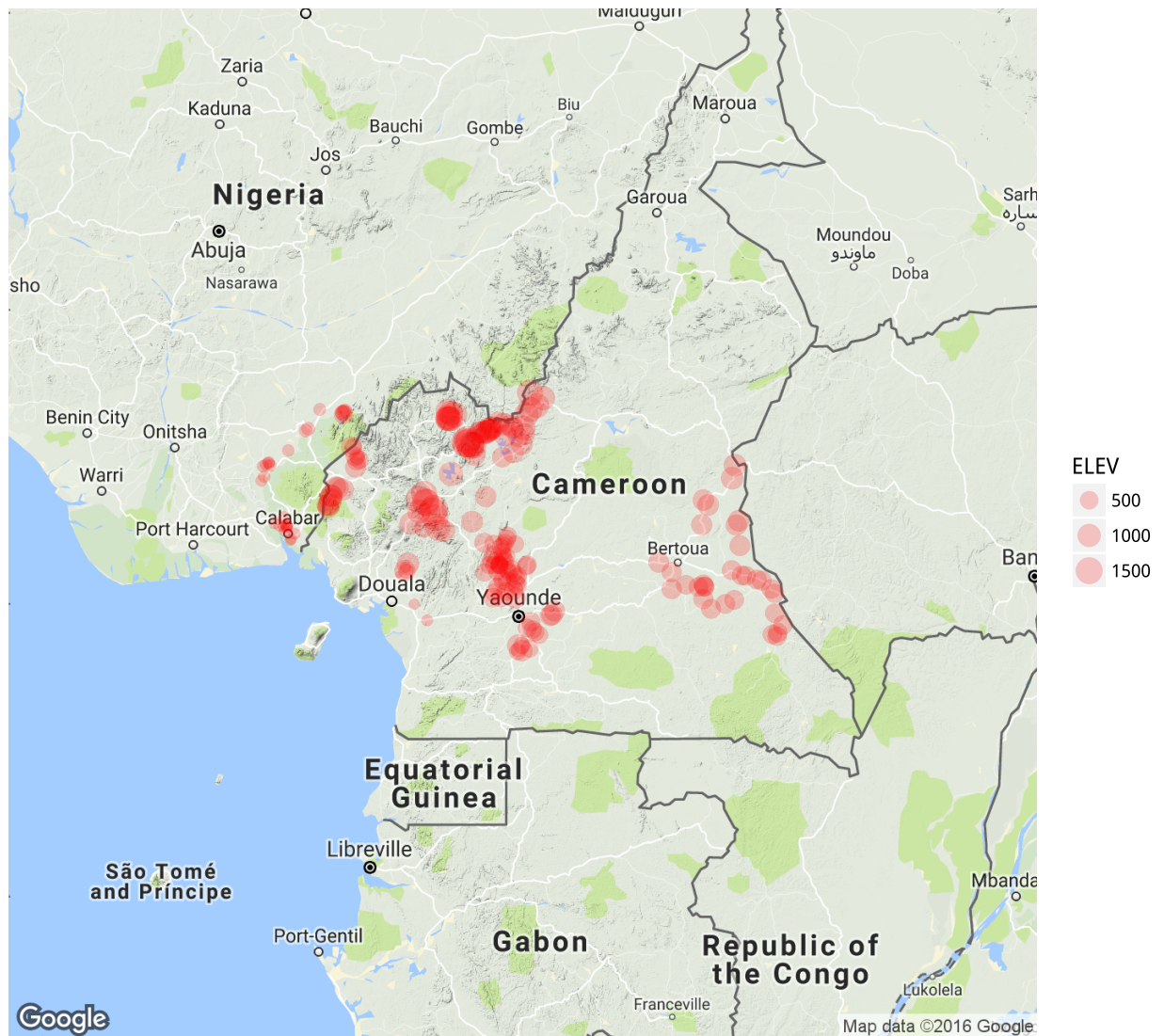


```
> ggmap(map, extent='device') +
+    geom_point(aes(x=lon, y=lat,size=No_pos),alpha=.2, colour="red", data=loaloa)
```
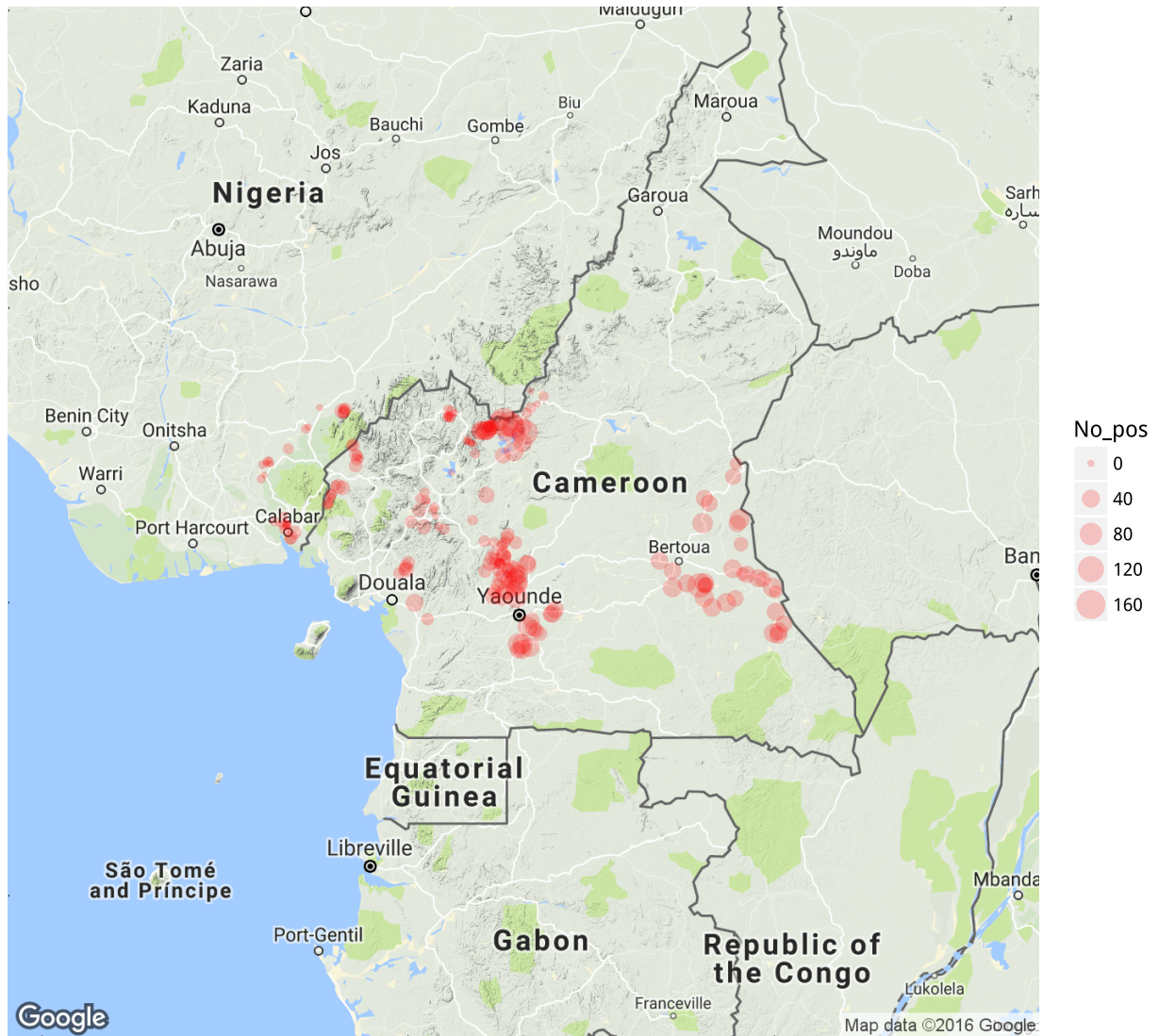
4 广义线性混合模型

4.1 符号说明

$x_i \in \mathbb{R}^2, p(x_i), m_i, Y_i, d(x_i), i = 1, 2, \cdots, 65$ 分别表示第 i 个村庄的坐标，疟疾流行度，抽样数目，血样中疟疾检测结果，与位置有关的其他变量。Y_i 表示一个向量，长度为 m_i，$d(x_i)$ 表示一个矩阵，行数为 m_i，列数是其它变量的个数（除村庄坐标和 pos 变量外，共 5 个）。

4.2 混合模型

at village level

$$Y_i \sim \text{Bin}(m_i, p(x_i))$$

$$log\{\frac{p(x_i)}{1 - p(x_i)}\} = d(x_i)'\beta + S(x_i) + Z_i$$

1. $\mathcal{S} = \{S(x) : x \in \mathbb{R}^2\}$ 是均值为 0，方差为 σ^2，相关函数为 $\rho(x, x') = \text{Corr}\{S(x), S(x')\}$ 的高斯过程；

2. 假定过程 $\mathcal{S}$ 是平稳且各向同性，则 $\text{Corr}\{S(x), S(x')\} = \rho(\|x, x'\|)$，$\| \cdot \|$ 表示欧氏距离；

3. $d(x_i)$ 是与位置 x_i 有关的协变量（固定效应）；

4. $S(x_i)$ 是与空间相关的随机效应；

5. Z_i 相互独立且服从 $N(0, \tau^2)$ 的随机变量（效应）。

补充：

1. $\mu_i = E[Y_i|S(\cdot)]$
2. $h(\mu_i) = \sum_{k=1}^{p} \beta_k d_k(x_i) + S(x_i)$
3. $h(\cdot)$ 是已知的联系函数，$d_k(\cdot)$ 是可观察的空间解释变量，β_k 是未知的空间回归参数。

5 模型拟合（参数估计和模型预测）

5.1 基于 profile 似然（应该不行）

5.2 基于似然推断与 MCML 算法（有待观察）

MCML：Monte Carlo Maximum likelihood

5.3 贝叶斯推断与 MCMC 算法（效率和精度可能有问题）

MCMC：Markov Chain Monte Carlo

5.4 近似贝叶斯推断与 INLA 算法（有希望）

INLA：Integrated Nested Laplace Approximation

6 FAQs

- **The MCMC-algorithm seems not to be mixing well. What to do ?** The general solution is to make longer run's. It is not unusual for me when doing Bayesian inference to make 2,000,000 iterations, storing every 2,000. The problem is most pronounced when phi is random and a normal prior with a large variance is used for beta. The solution here is to use the flat prior for beta instead of the normal.

- **Is inference for the nugget implemented ?** The relative nugget tausq.rel is fixed when doing Bayesian inference. I have no plans allowing a prior on tausq.rel for two reasons:

- I do not know how meaningful priors should look like
- For computational reasons, having a discrete prior on both phi and tausq.rel requires that a large number of matrices are precomputed and stored. Maximum likelihood estimation of the relative nugget is possible using either MCMC-MLE, which is implemented in the function likfit.glsm, or MCMC-EM, which has not yet been implemented.
- **Are improper priors dangerous to use ?** Not always, but the resulting posterior distribution may not exist (be improper). For the priors implemented in the geoRglm the posterior is proper, apart from when using the reciprocal prior for sigmasq where the posterior becomes improper.
- **Problem with random seed:** If you get an execution error like ".Random.seed[0] is not a valid Normal type", the problem is that the random seed is not defined. A solution is f.ex. to call rnorm(1) once before calling the function in geoRglm.
- **Multivariate analysis:** is not implemented in the package. In particular the analysis of the Malaria data in Diggle et al. (2002) cannot be replicated using geoRglm
- **Markov chain Monte Carlo EM :** as in Zhang 2002 is not yet implemented.

7 软件

```
> devtools::session_info()
```

```
setting   value
version   R version 3.3.2 (2016-10-31)
system    x86_64, mingw32
ui        RTerm
language  en
collate   Chinese (Simplified)_China.936
tz        Asia/Taipei
date      2016-12-28


package          * version  date        source
assertthat         0.1      2013-12-06  CRAN (R 3.3.2)
backports          1.0.4    2016-10-24  CRAN (R 3.3.2)
colorspace         1.3-2    2016-12-14  CRAN (R 3.3.2)
devtools           1.12.0   2016-06-24  CRAN (R 3.3.2)
digest             0.6.10   2016-08-02  CRAN (R 3.3.2)
evaluate           0.10     2016-10-11  CRAN (R 3.3.2)
geoR             * 1.7-5.2  2016-05-02  CRAN (R 3.3.2)
```

```
geosphere          1.5-5     2016-06-15 CRAN (R 3.3.2)
ggmap            * 2.6.1     2016-01-23 CRAN (R 3.3.2)
ggplot2          * 2.2.0     2016-11-11 CRAN (R 3.3.2)
gridExtra          2.2.1     2016-02-29 CRAN (R 3.3.2)
gtable             0.2.0     2016-02-26 CRAN (R 3.3.2)
highr              0.6       2016-05-09 CRAN (R 3.3.2)
htmltools          0.3.5     2016-03-21 CRAN (R 3.3.2)
jpeg               0.1-8     2014-01-23 CRAN (R 3.3.2)
knitr              1.15.1    2016-11-22 CRAN (R 3.3.2)
labeling           0.3       2014-08-23 CRAN (R 3.3.2)
lattice            0.20-34   2016-09-06 CRAN (R 3.3.2)
lazyeval           0.2.0     2016-06-12 CRAN (R 3.3.2)
magrittr           1.5       2014-11-22 CRAN (R 3.3.2)
mapproj            1.2-4     2015-08-03 CRAN (R 3.3.2)
maps               3.1.1     2016-07-27 CRAN (R 3.3.2)
MASS               7.3-45    2016-04-21 CRAN (R 3.3.2)
MBA                0.0-8     2014-04-29 CRAN (R 3.3.2)
memoise            1.0.0     2016-01-29 CRAN (R 3.3.2)
munsell            0.4.3     2016-02-13 CRAN (R 3.3.2)
plyr               1.8.4     2016-06-08 CRAN (R 3.3.2)
png                0.1-7     2013-12-03 CRAN (R 3.3.2)
proto              1.0.0     2016-10-29 CRAN (R 3.3.2)
RandomFields       3.1.24.1  2016-10-11 CRAN (R 3.3.2)
RandomFieldsUtils  0.3.3.1   2016-10-11 CRAN (R 3.3.2)
RColorBrewer     * 1.1-2     2014-12-07 CRAN (R 3.3.2)
Rcpp               0.12.8    2016-11-17 CRAN (R 3.3.2)
reshape2           1.4.2     2016-10-22 CRAN (R 3.3.2)
RgoogleMaps        1.4.1     2016-09-18 CRAN (R 3.3.2)
rjson              0.2.15    2014-11-03 CRAN (R 3.3.2)
rmarkdown          1.3       2016-12-21 CRAN (R 3.3.2)
rprojroot          1.1       2016-10-29 CRAN (R 3.3.2)
rticles            0.2       2016-04-24 CRAN (R 3.3.2)
scales             0.4.1     2016-11-09 CRAN (R 3.3.2)
showtext         * 0.4-5     2016-10-14 CRAN (R 3.3.2)
showtextdb         1.0       2015-03-10 CRAN (R 3.3.2)
sp                 1.2-4     2016-12-22 CRAN (R 3.3.2)
splancs            2.01-39   2016-08-23 CRAN (R 3.3.2)
```

```
stringi           1.1.2    2016-10-01 CRAN (R 3.3.2)
stringr           1.1.0    2016-08-19 CRAN (R 3.3.2)
sysfonts        * 0.5      2015-04-27 CRAN (R 3.3.2)
tibble            1.2      2016-08-26 CRAN (R 3.3.2)
viridis         * 0.3.4    2016-03-12 CRAN (R 3.3.2)
withr             1.0.2    2016-06-20 CRAN (R 3.3.2)
yaml              2.1.14   2016-11-12 CRAN (R 3.3.2)
```

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