```
library(knitr)
#knitr::spin("../../.tests/spline.est.r")
library(asreml4)
library(asreml4Plus)
library(MASS)
options(width = 110)


data(chkpeadat)
```

Warning in data(chkpeadat): data set 'chkpeadat' not found

```
asreml.options(design = TRUE)
asreml.obj <- asreml(fixed = Biomass.plant ~ Lines * TRT + Smarthouse/(vLanes + vPos),
                     random = ~Smarthouse:Zone + Smarthouse:spl(vLanes),
                     residual = ~Smarthouse:ar1(Lane):ar1(Position),
                     data = chkpeadat, trace = FALSE)
```

Model fitted using the gamma parameterization.
Spline: design points closer than 0.0023 have been merged.

```
asreml4:::summary.asreml(asreml.obj)$varcomp
```

```
##                                           component   std.error     z.ratio bound %ch
## Smarthouse:Zone                           0.6225635  1.40923506   0.4417741     P 0.0
## Smarthouse:spl(vLanes)                    4.2761480  2.56364724   1.6679939     P 0.1
## Smarthouse:Lane:Position(R)              11.7208066  0.76603168  15.3006813     P 0.0
## Smarthouse:Lane:Position!Lane!cor         0.1440545  0.06118142   2.3545460     U 0.0
## Smarthouse:Lane:Position!Position!cor     0.2247251  0.04801723   4.6800921     U 0.0
```

```
s2s <- asreml4:::summary.asreml(asreml.obj)$varcomp[grepl("Smarthouse:spl(vLanes)",
                                                   rownames(asreml4:::summary.asreml(asreml.obj)$
                                                   fixed = TRUE), "component"]
Zasr <- as.matrix(asreml.obj$design[,753:796])
s2s*mean(diag(Zasr%*%t(Zasr)))
```

[1] 8.379266

```
asreml.obj$coefficients$random[grep("spl(vLanes)",
                                    rownames(asreml.obj$coefficients$random), fixed=TRUE)]
```

```
##  [1]   0.27031407 -0.09263423 -0.41699684 -0.19783486 -0.21611371   0.23827409   0.82440505   1.18382545
##  [9]   1.18191741   0.08470003 -0.68026784 -0.60034769 -0.54754174 -0.76228095  -1.17330139 -0.59010874
## [17]   0.23055901   0.39025386 -0.24816860 -0.57609655 -0.53605078 -0.21129726   0.28273314 -0.35231624
## [25]  -1.23161868 -1.24341393 -0.73297221 -0.55797284 -1.53168335 -1.92680478  -0.49237602 -0.04599778
## [33]   0.13080269  0.69627426  1.60000067   1.75738403  1.58140458  1.81082469   1.27163587  0.45342852
## [41]  -1.27910915 -1.64525729 -0.79937260  0.09235558
```

```
dat <- chkpeadat


Zasr <- Zasr / sqrt(mean(diag(Zasr%*%t(Zasr))))
dat <- cbind(dat, as.data.frame(as.matrix(Zasr)))
names(dat)[22:65] <- paste("V",1:44, sep="")
g.asr <- asreml(fixed = Biomass.plant ~ Lines * TRT + Smarthouse/(vLanes + vPos),
                random = ~Smarthouse:Zone + grp(spl.vLanes),
                residual = ~Smarthouse:ar1(Lane):ar1(Position),
                group = list(spl.vLanes=22:65),
                data = dat, trace = FALSE)
```

```r
## Model fitted using the gamma parameterization.
asreml4:::summary.asreml(g.asr)$varcomp
```

```
##                                        component  std.error    z.ratio bound %ch
## Smarthouse:Zone                        0.6225391 1.40904233  0.4418172     P 0.1
## grp(spl.vLanes)                        8.3791087 5.02232955  1.6683710     P 0.1
## Smarthouse:Lane:Position(R)           11.7210565 0.76606858 15.3002705     P 0.0
## Smarthouse:Lane:Position!Lane!cor      0.1440555 0.06118110  2.3545750     U 0.0
## Smarthouse:Lane:Position!Position!cor  0.2247326 0.04801689  4.6802813     U 0.0
```

```r
knot.points <- unique(chkpeadat$vLanes)
Xs <- matrix(cbind(rep(1, 24), knot.points), ncol = 2)
ZvL <- Zspline(knot.points)
mean(diag(ZvL%*%t(ZvL)))
```

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

```r
t(ZvL) %*% Xs
```

```
##                [,1]          [,2]
##  [1,] -1.006140e-16  6.106227e-16
##  [2,] -2.359224e-16  1.221245e-15
##  [3,]  5.759282e-16 -3.108624e-15
##  [4,] -4.302114e-16  4.996004e-15
##  [5,]  7.771561e-16 -5.329071e-15
##  [6,]  5.273559e-16 -2.220446e-15
##  [7,]  8.326673e-16 -4.884981e-15
##  [8,] -1.804112e-15  1.154632e-14
##  [9,]  8.049117e-16 -7.327472e-15
## [10,] -1.026956e-15  4.440892e-15
## [11,]  1.075529e-15 -2.109424e-15
## [12,] -2.220446e-15  1.154632e-14
## [13,]  1.443290e-15 -4.385381e-15
## [14,] -1.110223e-15 -1.776357e-15
## [15,]  5.551115e-16 -4.884981e-15
## [16,] -6.661338e-16  2.664535e-15
## [17,] -1.665335e-15  5.329071e-15
## [18,]  1.332268e-15 -5.329071e-15
## [19,] -2.220446e-16  1.776357e-15
## [20,]  3.330669e-16 -4.440892e-16
## [21,]  4.996004e-16 -4.440892e-16
## [22,] -1.387779e-17  0.000000e+00
```

```r
ZSvL <- kronecker(diag(1, nrow=2), ZvL)
dat <- chkpeadat
dat$f.vLanes <- as.factor(dat$vLanes)
Z <- model.matrix(~ - 1 + f.vLanes:Smarthouse, data = dat)
Z <- Z %*% ZSvL
dat <- cbind(dat, as.data.frame(Z))
t.asr <- asreml(fixed = Biomass.plant ~ Lines * TRT + Smarthouse/(vLanes + vPos),
                random = ~Smarthouse:Zone + grp(spl.vLanes),
                residual = ~Smarthouse:ar1(Lane):ar1(Position),
                group = list(spl.vLanes=23:66),
                data = dat, trace = FALSE)
```

Model fitted using the gamma parameterization.

```r
asreml4:::summary.asreml(t.asr)$varcomp
```

```
##                                      component   std.error     z.ratio bound %ch
## Smarthouse:Zone                      0.6114686  1.40654884   0.4347297     P   0
## grp(spl.vLanes)                      8.3861549  5.00111756   1.6768562     P   0
## Smarthouse:Lane:Position(R)         11.6966945  0.76565866  15.2766436     P   0
## Smarthouse:Lane:Position!Lane!cor    0.1445167  0.06120638   2.3611380     U   0
## Smarthouse:Lane:Position!Position!cor 0.2229755 0.04820227   4.6258295     U   0
```

```r
s2s_t <- asreml4:::summary.asreml(t.asr)$varcomp[grepl("grp(spl.vLanes)",
                                       rownames(asreml4:::summary.asreml(t.asr)$varcomp
                                       fixed = TRUE), "component"]
s2s_t*sum(diag(Z%*%t(Z)))/nrow(Z)
```

```
## [1] 8.386155
```