Correlation Function

Correlations in bdots

This vignette is created to illustrate the use of the `bdotsCorr` function, which finds the correlation between a fixed value in our dataset and the collection of fitted curves at each time points for each of the groups fit in `bdotsFit`.

First, let's take an existing dataset and add a fixed value for each of the subjects

```
library(bdots)
library(data.table)

## Let's work with cohort_unrelated dataset, as it has multiple groups
dat <- as.data.table(cohort_unrelated)

## And add a fixed value for which we want to find a correlation
dat[, val := rnorm(1), by = Subject]

head(dat)
```

```
##    Subject Time DB_cond Fixations LookType Group      val
## 1:       1    0      50  0.011364   Cohort    50 -0.58118
## 2:       1    4      50  0.011364   Cohort    50 -0.58118
## 3:       1    8      50  0.011364   Cohort    50 -0.58118
## 4:       1   12      50  0.011364   Cohort    50 -0.58118
## 5:       1   16      50  0.022727   Cohort    50 -0.58118
## 6:       1   20      50  0.022727   Cohort    50 -0.58118
```

Now, we go about creating our fitted object as usual

```
## Create regular fit in bdots
fit <- bdotsFit(data = dat,
                subject = "Subject",
                time = "Time",
                group = c("LookType", "Group"),
                y = "Fixations", curveType = doubleGauss2(),
                cores = 2)
```

Using this fit object, we now introduce the `bdotsCorr` function, taking four arguments:

1. `bdObj`, any object returned from a `bdotsFit` call
2. `val`, a length one character vector of the value with which we want to correlate. `val` should be a column in our original dataset, and it should be numeric
3. `ciBands`, a boolean indicating whether or not we want to return 95% confidence intervals. Default is `FALSE`
4. `method`, paralleling the `method` argument in `cor` and `cor.test`. The default is `pearson`.

```
## Returns a data.table of class bdotsCorrObj
corr_ci <- bdotsCorr(fit, val = "val", ciBands = TRUE)
head(corr_ci)
```

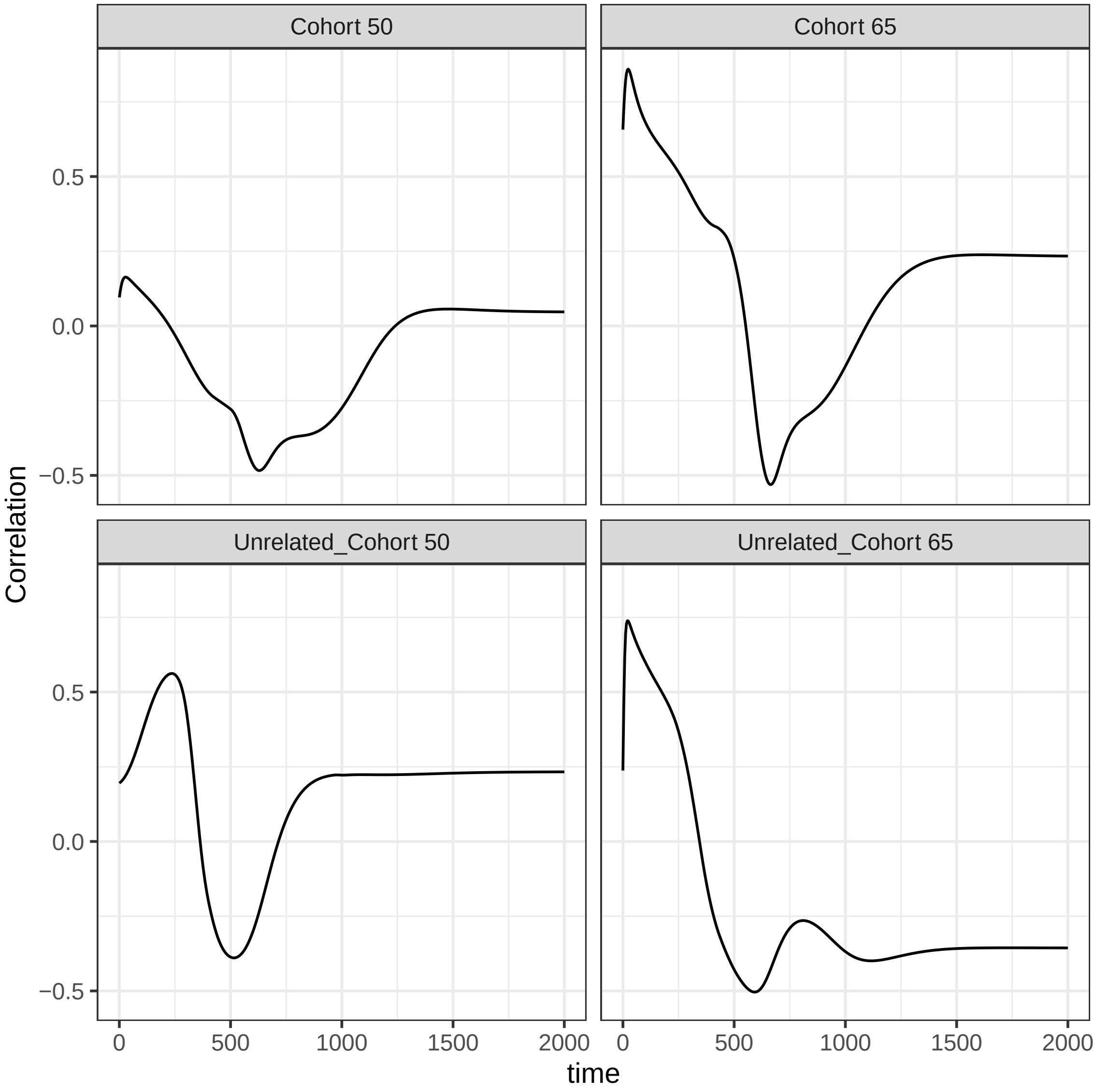
```
##    time Correlation    lower   upper     Group Group1 Group2
## 1:    0    0.095552 -0.60709 0.71434 Cohort 50 Cohort     50
## 2:    4    0.115780 -0.59402 0.72422 Cohort 50 Cohort     50
## 3:    8    0.132659 -0.58281 0.73227 Cohort 50 Cohort     50
## 4:   12    0.145523 -0.57408 0.73829 Cohort 50 Cohort     50
## 5:   16    0.154420 -0.56795 0.74241 Cohort 50 Cohort     50
## 6:   20    0.159896 -0.56413 0.74491 Cohort 50 Cohort     50
```

```
## Same, without confidence intervals
corr_noci <- bdotsCorr(fit, val = "val")
head(corr_noci)
```

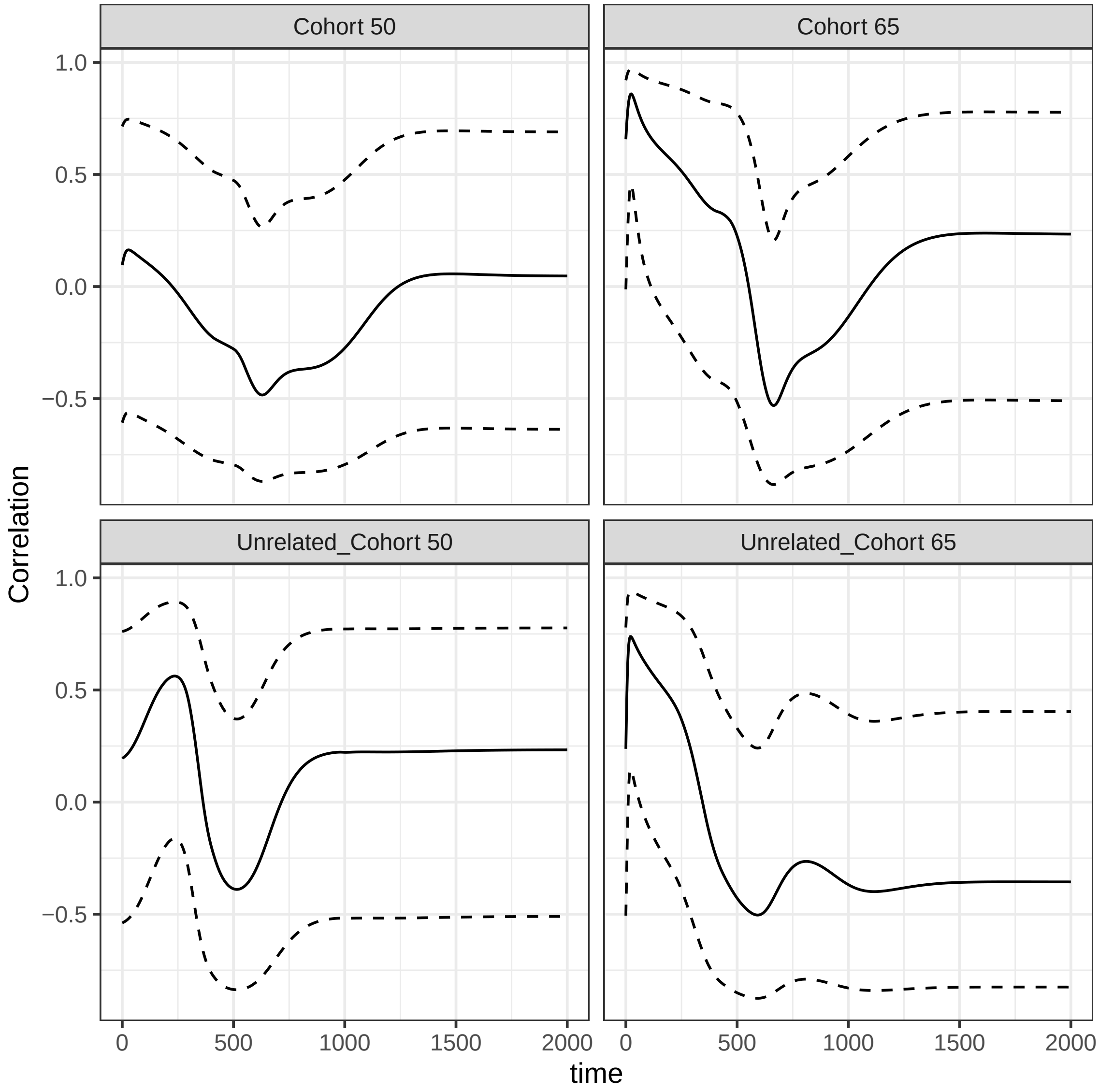
```
##    time Correlation     Group Group1 Group2
## 1:    0    0.095552 Cohort 50 Cohort     50
## 2:    4    0.115780 Cohort 50 Cohort     50
## 3:    8    0.132659 Cohort 50 Cohort     50
## 4:   12    0.145523 Cohort 50 Cohort     50
## 5:   16    0.154420 Cohort 50 Cohort     50
## 6:   20    0.159896 Cohort 50 Cohort     50
```

From here, we are able to use the `data.tables` themselves for whatever we may be interested in. We also have a plotting method associated with this object

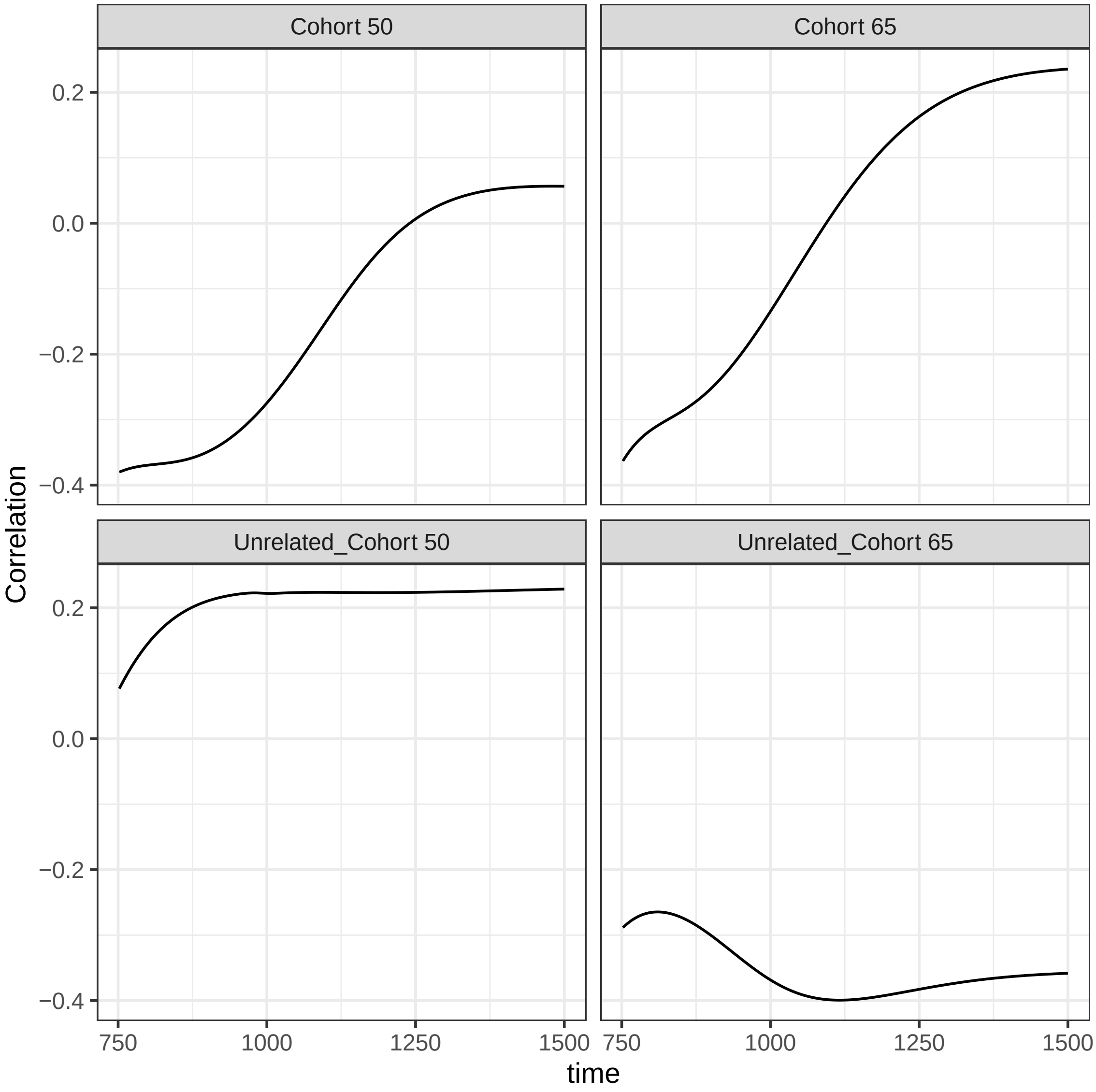
```
## Default is no bands
plot(corr_ci)
```



```r
## Try again with bands
plot(corr_ci, ciBands = TRUE)
```

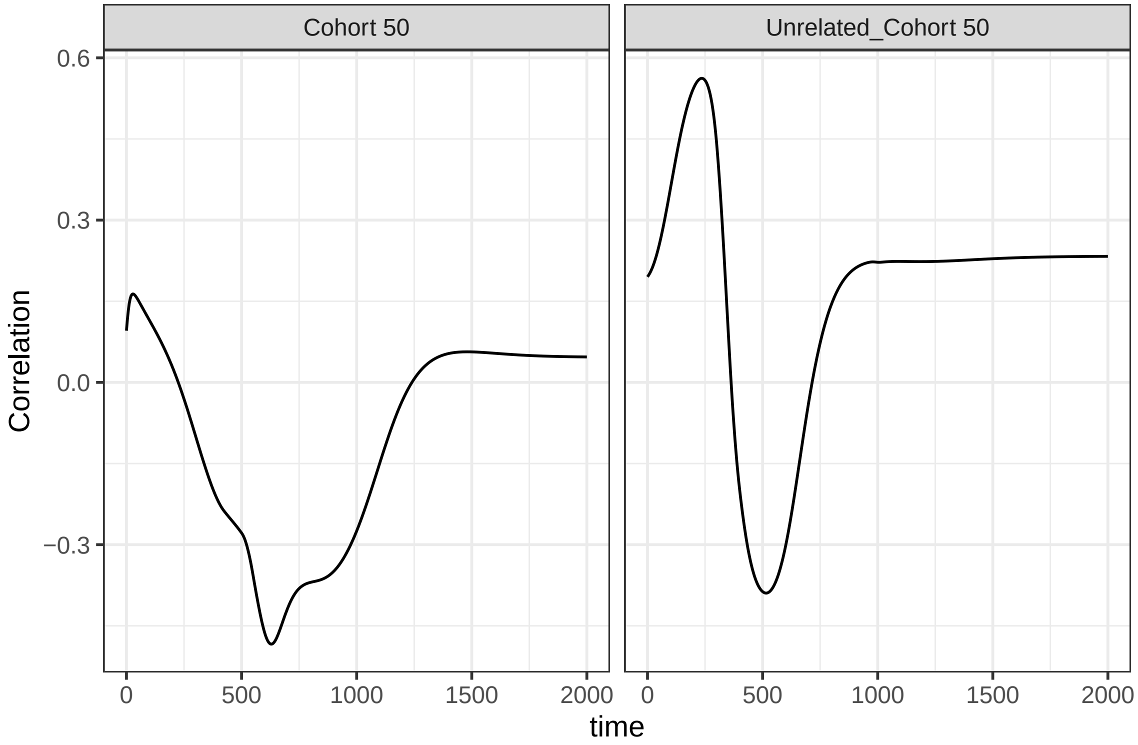


```r
## Narrow in on a particular window
plot(corr_ci, window = c(750, 1500))
```



Because this object is a `data.table`, we have full use of subsetting capabilities for our plots

```
plot(corr_ci[Group2 == "50", ])
```


Cohort 50
Unrelated_Cohort 50
Correlation
0.6
0.3
0.0
−0.3
0
500
1000
1500
2000
0
500
1000
1500
2000
time