Xeva Tutorial

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Load Xeva

Load Xeva library and data.

```r
library(Xeva)
cdf = readRDS("~/CXP/Xeva/DATA-raw/celineData.Rds")
head(ModelInfo(cdf))
```

```
##                                    model.id                    donor
## PHLC1106_P5.501.A1.1 PHLC1106_P5.501.A1.1 11101S-213RC-312S(F)-412S-
## PHLC1106_P5.504.A4.1 PHLC1106_P5.504.A4.1 11101S-213RC-312S(F)-412S-
## PHLC1106_P5.506.B1.1 PHLC1106_P5.506.B1.1 11101S-213RC-312S(F)-412S-
## PHLC1106_P5.507.B2.1 PHLC1106_P5.507.B2.1 11101S-213RC-312S(F)-412S-
## PHLC1106_P5.508.B3.1 PHLC1106_P5.508.B3.1 11101S-213RC-312S(F)-412S-
## PHLC1106_P5.511.C1.1 PHLC1106_P5.511.C1.1 11101S-213RC-312S(F)-412S-
##                         dob sex
## PHLC1106_P5.501.A1.1 Aug31.14   F
## PHLC1106_P5.504.A4.1 Aug31.14   F
## PHLC1106_P5.506.B1.1 Aug31.14   F
## PHLC1106_P5.507.B2.1 Aug31.14   F
## PHLC1106_P5.508.B3.1 Aug31.14   F
## PHLC1106_P5.511.C1.1 Sep14.14   F
##
## PHLC1106_P5.501.A1.1 /home/arvind/CXP/XG/Data/Celine_Data/Nhu-An_3Jan2017/PHLC110 Ludo (Every Mon) Ma
## PHLC1106_P5.504.A4.1 /home/arvind/CXP/XG/Data/Celine_Data/Nhu-An_3Jan2017/PHLC110 Ludo (Every Mon) Ma
## PHLC1106_P5.506.B1.1 /home/arvind/CXP/XG/Data/Celine_Data/Nhu-An_3Jan2017/PHLC110 Ludo (Every Mon) Ma
## PHLC1106_P5.507.B2.1 /home/arvind/CXP/XG/Data/Celine_Data/Nhu-An_3Jan2017/PHLC110 Ludo (Every Mon) Ma
## PHLC1106_P5.508.B3.1 /home/arvind/CXP/XG/Data/Celine_Data/Nhu-An_3Jan2017/PHLC110 Ludo (Every Mon) Ma
## PHLC1106_P5.511.C1.1 /home/arvind/CXP/XG/Data/Celine_Data/Nhu-An_3Jan2017/PHLC110 Ludo (Every Mon) Ma
##                         PHLC biobase.id patient.id
## PHLC1106_P5.501.A1.1 PHLC1106       <NA>       <NA>
## PHLC1106_P5.504.A4.1 PHLC1106       <NA>       <NA>
## PHLC1106_P5.506.B1.1 PHLC1106       <NA>       <NA>
## PHLC1106_P5.507.B2.1 PHLC1106       <NA>       <NA>
## PHLC1106_P5.508.B3.1 PHLC1106       <NA>       <NA>
## PHLC1106_P5.511.C1.1 PHLC1106       <NA>       <NA>
```
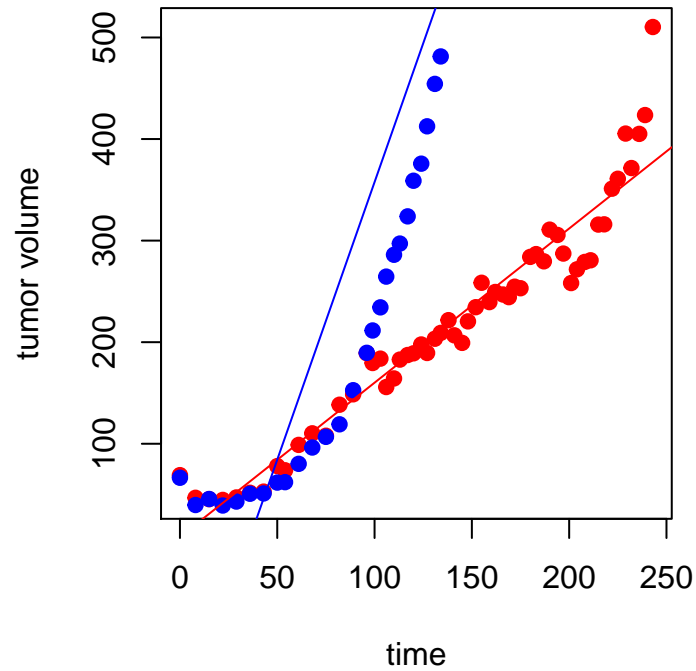
Models which belongs to same batch are in one list which is stored in expDesign slot. For example

```r
print(batchNames(cdf))
```

```
##    PHLC1106_P5    PHLC111_P7    PHLC119_P5    PHLC153_P6    PHLC181_P7
## "PHLC1106_P5"  "PHLC111_P7"  "PHLC119_P5"  "PHLC153_P6"  "PHLC181_P7"
##     PHLC189_P5    PHLC191_P5    PHLC191_P7    PHLC196_P5    PHLC215_P5
## "PHLC189_P5"  "PHLC191_P5"  "PHLC191_P7"  "PHLC196_P5"  "PHLC215_P5"
##     PHLC229_P6    PHLC235_P4    PHLC655_P7     PHLC82_P5
## "PHLC229_P6"  "PHLC235_P4"  "PHLC655_P7"   "PHLC82_P5"
```

To calculate angle between the treatment and control samples of this batch

```
batchNames = batchNames(cdf)
expDesign  = expDesign(cdf, batchNames[4])
ang = calculateAngle(cdf, expDesign, plot=TRUE)
```



```
print(ang)
```

```
## [1] 23.00287
```