Xeva Tutorial

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Load Xeva

Load Xeva library and data.

```
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>
```

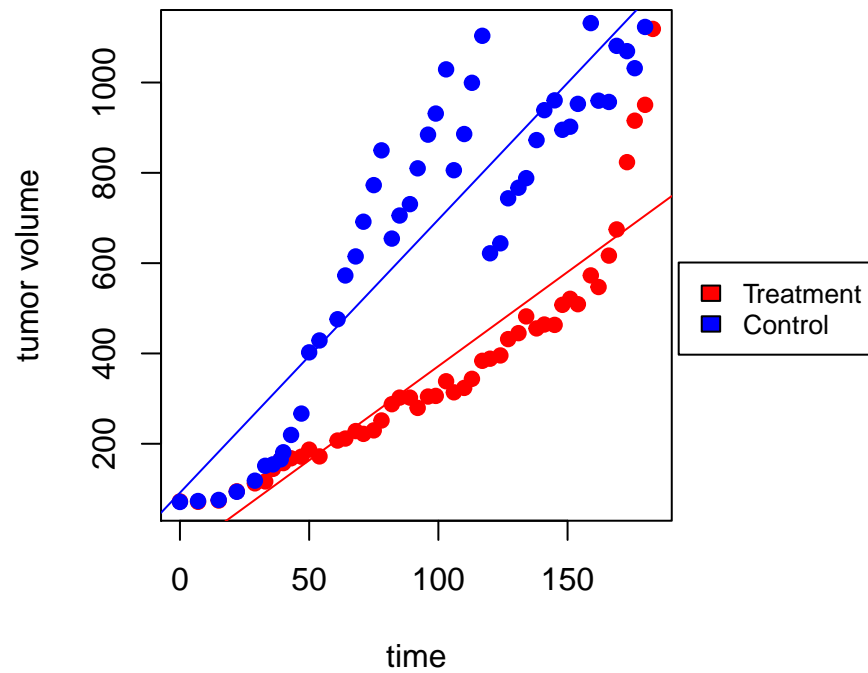Models which belongs to same batch are in one list which is stored in expDesign slot. For example

```
print(cdf@expDesign[[1]])
```

```
## $batch.name
## [1] "PHLC1106_P5"
##
## $treatment
```

```
## [1] "PHLC1106_P5.502.A2.1" "PHLC1106_P5.503.A3.1" "PHLC1106_P5.505.A5.1"
## [4] "PHLC1106_P5.509.B4.1" "PHLC1106_P5.510.B5.1" "PHLC1106_P5.512.C2.1"
##
## $control
## [1] "PHLC1106_P5.501.A1.1" "PHLC1106_P5.504.A4.1" "PHLC1106_P5.506.B1.1"
## [4] "PHLC1106_P5.507.B2.1" "PHLC1106_P5.508.B3.1" "PHLC1106_P5.511.C1.1"
```

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

```
batch = cdf@expDesign[[1]]
ang = calculateAngle(cdf, batch, plot=TRUE)
```



```
print(ang)
```

```
## [1] 4.100286
```