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)
```
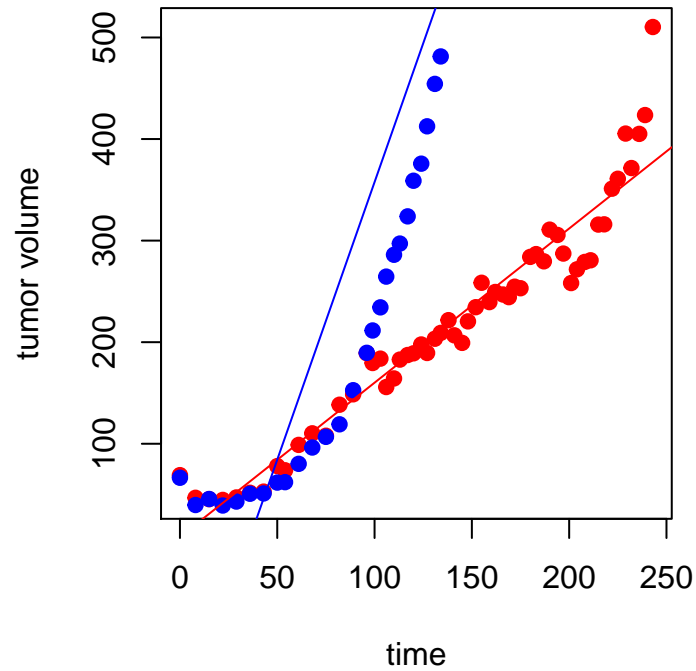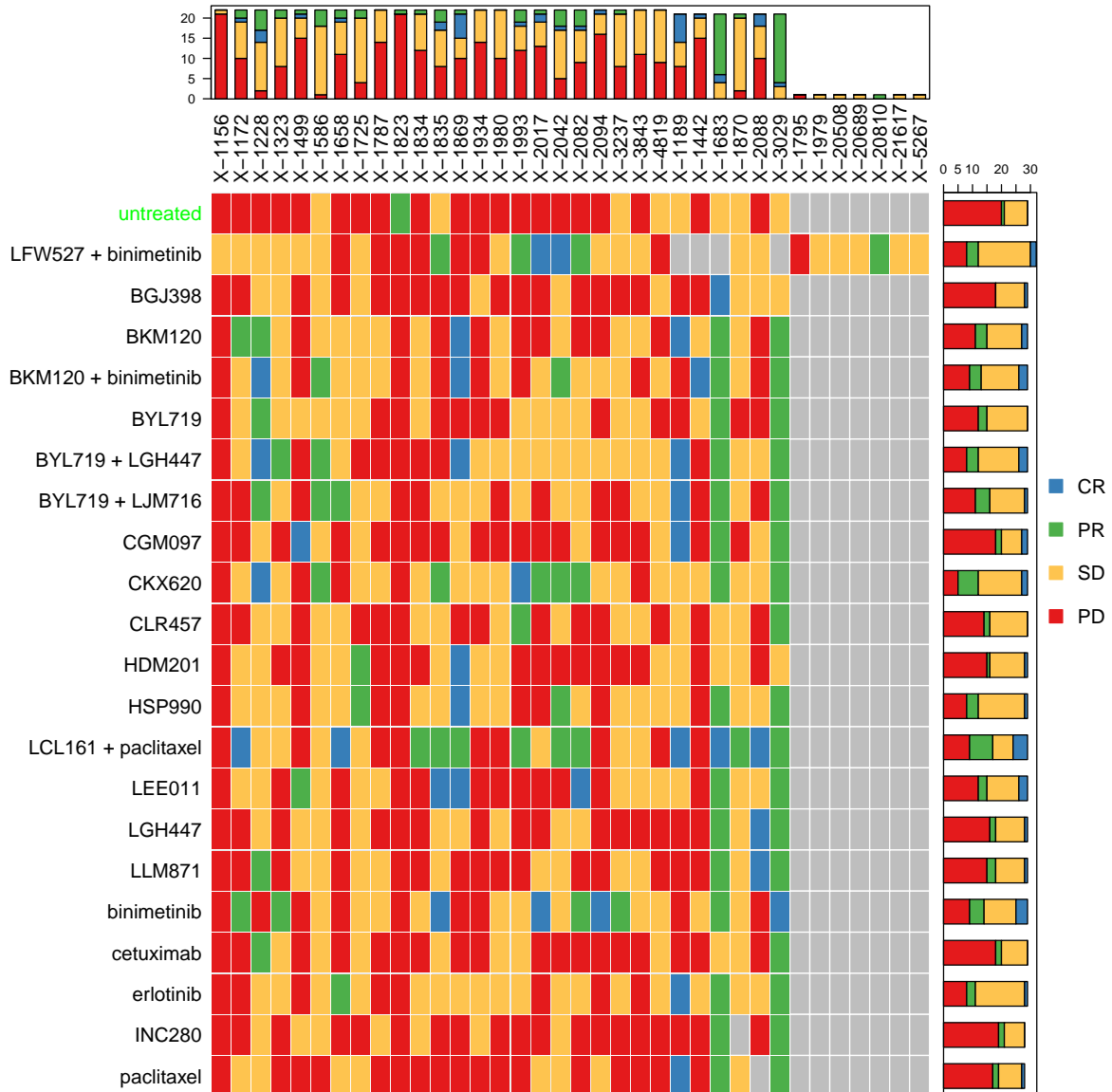


```
print(ang)
```

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

```
data(pdxe)
df = getmRECIST(pdxe)
## add tumor.type information
dfMap = mapModelSlotIds(object=pdxe, id=df$model.id, id.name="model.id", map.to="tumor.type")
dfx = merge(df, dfMap, by.x = "model.id", by.y = "model.id")
lungDf = dfx[dfx$tumor.type=="NSCLC", ]#c("model.id", "biobase.id", "drug.join.name", "mRECIST", "tumor
#pdf(file="DATA-raw/mRECIST_plot_NSCLC.pdf", width=12, height=10)
plotmRECIST(lungDf, groupBy = "biobase.id", control.name = "untreated")
```



```
#dev.off()
```