Xeva Tutorial

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Load Xeva

Load Xeva library and data.

```
library(Xeva)
data(lpdx)
head(modelInfo(lpdx))
```

```
##                                  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     PHLC biobase.id patient.id
## PHLC1106_P5.501.A1.1 Aug31.14   F PHLC1106   PHLC1106   PHLC1106
## PHLC1106_P5.504.A4.1 Aug31.14   F PHLC1106   PHLC1106   PHLC1106
## PHLC1106_P5.506.B1.1 Aug31.14   F PHLC1106   PHLC1106   PHLC1106
## PHLC1106_P5.507.B2.1 Aug31.14   F PHLC1106   PHLC1106   PHLC1106
## PHLC1106_P5.508.B3.1 Aug31.14   F PHLC1106   PHLC1106   PHLC1106
## PHLC1106_P5.511.C1.1 Sep14.14   F PHLC1106   PHLC1106   PHLC1106
```

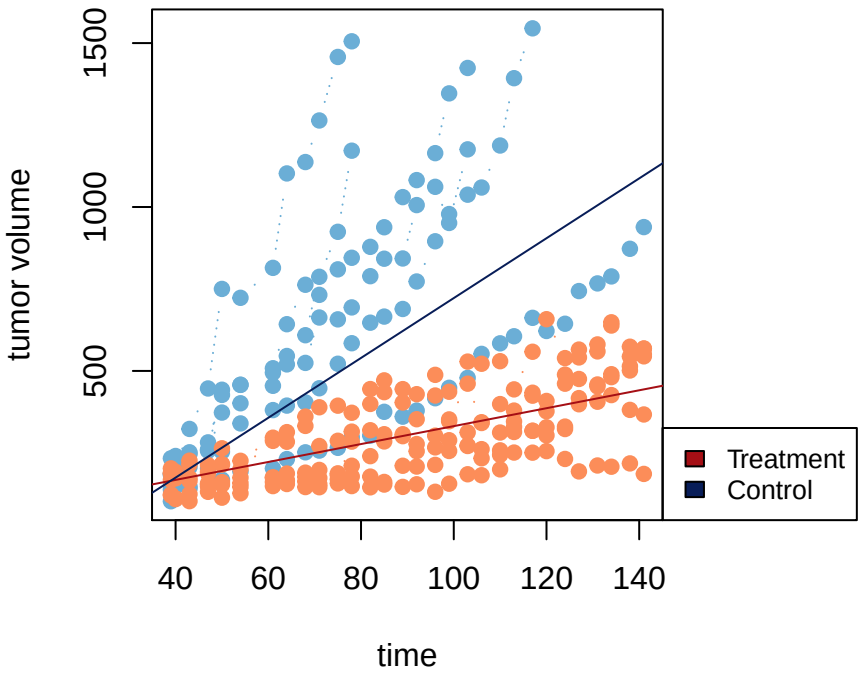
Models which belongs to same batch are in one list which is stored in expDesign slot. For example

```
print(batchNames(lpdx))
```

```
##   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

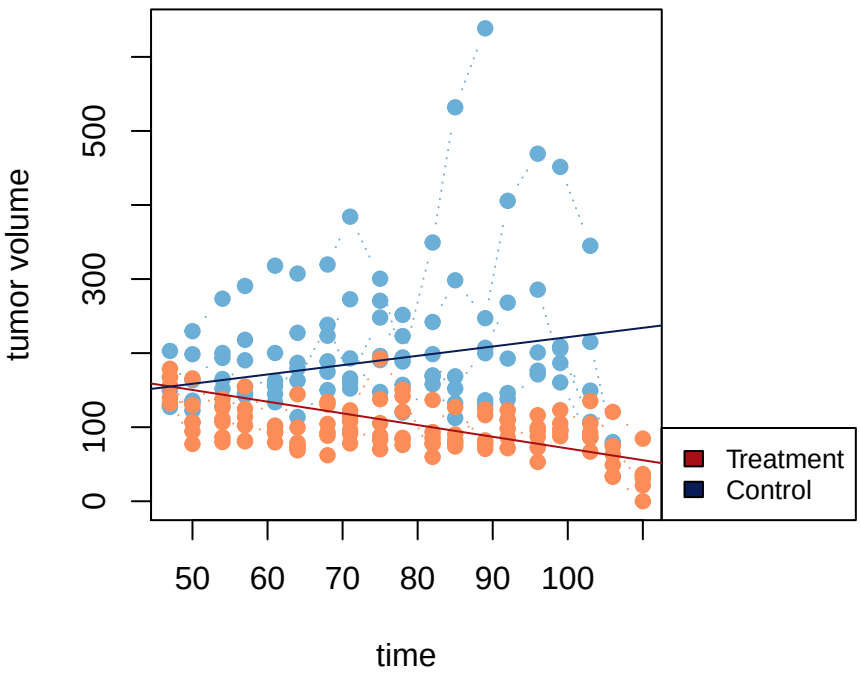
```
batchNames <- batchNames(lpdx)
expDesign  <- expDesign(lpdx, batchNames[1])
ang <- calculateAngle(lpdx, expDesign, treatment.only = TRUE, plot=TRUE)
```

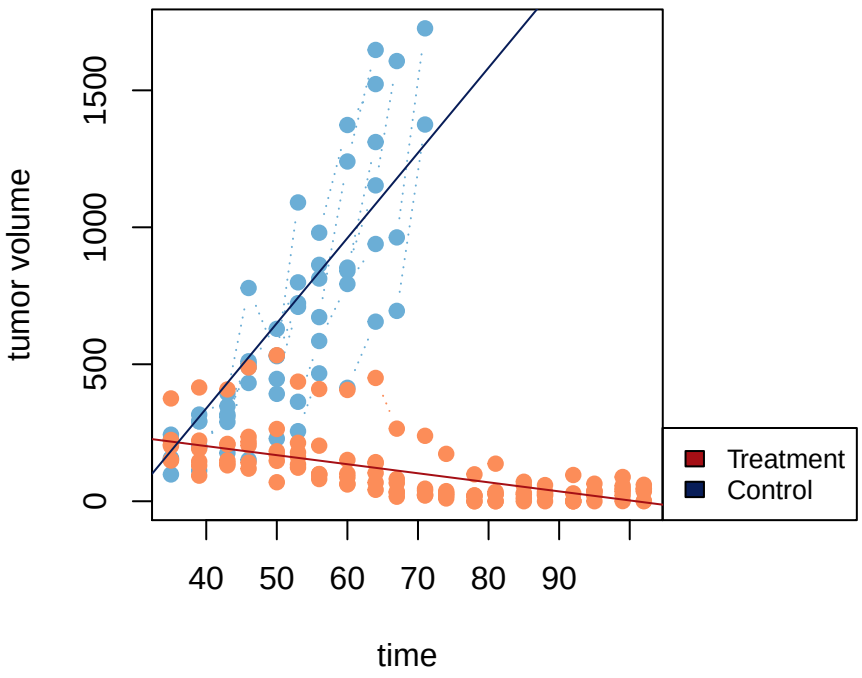


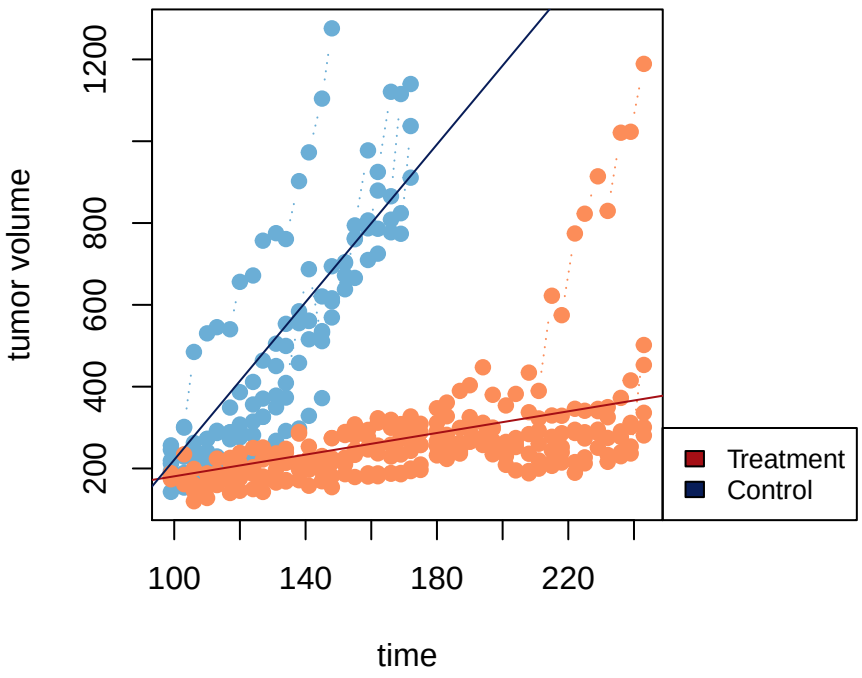

```
print(ang)
```

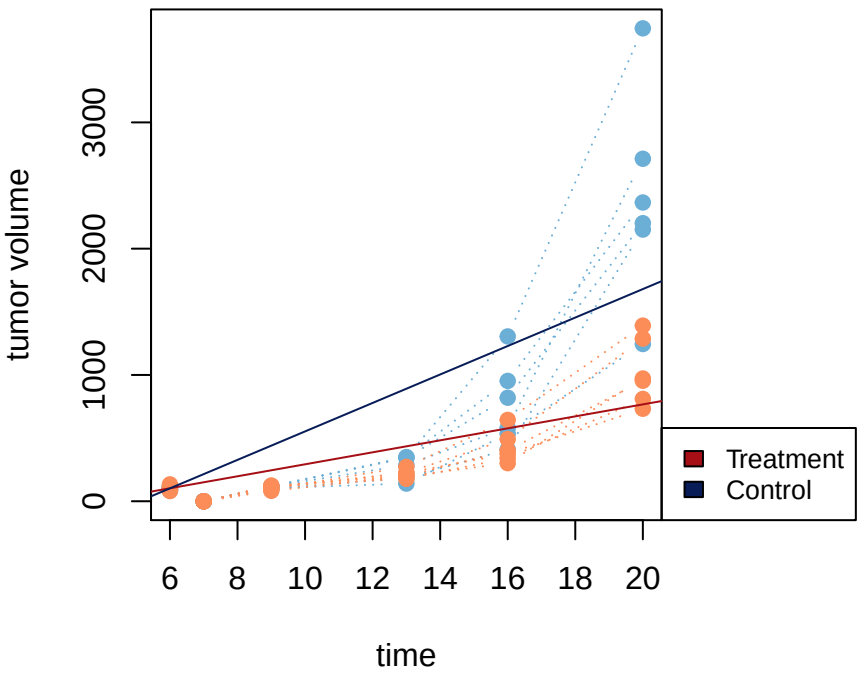
```
## $PHLC1106_P5
## [1] 13.84247
```

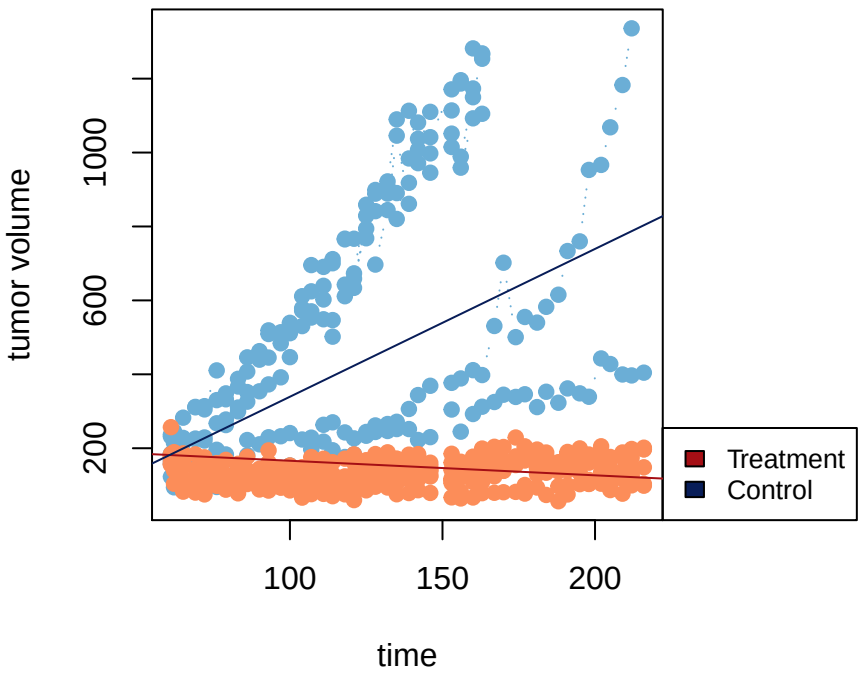
```
#par(mfrow=c(5,3))
for(I in batchNames)
{
  expDesign  <- expDesign(lpdx, I)
  ang <- calculateAngle(lpdx, expDesign, treatment.only = TRUE, plot=TRUE)
#  print(ang)
}
```

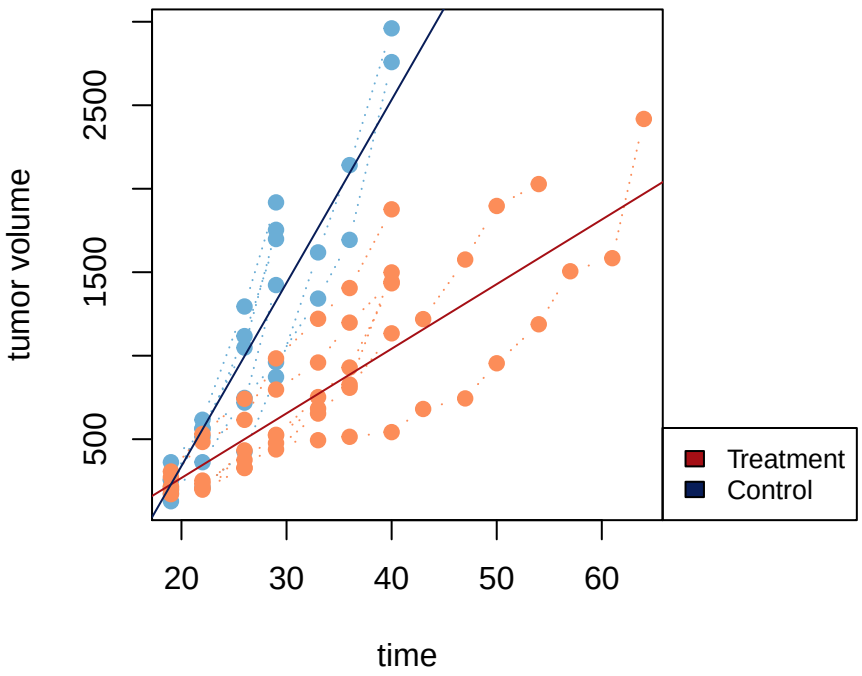

tumor volume
0
100
300
500
50
60
70
80
90
100
time
Treatment
Control

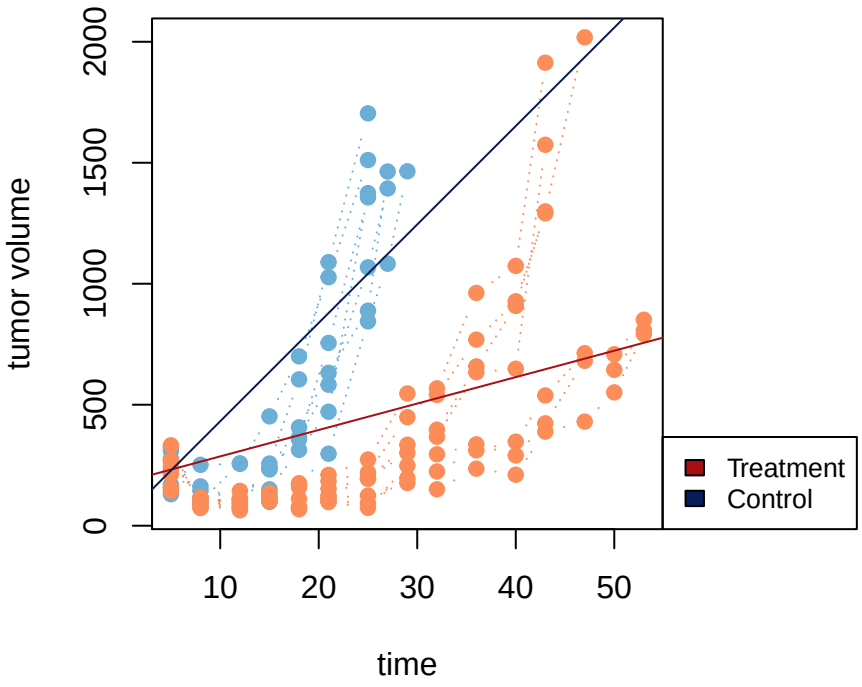

tumor volume
0
500
1000
1500
40
50
60
70
80
90
time
Treatment
Control

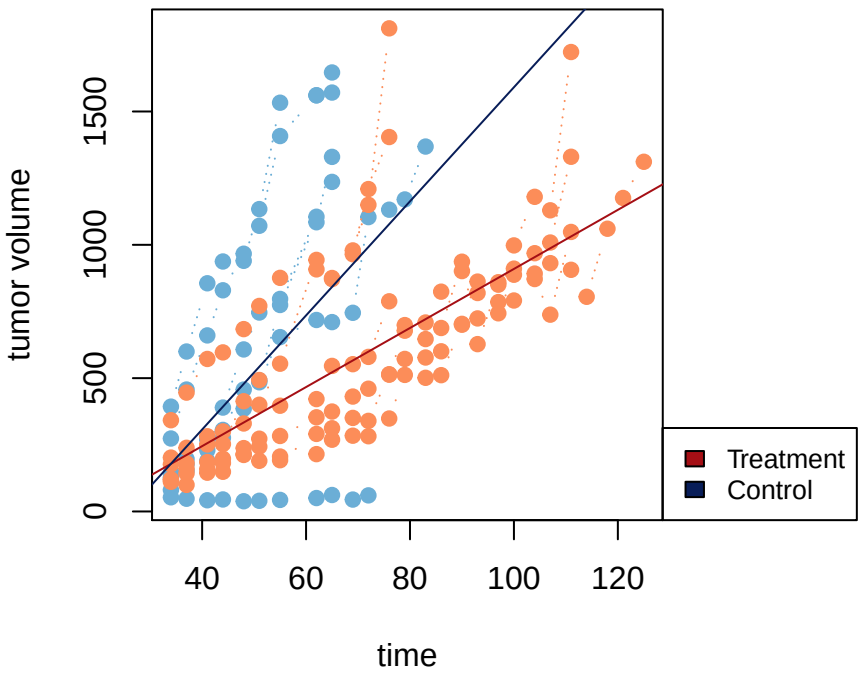

tumor volume
200
400
600
800
1200
100
140
180
220
time
Treatment
Control

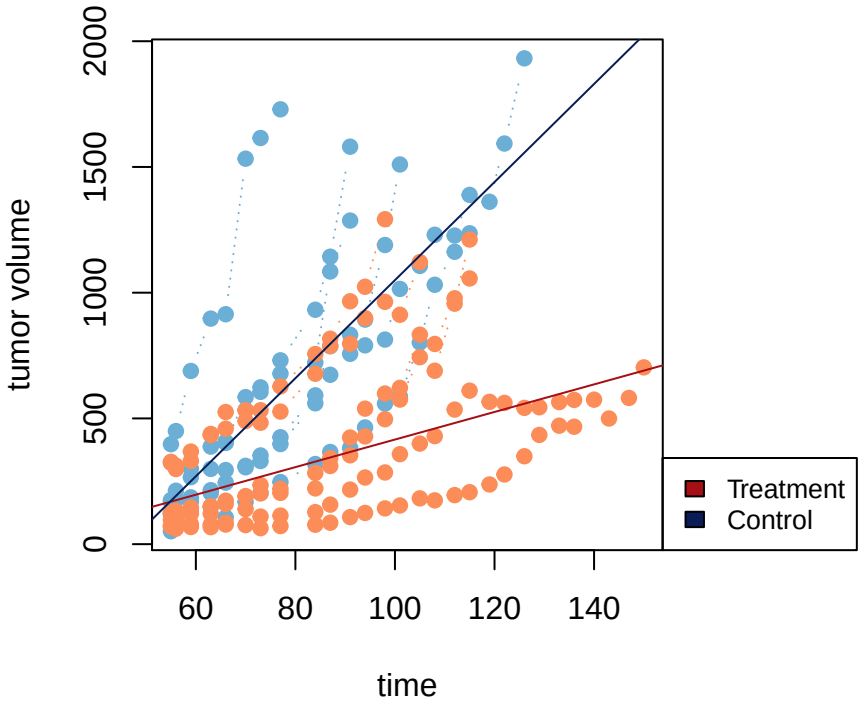

tumor volume
0
1000
2000
3000
6
8
10
12
14
16
18
20
time
Treatment
Control

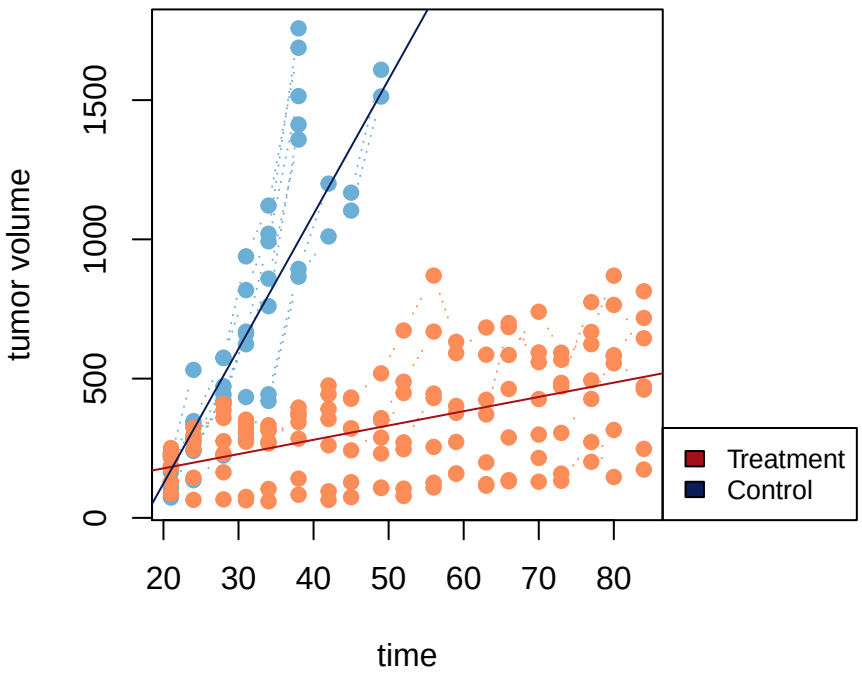

tumor volume
200
600
1000
100
150
200
time
Treatment
Control

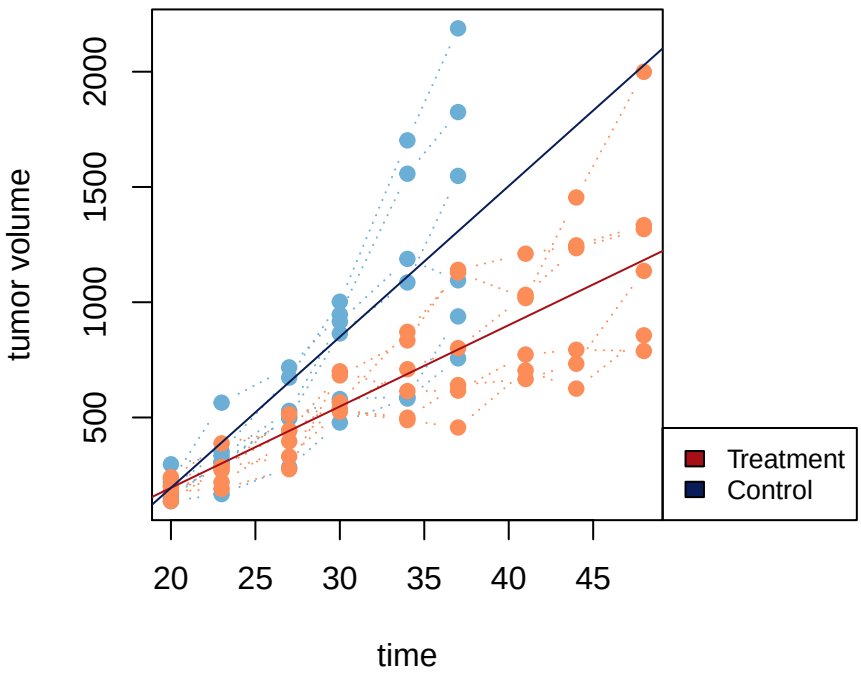

tumor volume
500
1500
2500
20
30
40
50
60
time
Treatment
Control

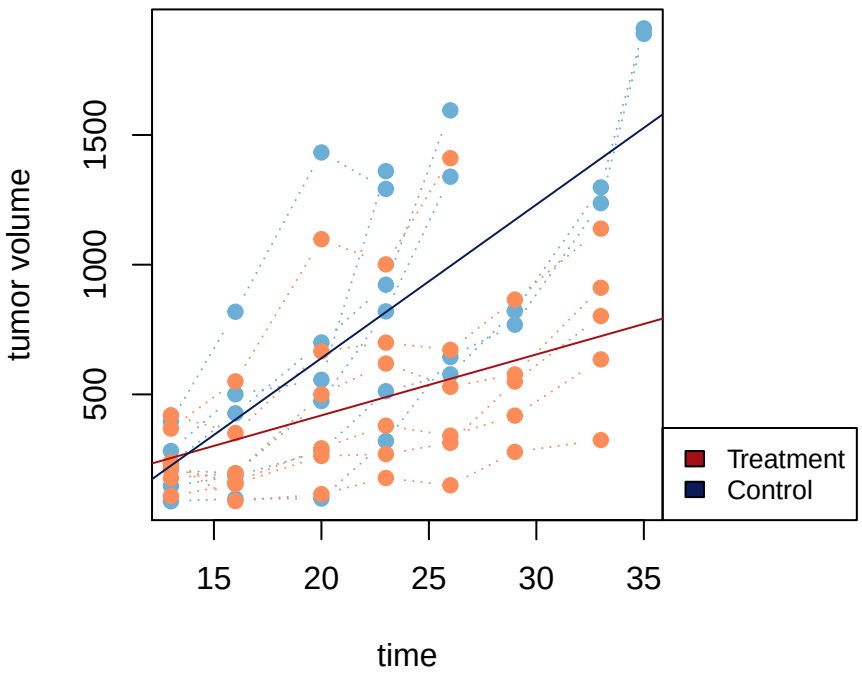

tumor volume
0
500
1000
1500
2000
10
20
30
40
50
time
Treatment
Control

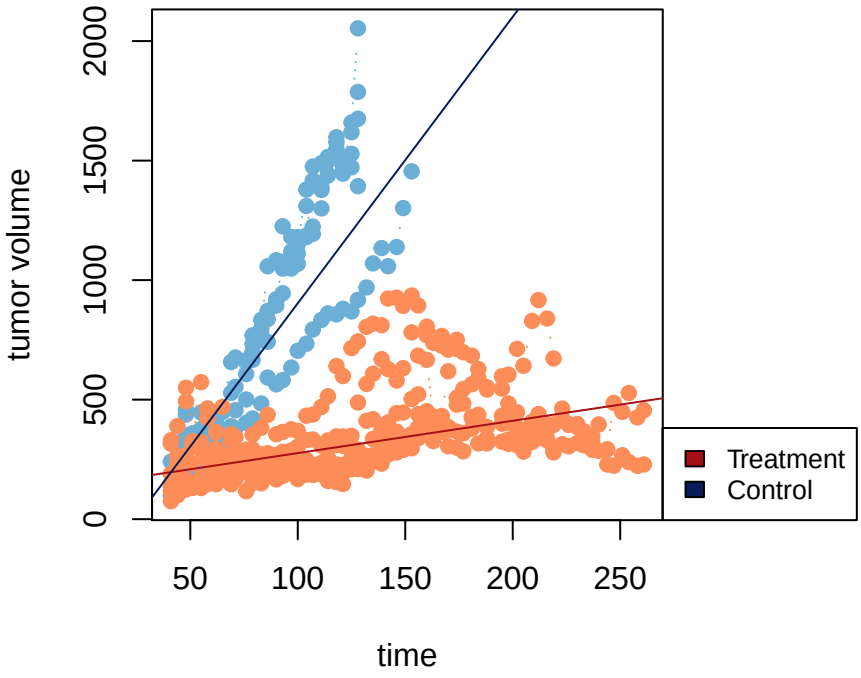

tumor volume
0
500
1000
1500
40
60
80
100
120
time
Treatment
Control


tumor volume
0
500
1000
1500
2000
60
80
100
120
140
time
Treatment
Control


tumor volume
0
500
1000
1500
20
30
40
50
60
70
80
time
Treatment
Control


tumor volume
500
1000
1500
2000
20
25
30
35
40
45
time
Treatment
Control


tumor volume
500
1000
1500
15
20
25
30
35
time
Treatment
Control



Summarize Response of PDXs Get slop of each model and combine summarize all model slop which belongs to same patient by "mean"

```
lpdx_slop <- summarizeResponse(lpdx, response.measure = "slop",
                               group.by="patient.id", summary.stat = "mean")
```

Get angle between treatment and control model ids. For each batch it will give one angle value

```
lpdx_angle <- summarizeResponse(lpdx, response.measure = "angle")
```

Get mutation expression profile

```
ldxe_mut <- getMolecularProfiles(lpdx, data.type="mutation")
print(ldxe_mut)
```

```
## ExpressionSet (storageMode: lockedEnvironment)
## assayData: 2666 features, 11 samples
##   element names: exprs
## protocolData: none
## phenoData
##   sampleNames: PHLC1106 PHLC111 ... PHLC82 (11 total)
##   varLabels: PHLC.ID X.ID
##   varMetadata: labelDescription
## featureData
##   featureNames: RERE SPATA21 ... MTMR1 (2666 total)
```

```
##   fvarLabels: probe.Id
##   fvarMetadata: labelDescription
## experimentData: use 'experimentData(object)'
## Annotation: MUT
```

The sample names in expression set are called biobase.id in model slot. Sample names from the expression set canb be be mapped to individual PDX model.ids as

```
# get sample names
library(Biobase)
```

```
## Loading required package: BiocGenerics
```

```
## Loading required package: parallel
```

```
##
## Attaching package: 'BiocGenerics'
```

```
## The following objects are masked from 'package:parallel':
##
##     clusterApply, clusterApplyLB, clusterCall, clusterEvalQ,
##     clusterExport, clusterMap, parApply, parCapply, parLapply,
##     parLapplyLB, parRapply, parSapply, parSapplyLB
```

```
## The following objects are masked from 'package:stats':
##
##     IQR, mad, xtabs
```

```
## The following objects are masked from 'package:base':
##
##     Filter, Find, Map, Position, Reduce, anyDuplicated, append,
##     as.data.frame, cbind, colnames, do.call, duplicated, eval,
##     evalq, get, grep, grepl, intersect, is.unsorted, lapply,
##     lengths, mapply, match, mget, order, paste, pmax, pmax.int,
##     pmin, pmin.int, rank, rbind, rownames, sapply, setdiff, sort,
##     table, tapply, union, unique, unsplit, which, which.max,
##     which.min
```

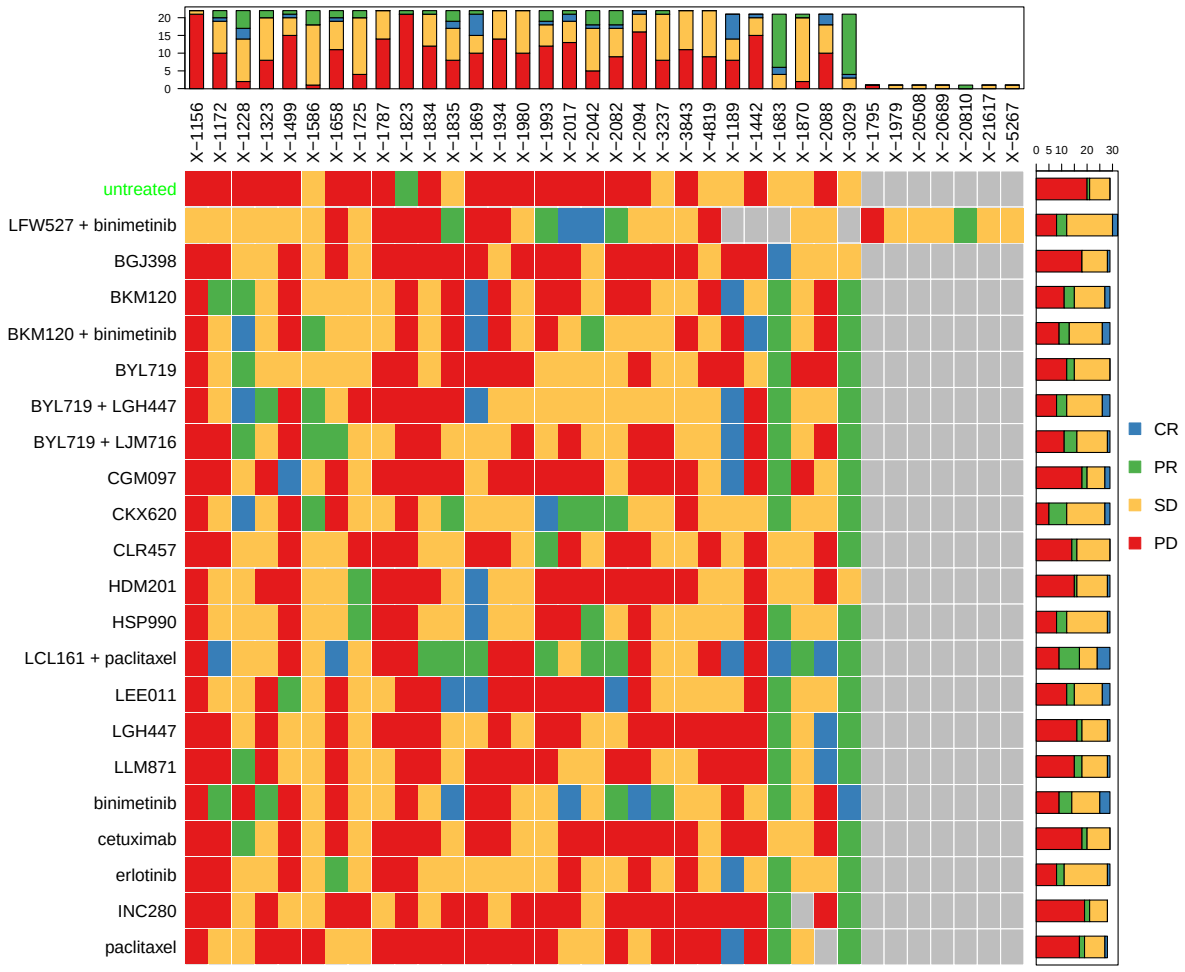
```
## Welcome to Bioconductor
##
##     Vignettes contain introductory material; view with
##     'browseVignettes()'. To cite Bioconductor, see
##     'citation("Biobase")', and for packages 'citation("pkgname")'.
```

```
sn <- Biobase::sampleNames(ldxe_mut)
smap <- mapModelSlotIds(lpdx, id=sn, id.name = "biobase.id", map.to = "model.id")
head(smap)
```

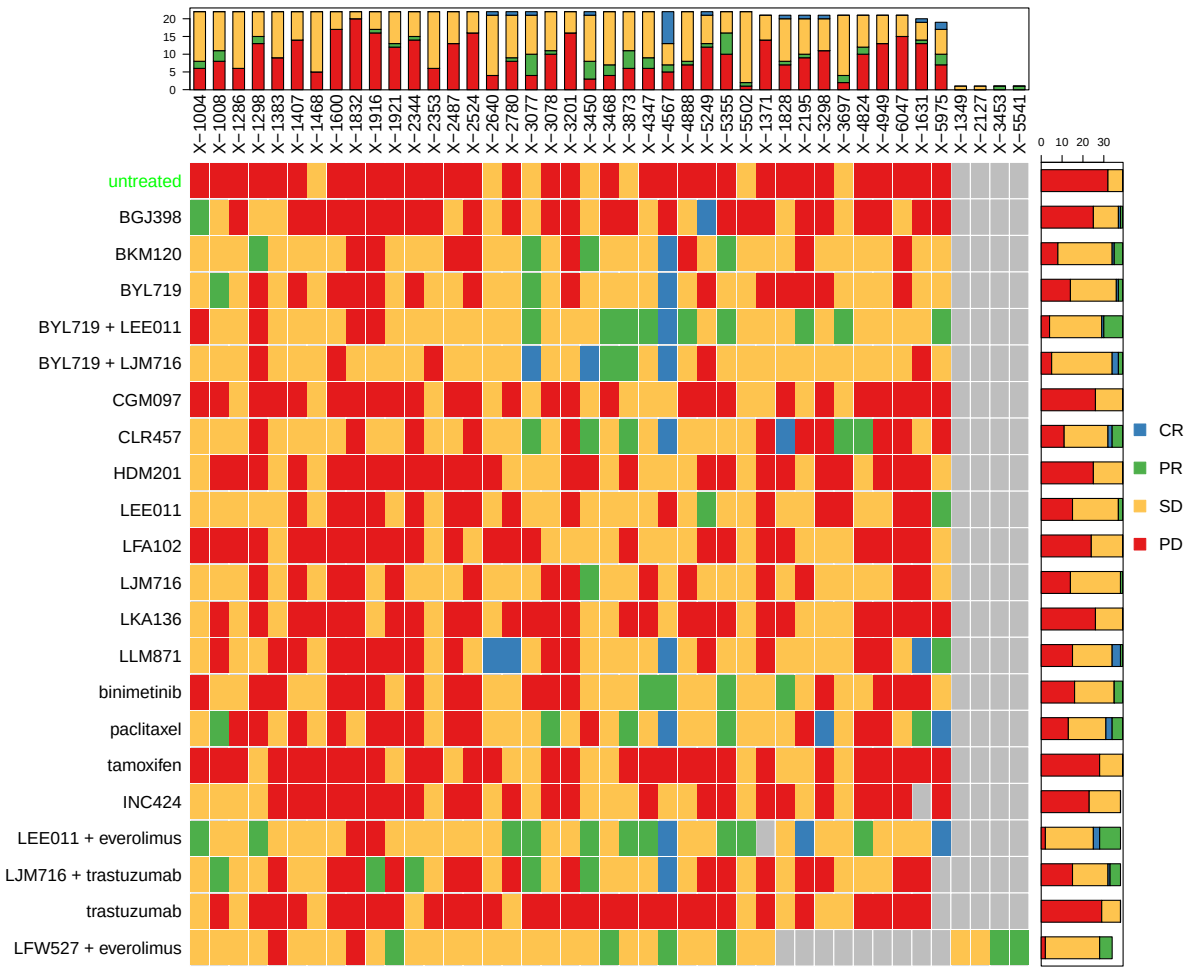
```
##                      biobase.id             model.id
## PHLC1106_P5.501.A1.1   PHLC1106 PHLC1106_P5.501.A1.1
## PHLC1106_P5.504.A4.1   PHLC1106 PHLC1106_P5.504.A4.1
## PHLC1106_P5.506.B1.1   PHLC1106 PHLC1106_P5.506.B1.1
## PHLC1106_P5.507.B2.1   PHLC1106 PHLC1106_P5.507.B2.1
## PHLC1106_P5.508.B3.1   PHLC1106 PHLC1106_P5.508.B3.1
## PHLC1106_P5.511.C1.1   PHLC1106 PHLC1106_P5.511.C1.1
```

Create mRECIST plot for PDXE Lung Cancer data

```
data(pdxe)
df <- getmRECIST(pdxe)
## add tumor.type information
dfMap <- mapModelSlotIds(object=pdxe, id=df$model.id, id.name="model.id",
                         map.to="tumor.type", unique = FALSE)
if(all(df$model.id==dfMap$model.id)) {df$tumor.type = dfMap$tumor.type}
lungDf = df[df$tumor.type=="NSCLC", ]
#pdf(file="DATA-raw/mRECIST_plot_NSCLC.pdf", width=12, height=10)
plotmRECIST(lungDf, groupBy = "biobase.id", control.name = "untreated")
```




```
#pdf(file="DATA-raw/mRECIST_plot_BRCA.pdf", width=12, height=10)
brDF = df[df$tumor.type=="BRCA", ]
plotmRECIST(brDF, groupBy = "biobase.id", control.name = "untreated")
```




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

Creat mR vs slop bar-plot

```
data(pdxe)

pm = modelInfo(pdxe)
lungPID = unique(pm[pm$tumor.type=="NSCLC", "patient.id"])

pdxe_slop <- summarizeResponse(pdxe, response.measure = "slop",
                               group.by="patient.id", summary.stat = "mean")

lung_pdxe_slope <- pdxe_slop[, lungPID]

##-------
pdxe_mR <- summarizeResponse(pdxe, response.measure = "mRECIST_recomputed",
                               group.by="patient.id")

lung_pdxe_mR = pdxe_mR[, lungPID]
```

```
slope=c(); mR=c()
for(dn in rownames(lung_pdxe_slope))
{
  for(pi in colnames(lung_pdxe_slope))
  {
    v = c(lung_pdxe_slope[dn,pi], lung_pdxe_mR[dn,pi])
    if(!is.na(v[1]) & !is.na(v[1]))
    { slope = c(slope,v[1]); mR=c(mR,v[2]) }
  }
}

df = data.frame(mR= mR, slope= as.numeric(slope), stringsAsFactors = FALSE)
df$mR= factor(df$mR, c("CR", "PR", "SD", "PD"))

colPalette = c("#377eb8", "#4daf4a", "#fec44f", "#e41a1c")
boxplot(slope~mR, data=df, col=colPalette,
  main="mRECIST vs slope", xlab="mRECIST", ylab="slope")
```