

Xeva Tutorial

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Load Xeva

Load Xeva library and data

```
library(Xeva)
data(pdx)
```

Access experiment slot

Get all model.id for which drug “paclitaxel” was used and tumor.type is “BRCA”

```
modelIds = getModelIds(pdx, drug="paclitaxel", drug.match.exact=TRUE, tumor.type="BRCA")
print(modelIds)
```

```
## [1] "X.1004.pael" "X.1008.pael" "X.1286.pael" "X.1298.pael" "X.1371.pael"
## [6] "X.1383.pael" "X.1407.pael" "X.1468.pael" "X.1600.pael" "X.1631.pael"
## [11] "X.1828.pael" "X.1832.pael" "X.1916.pael" "X.1921.pael" "X.2195.pael"
## [16] "X.2344.pael" "X.2353.pael" "X.2487.pael" "X.2524.pael" "X.2640.pael"
## [21] "X.2780.pael" "X.3077.pael" "X.3078.pael" "X.3201.pael" "X.3298.pael"
## [26] "X.3450.pael" "X.3468.pael" "X.3697.pael" "X.3873.pael" "X.4347.pael"
## [31] "X.4567.pael" "X.4824.pael" "X.4888.pael" "X.4949.pael" "X.5249.pael"
## [36] "X.5355.pael" "X.5502.pael" "X.5975.pael" "X.6047.pael"
```

To get the data for a model id

```
df = getExperiment(pdx, model.id="X.1655.LE11.biiib")
head(df)
```

```
##   time volume body.weight volume.change average.response
## 1    0 200.93      24.1      0.000000      0.0000000
## 2    3 203.64      24.8      1.348728      0.6743642
## 3    7 220.28      24.5      9.630219      3.6596493
## 4   10 212.34      25.6      5.678595      4.1643856
## 5   14 207.00      25.3      3.020953      3.9356990
## 6   20 158.37      25.5     -21.181506     -0.2505018
##   body.weight.change      model.id      drug.join.name
## 1      0.000000 X.1655.LE11.biiib LEE011 + binimetinib
## 2      2.904564 X.1655.LE11.biiib LEE011 + binimetinib
## 3      1.659751 X.1655.LE11.biiib LEE011 + binimetinib
## 4      6.224066 X.1655.LE11.biiib LEE011 + binimetinib
## 5      4.979253 X.1655.LE11.biiib LEE011 + binimetinib
## 6      5.809129 X.1655.LE11.biiib LEE011 + binimetinib
##   drug.names.drug.1 drug.names.drug.2
## 1      LEE011      binimetinib
```

```
## 2          LEE011      binimetinib
## 3          LEE011      binimetinib
## 4          LEE011      binimetinib
## 5          LEE011      binimetinib
## 6          LEE011      binimetinib
##              experiment.id best.response.time
## 1 X.1655.LE11.biib.LEE011 + binimetinib      65
## 2 X.1655.LE11.biib.LEE011 + binimetinib      65
## 3 X.1655.LE11.biib.LEE011 + binimetinib      65
## 4 X.1655.LE11.biib.LEE011 + binimetinib      65
## 5 X.1655.LE11.biib.LEE011 + binimetinib      65
## 6 X.1655.LE11.biib.LEE011 + binimetinib      65
## best.response.value best.response.index best.average.response.time
## 1 -47.5140596227542          17          84
## 2 -47.5140596227542          17          84
## 3 -47.5140596227542          17          84
## 4 -47.5140596227542          17          84
## 5 -47.5140596227542          17          84
## 6 -47.5140596227542          17          84
## best.average.response.value best.average.response.index mRECIST
## 1 -18.9353715748087          19      SD
## 2 -18.9353715748087          19      SD
## 3 -18.9353715748087          19      SD
## 4 -18.9353715748087          19      SD
## 5 -18.9353715748087          19      SD
## 6 -18.9353715748087          19      SD
```

To get all mode

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When you click the **Knit** button a document will be generated that includes both content as well as the output of any embedded R code chunks within the document. You can embed an R code chunk like this:

```
summary(cars)
```

```
##      speed      dist
## Min.   : 4.0    Min.   :  2.00
## 1st Qu.:12.0    1st Qu.: 26.00
## Median :15.0    Median : 36.00
## Mean   :15.4    Mean   : 42.98
## 3rd Qu.:19.0    3rd Qu.: 56.00
## Max.   :25.0    Max.   :120.00
```

Including Plots

You can also embed plots, for example:



Note that the `echo = FALSE` parameter was added to the code chunk to prevent printing of the R code that generated the plot.