

The Xeva user’s guide

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1 Introduction

The Xeva package provides efficient and powerful functions for patient driven xenograft (PDX) based pharmacogenomic data analysis.

2 Installation and Settings

Xeva requires that several packages are installed. However, all dependencies are available from CRAN or Bioconductor.

```
source('http://bioconductor.org/biocLite.R')
biocLite('Xeva')
```

Load Xeva into your current workspace:

```
library(Xeva)
```

Load PDXE breast cancer dataset:

```
data(brca)
print(brca)

## Xeva-set name: PDXE.BRCA
## Creation date: Mon Aug 27 11:16:00 2018
## Number of models: 849
## Number of drugs: 22
## Moleculer dataset: RNASeq, mutation, microArray, cnv
```

3 Definations

Before we further dive into the analysis and visualization, it is important to understand terms used in the Xeva package. In a Xeva object, the experiment slot stores each individual PDX/mouse data. This data is stored using the class `pdxModel` and a unique id called *model.id* is given to each PDX model. Therefore *model.id* represents individual mouse/PDX id. We can visualize data for an exampl

4 PDX Data Access

To store and access the data **Xeva** uses XevaSet class. Xeva stores data for each individual PDX model. We can see the information about models using:

```
brca.mod <- modelInfo(brca)
brca.mod[1:4, ]

##           model.id tissue  tissue.name patient.id      drug
## X.1004.BG98 X.1004.BG98  BRCA Breast Cancer    X-1004    BGJ398
## X.1004.biib X.1004.biib  BRCA Breast Cancer    X-1004 binimetinib
## X.1004.BK20 X.1004.BK20  BRCA Breast Cancer    X-1004    BKM120
## X.1004.BY19 X.1004.BY19  BRCA Breast Cancer    X-1004    BYL719
```

5 PDX Model Response

Xeva can effectively summarize the PDX response data. Here we summarize the **mRECIST** values for models in the dataset:

```
brca.mr <- summarizeResponse(brca, response.measure = "mRECIST")
brca.mr[1:5, 1:4]

##           X-1004 X-1008 X-1286 X-1298
## BGJ398          PR     SD      PD      SD
## binimetinib      PD     SD      SD      PD
## BKM120           SD     SD      SD      PR
## BYL719           SD     PR      SD      PD
## BYL719 + LEE011  PD     SD      SD      PD
```

These **mRECIST** values can be visualized as:

```
plotmRECIST(brca.mr, control.name = "untreated")
```

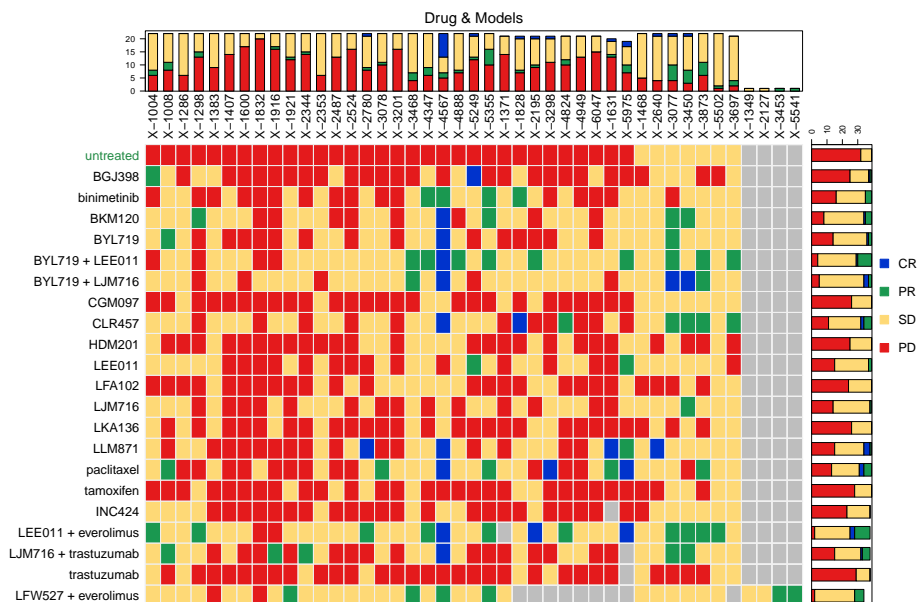


Figure 1: mRECIST plot for PDX breast cancer data

6 Visualizing PDX Growth Curve

```
plotBatch(brca, batch = "X-4567.BKM120")
```

```
plotBatch(brca, patient.id="X-4567", drug="BKM120", control.name="untreated")
```

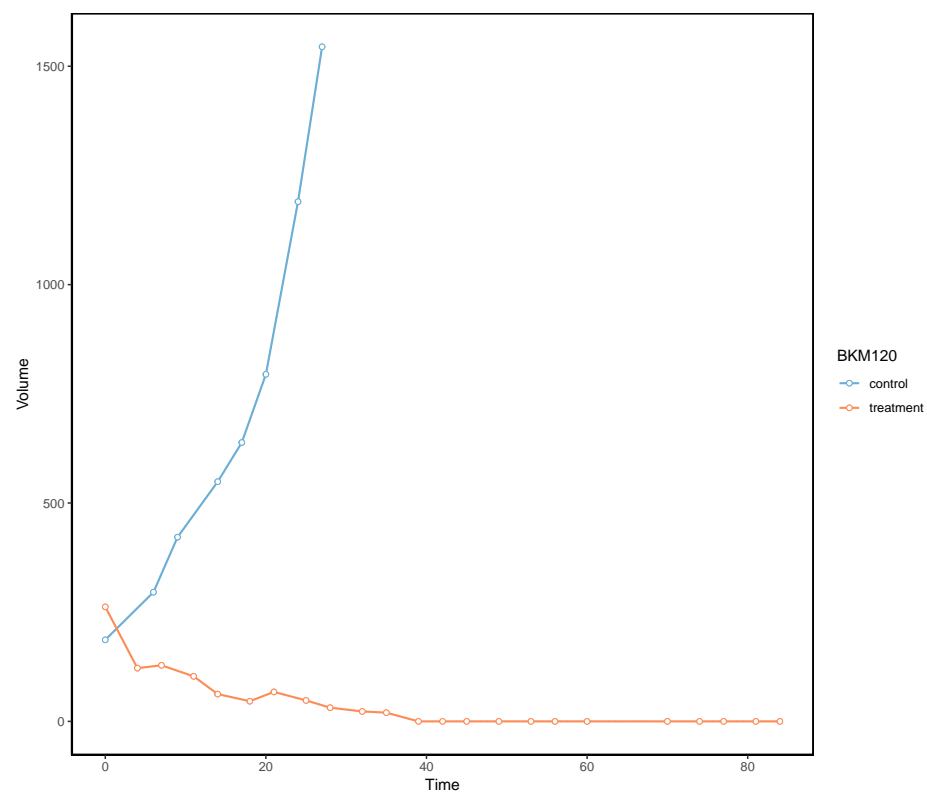


Figure 2: mRECIST plot for PDXE breast cancer data

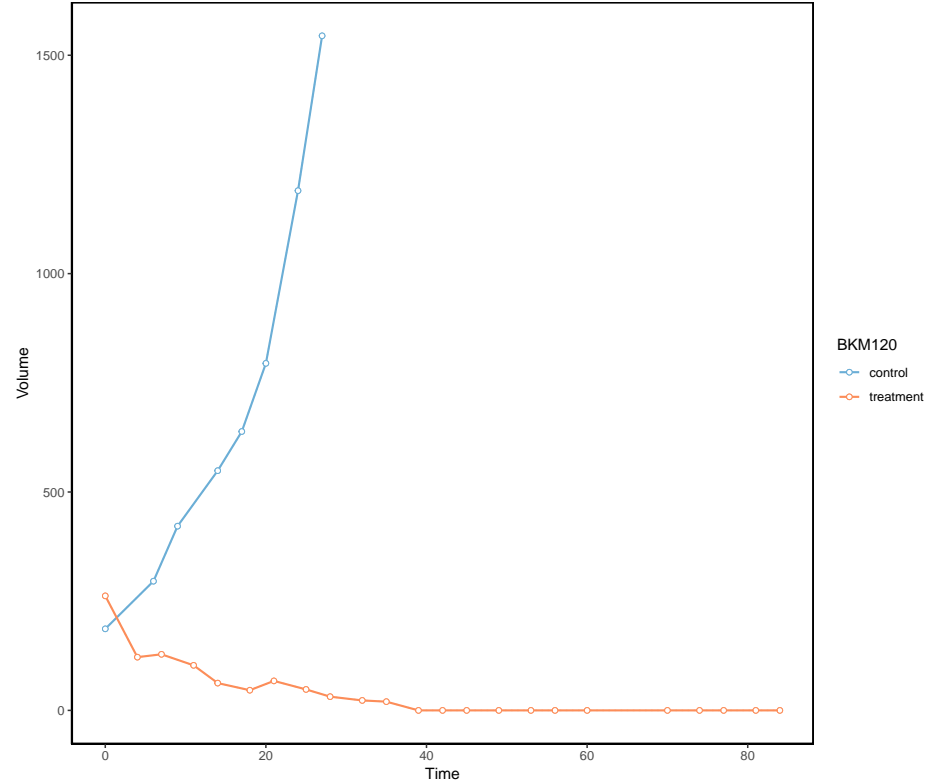


Figure 3: mRECIST plot for PDXE breast cancer data