

Xeva Tutorial

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

Load Xeva library and PDXE breast cancer dataset

```
library(Xeva)
data(brca)
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
```

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

```
brca.mod <- modelInfo(brca)
head(brca.mod)
```

```
##               model.id tissue  tissue.name patient.id
## X.1004.BG98      X.1004.BG98  BRCA Breast Cancer    X-1004
## X.1004.biib      X.1004.biib  BRCA Breast Cancer    X-1004
## X.1004.BK20      X.1004.BK20  BRCA Breast Cancer    X-1004
## X.1004.BY19      X.1004.BY19  BRCA Breast Cancer    X-1004
## X.1004.BY19.LE11 X.1004.BY19.LE11 BRCA Breast Cancer X-1004
## X.1004.BY19.LJ16 X.1004.BY19.LJ16 BRCA Breast Cancer X-1004
##               drug
## X.1004.BG98      BGJ398
## X.1004.biib      binimetinib
## X.1004.BK20      BKM120
## X.1004.BY19      BYL719
## X.1004.BY19.LE11 BYL719 + LEE011
## X.1004.BY19.LJ16 BYL719 + LJM716
```

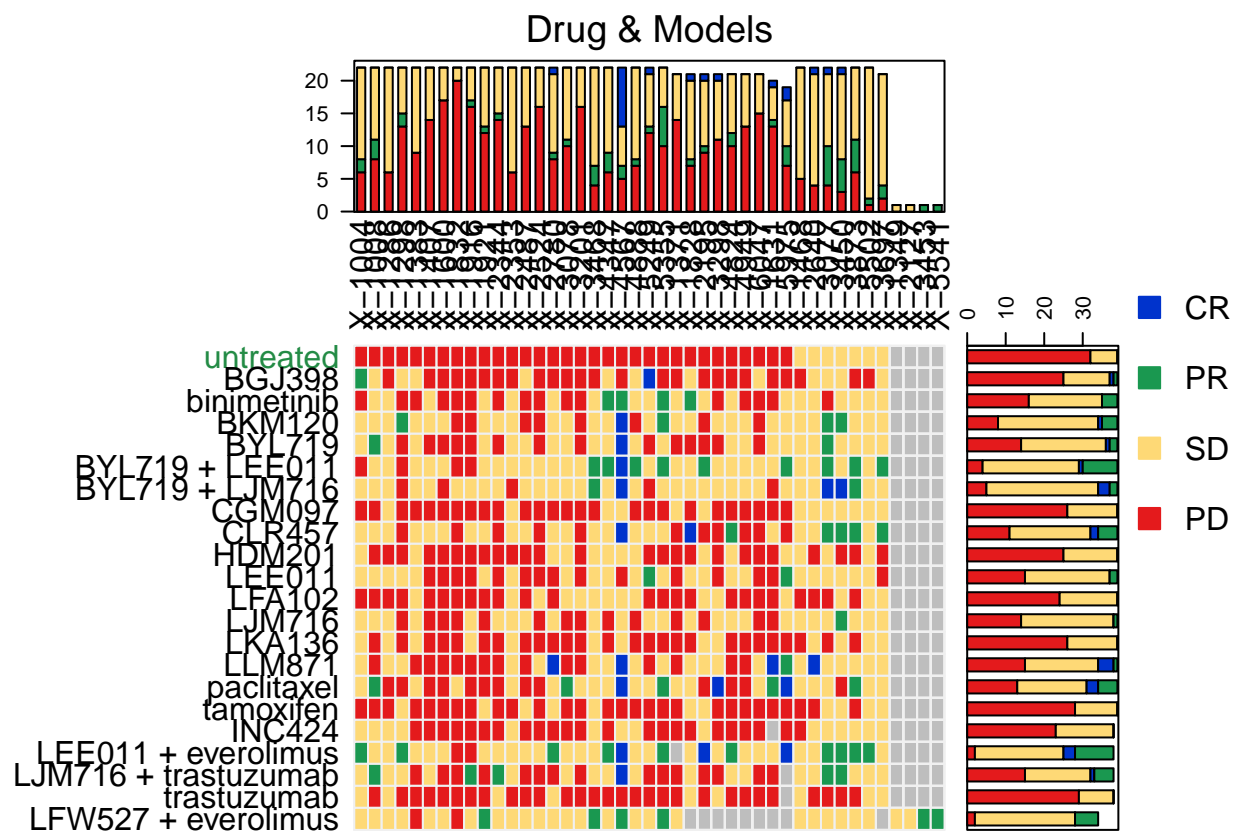
Create the mRECIST plot for data

```
brca.mr <- summarizeResponse(brca, response.measure = "mRECIST")
head(brca.mr)
```

```
##           X-1004 X-1008 X-1286 X-1298 X-1349 X-1371 X-1383 X-1407
## BGJ398         PR    SD    PD    SD    <NA>    PD    SD    PD
## binimetinib    PD    SD    SD    PD    <NA>    SD    PD    SD
## BKM120         SD    SD    SD    PR    <NA>    SD    SD    SD
## BYL719         SD    PR    SD    PD    <NA>    PD    SD    PD
## BYL719 + LEE011 PD    SD    SD    PD    <NA>    SD    SD    SD
## BYL719 + LJM716 SD    SD    SD    PD    <NA>    SD    SD    SD
##           X-1468 X-1600 X-1631 X-1828 X-1832 X-1916 X-1921 X-2127
## BGJ398         PD    PD    PD    SD    PD    PD    PD    <NA>
## binimetinib    SD    PD    PD    PR    PD    PD    SD    <NA>
```

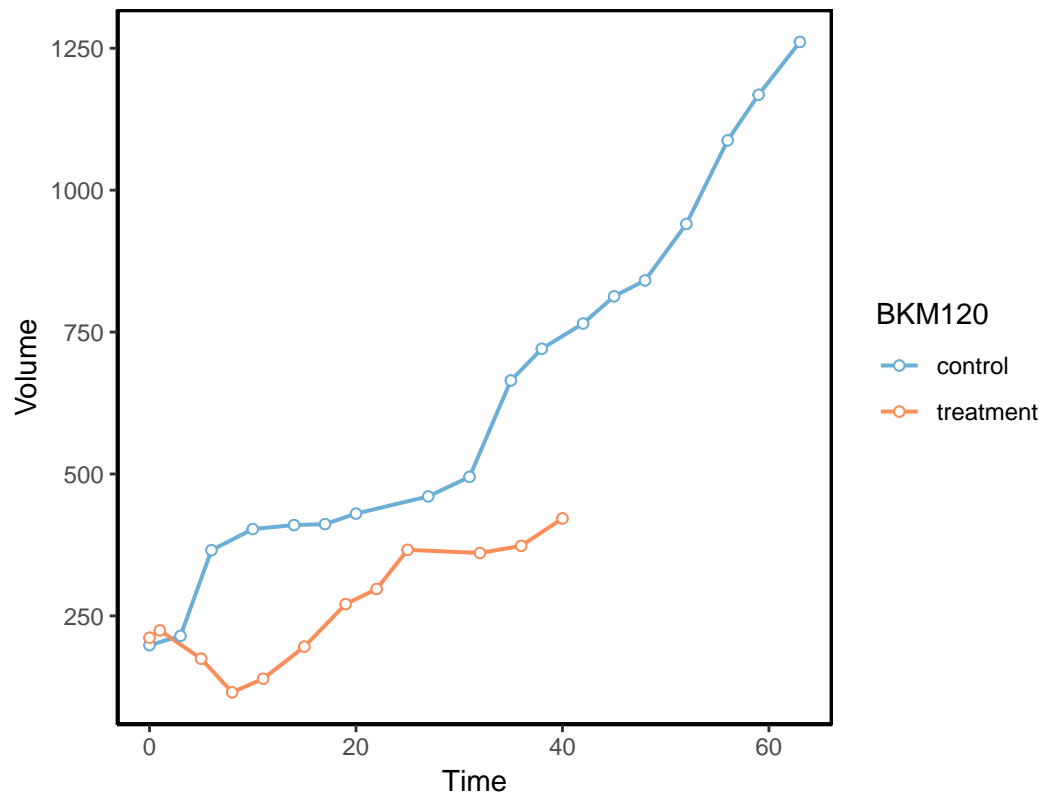
## BKM120	SD	SD	SD	SD	PD	PD	SD	<NA>
## BYL719	SD	PD	SD	PD	PD	PD	SD	<NA>
## BYL719 + LEE011	SD	SD	SD	SD	PD	PD	SD	<NA>
## BYL719 + LJM716	SD	PD	PD	SD	SD	SD	SD	<NA>
##	X-2195	X-2344	X-2353	X-2487	X-2524	X-2640	X-2780	X-3077
## BGJ398	PD	PD	PD	SD	PD	SD	PD	SD
## binimetinib	SD	PD	SD	PD	PD	SD	SD	PD
## BKM120	PD	SD	SD	PD	PD	SD	SD	PR
## BYL719	PD	PD	SD	SD	PD	SD	SD	PR
## BYL719 + LEE011	PR	SD	SD	SD	SD	SD	SD	PR
## BYL719 + LJM716	SD	SD	PD	SD	SD	SD	SD	CR
##	X-3078	X-3201	X-3298	X-3450	X-3453	X-3468	X-3697	X-3873
## BGJ398	PD	PD	PD	SD	<NA>	PD	SD	PD
## binimetinib	PD	PD	PD	SD	<NA>	SD	SD	SD
## BKM120	SD	PD	SD	PR	<NA>	SD	SD	SD
## BYL719	SD	PD	PD	SD	<NA>	SD	SD	SD
## BYL719 + LEE011	SD	SD	SD	SD	<NA>	PR	PR	PR
## BYL719 + LJM716	SD	SD	SD	CR	<NA>	PR	SD	PR
##	X-4347	X-4567	X-4824	X-4888	X-4949	X-5249	X-5355	X-5502
## BGJ398	SD	PD	PD	SD	PD	CR	PD	PD
## binimetinib	PR	PR	SD	SD	PD	SD	PR	SD
## BKM120	SD	CR	SD	PD	SD	SD	PR	SD
## BYL719	SD	CR	SD	SD	SD	PD	SD	SD
## BYL719 + LEE011	PR	CR	SD	PR	SD	SD	PR	SD
## BYL719 + LJM716	SD	CR	SD	SD	SD	PD	SD	SD
##	X-5541	X-5975	X-6047					
## BGJ398	<NA>	PD	SD					
## binimetinib	<NA>	SD	PD					
## BKM120	<NA>	SD	PD					
## BYL719	<NA>	SD	PD					
## BYL719 + LEE011	<NA>	PR	SD					
## BYL719 + LJM716	<NA>	SD	SD					

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



Plot PDX curve for a drug

```
plotBatch(brca, batch = "X-5249.BKM120")
```



```
plotBatch(brca, patient.id = "X-5249", drug = "BKM120", control.name = "untreated")
```

