2021-10-01-BIO392-CNV-freq.Rmd

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1 10 2021

Step 1: Install package

```
if (!require(devtools)){
    install.packages('devtools')
}
```

```
## Loading required package: devtools
```

```
## Loading required package: usethis
```

```
#install API package for progenetix database
devtools::install_github('progenetix/pgxRpi')
```

```
## Skipping install of 'pgxRpi' from a github remote, the SHA1 (ad1cf8a1) has not changed since last ins
##   Use `force = TRUE` to force installation
```

```
library(pgxRpi)
```

Step2: Search NCIt code

```
codes <- c("NCIT:C3058",
           "NCIT:C9245",
           "NCIT:C2926",
           "NCIT:C4349",
           "NCIT:C3224")

# Glioblastoma                    (NCIT:C3058)
# Lung Non-Small Cell Carcinoma   (NCIT:C2926)
# Invasive Breast Carcinoma       (NCIT:C9245)
# Colon Adenocarcinoma            (NCIT:C4349)
# Melanoma                        (NCIT:C3224)
```

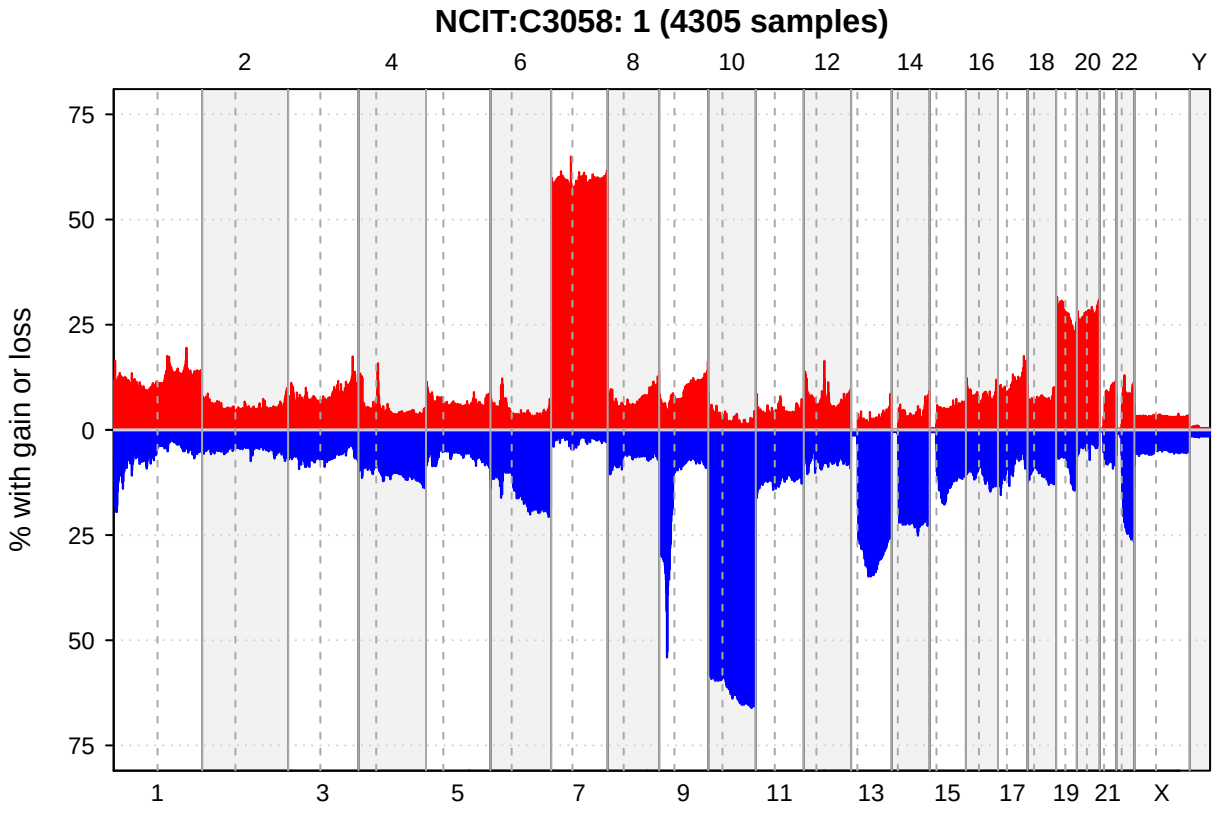
Step3: Access the CNV frequency data from samples with esophageal adenocarcinoma

Step4: Visualize data

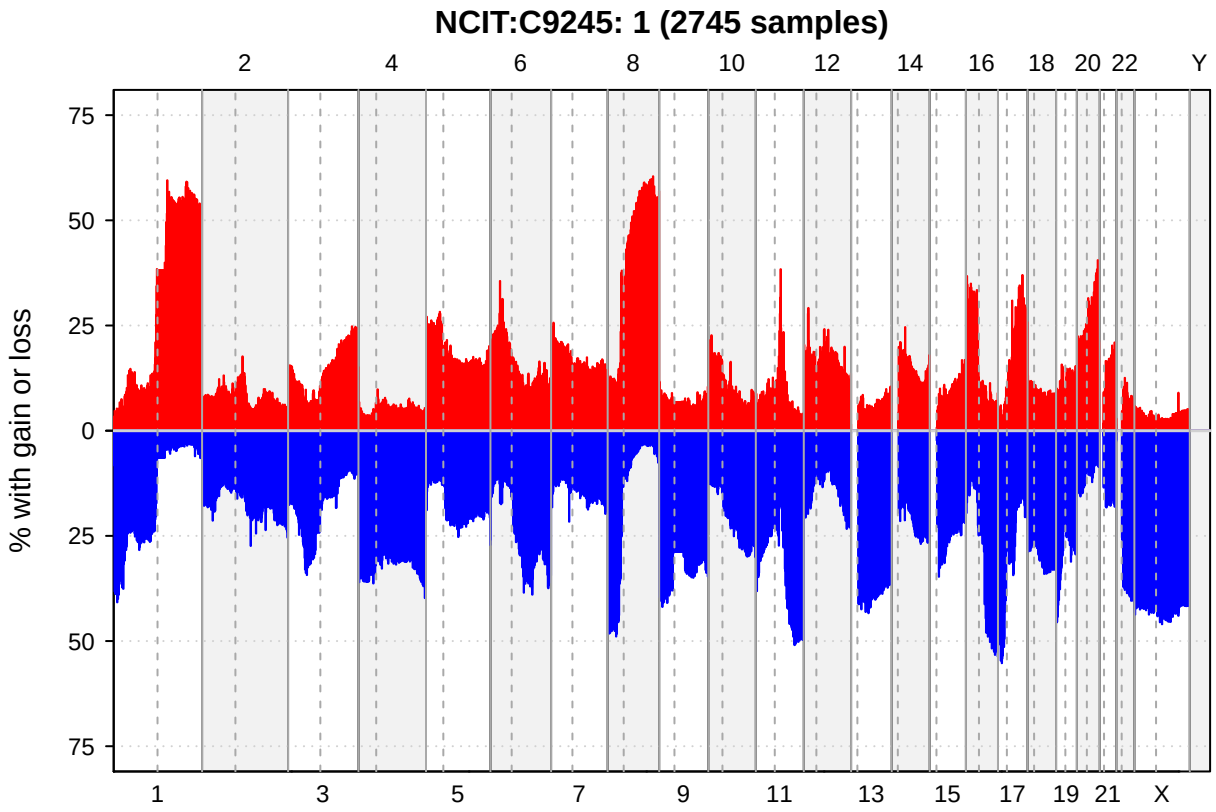
```
for (i in codes)
  {
  freq <- pgxLoader(type='frequency', output='pgxseg',filters=i,
```

```
                    codematches=T)
  pgxFreqplot(freq)
}
```

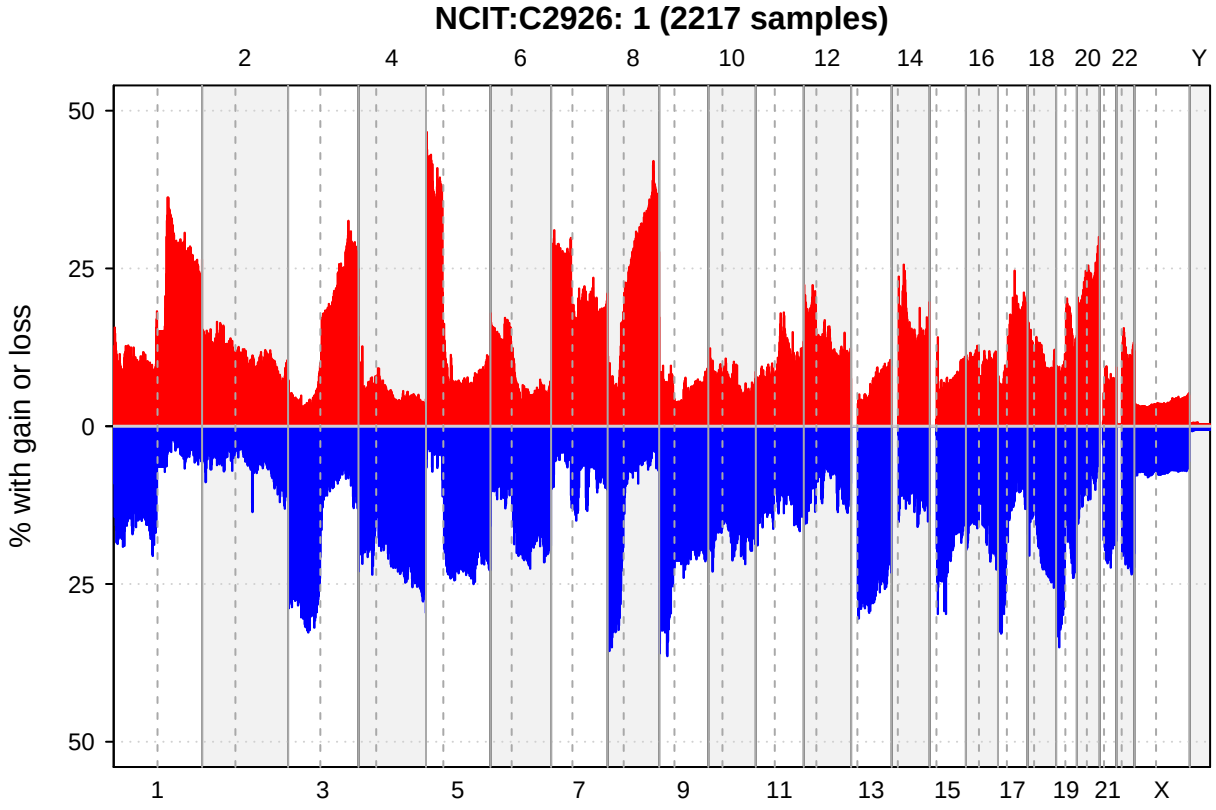
```
##
##  accessing IntervalFrequencies service from Progenetix
```



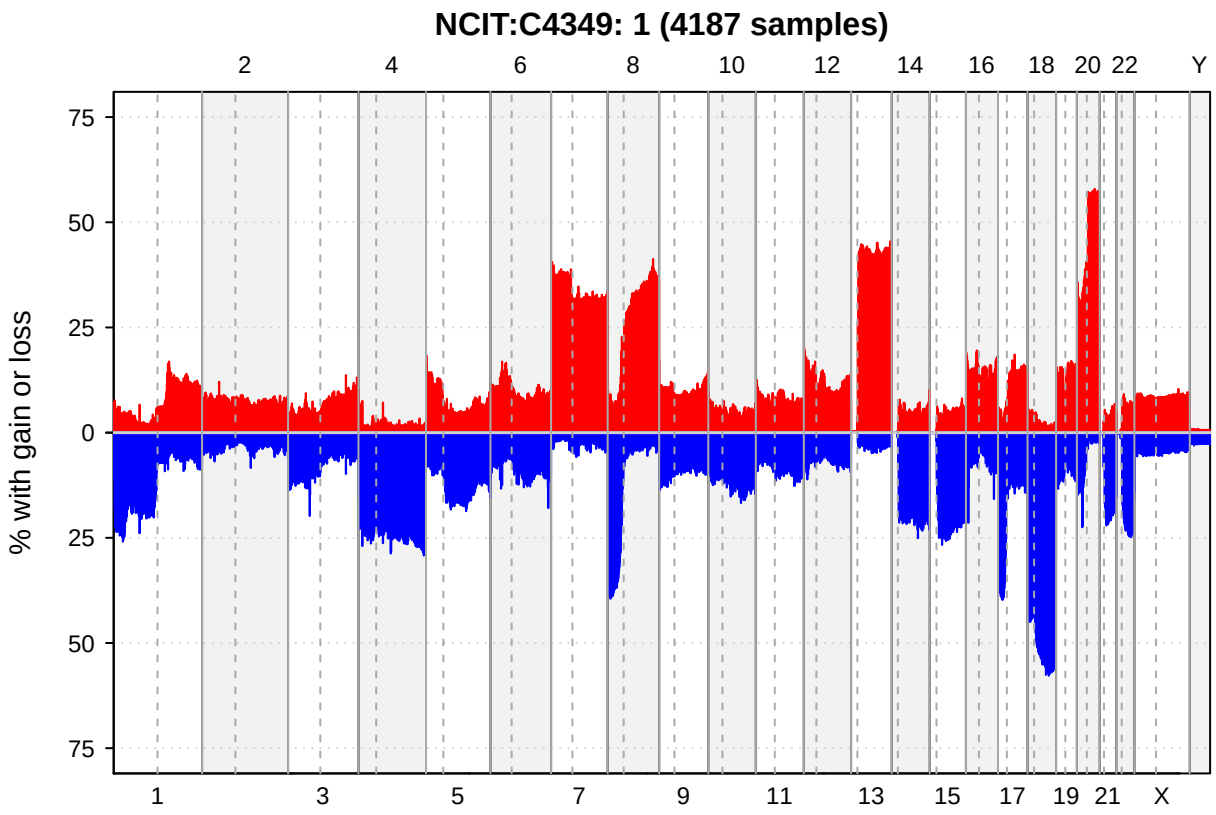

```
##
##  accessing IntervalFrequencies service from Progenetix
```



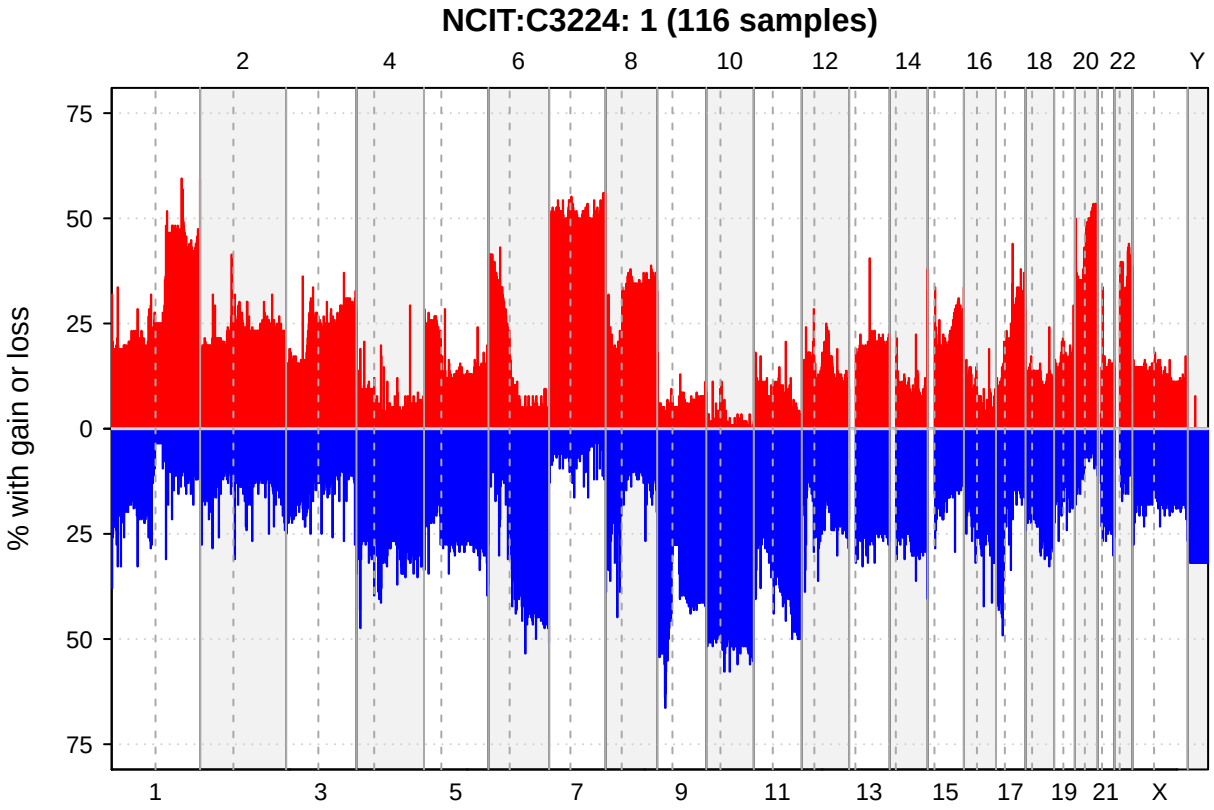

```
##
##  accessing IntervalFrequencies service from Progenetix
```



```
##
##  accessing IntervalFrequencies service from Progenetix
```




```
##
##  accessing IntervalFrequencies service from Progenetix
```



Step5: Analyse the data

Glioblastoma (NCIT:C3058)

Major occurences of gain events on chromosome 7 and loss events on chromosome 8.

Lung Non-Small Cell Carcinoma (NCIT:C2926)

Major occurences of gain events on chromosome 2 and 8.

Invasive Breast Carcinoma (NCIT:C9245)

Through the wohle genome gains and lossed of about 25%.

Colon Adenocarcinoma (NCIT:C4349)

Major occurences of gain events on chromosome 7,8,13,21 and loss events on chromosome 18.

Melanoma (NCIT:C3224)

Through the wohle genome gains and lossed of about 25%. And Major occurences of gain events on chromosome 2,7,20 and loss events on chromosome 9,10.