

Average Bar Graph using Cibersort Data: Bladder Cancer

Plot Average Bar Graph using Cibersort Data - R Markdown

- Read in output from Cibersort online (tumor samples)
- Read in output from Cibersort online (normal samples)
- Create one cibersort object for each group of interest.
- For each group of interest
 - Plot average bar for each group

Read in cibersort output from online web - tumor samples

```
# Read in cibersort output - rows are samples, columns are immune cell types
inputBLCA_tumor = read.csv("input/CIBERSORTx_Tumor_Results.txt",
                           header=TRUE, row.names=1, sep="\t")
knitr::kable(inputBLCA_tumor[1:5, 1:4], caption = "Bladder Cancer Tumor")
```

Table 1: Bladder Cancer Tumor

	B.cells.naive	B.cells.memory	Plasma.cells	T.cells.CD8
GSM340547	0.0000000	0.1478116	0.0000000	0.0699226
GSM340548	0.0000000	0.1167400	0.1668580	0.0000000
GSM340549	0.0243214	0.0000000	0.0014384	0.1269212
GSM340550	0.1223687	0.0000000	0.0045003	0.1051648
GSM340551	0.0000000	0.0296045	0.0407549	0.0000000

Read in cibersort output from online web - normal samples

```
# Read in cibersort output - rows are samples, columns are immune cell types
inputBLCA_normal = read.csv("input/CIBERSORTx_Normal_Results.txt",
                             header=TRUE, row.names=1, sep="\t")
knitr::kable(inputBLCA_normal[1:5, 1:4], caption = "Bladder cancer Normal")
```

Table 2: Bladder cancer Normal

	B.cells.naive	B.cells.memory	Plasma.cells	T.cells.CD8
GSM340537	0.0595902	0	0.0208277	0.0054900
GSM340538	0.0118495	0	0.0882123	0.2068398
GSM340539	0.0000000	0	0.0652977	0.1781057
GSM340540	0.0000000	0	0.0000000	0.1562189

	B.cells.naive	B.cells.memory	Plasma.cells	T.cells.CD8
GSM340541	0.0440019	0	0.0000000	0.1522319

Create cibersort data objects

```
cibersortDataTumor <- inputBLCA tumor
cibersortDataNormal <- inputBLCA normal
```

Call function for each group to plot average bar graph

Output will be a set of graphs in the “outputFolderName” folder

```
source("functionAvgBarPlot.R")
```

```
## Warning: package 'plyr' was built under R version 4.3.2
```

```
## -----
```

```
## You have loaded plyr after dplyr - this is likely to cause problems.
## If you need functions from both plyr and dplyr, please load plyr first, then dplyr:
## library(plyr); library(dplyr)
```

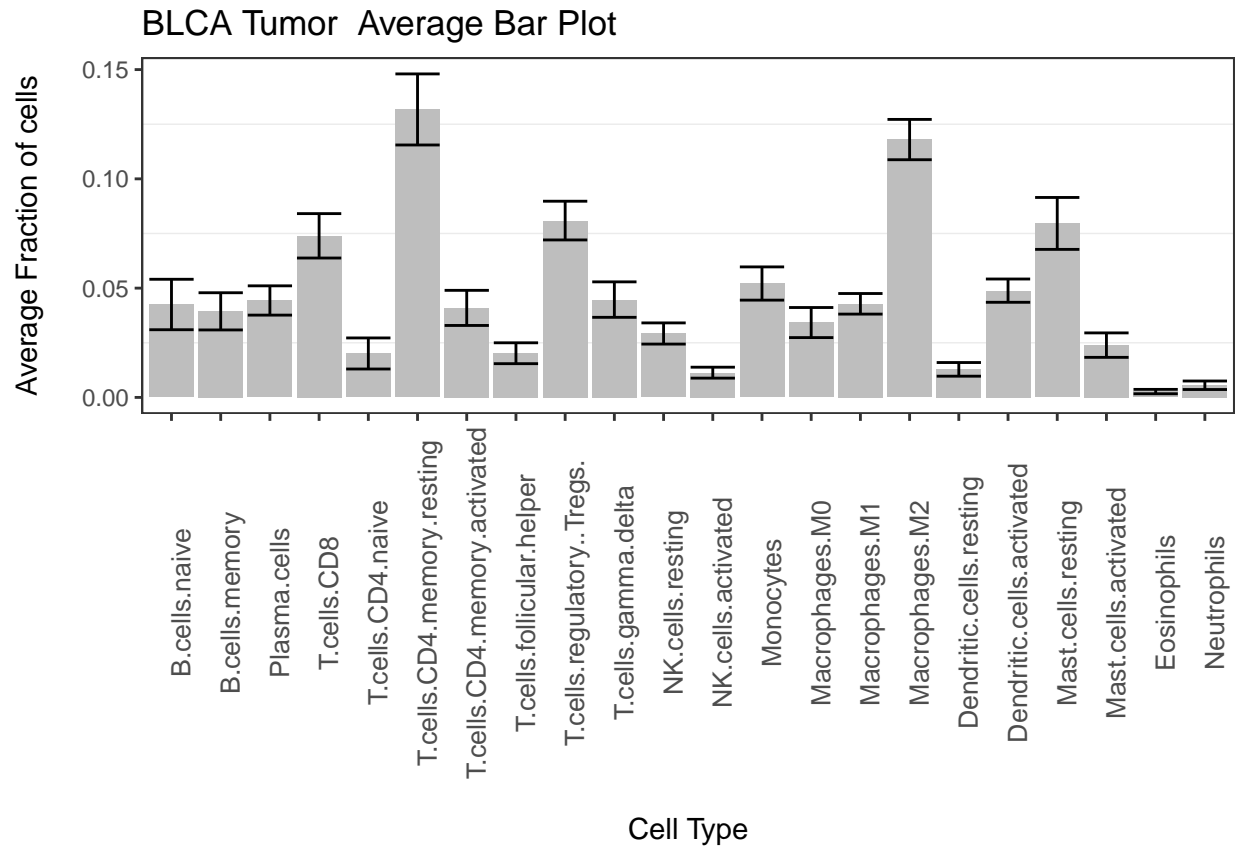
```
## -----
```

```
##
## Attaching package: 'plyr'
```

```
## The following objects are masked from 'package:dplyr':
##
##   arrange, count, desc, failwith, id, mutate, rename, summarise,
##   summarize
```

```
#calling function for BLCA Tumor
objectPlotTumor <- functionAvgBarPlot(
  cibersortData = cibersortDataTumor, #set Cibersort Data object for plotting
  outputFileName = "2023_Ciber_BLCA Tumor_AvgBarPlot", #set output file name
  outputFolderName = "output", #Set output folder name
  title1 = "BLCA Tumor Average Bar Plot", #Change Title
  num1 = 22) #Number of cell types to plot
```

```
#insert object into the Rmarkdown document
objectPlotTumor
```



```
### calling function for BLCA Tumor No-relapse
objectPlotNormal <- functionAvgBarPlot(
  ciphersortData = ciphersortDataNormal, #set Ciphersort Data object for plotting
  outputFileName = "2023_Ciber_BLCANormal_AvgBarPlot",
  #set output file name
  outputFolderName = "output", #Set output folder name
  title1 = "BLCA Normal Average Bar Plot",
  num1 = 22)

#insert object into the Rmarkdown
objectPlotNormal
```

