

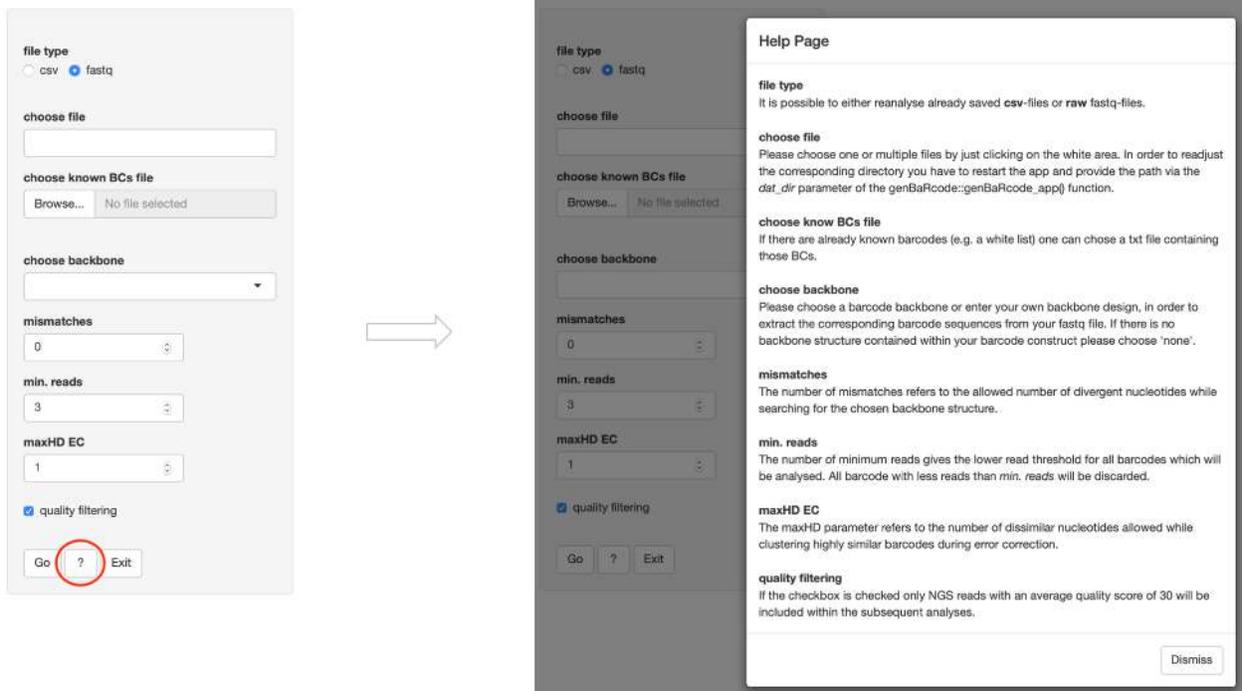
# Introduction to the genBaRcode GUI

There is also a shiny-app included within the package, allowing you to use all main functionality of the package without typing any line of code at all. Or if you are well capable of programming you can also use it as a convenient method to learn about the possibilities of the package. There is an app-internal help and there is also an option to inspect the source code necessary to redo all in-app done analyses. You can start the app with the `genBaRcode_app()` command and if you already have a data file which you are dying to analyze you just need to provide the path to the directory (`dat_dir`) of this particular file and you can chose it from within the app. If you have none and no path provided, the package's internal example file will be available for exemplary analysis.

```
# start Shiny app with the package internal test data file
genBaRcode_app()

# start Shiny app with access to a predefined directory
genBaRcode_app(dat_dir = "/path/to/my/data/")
```

After starting the app, the user has to provide basic informations like file type, file name, backbone structure, etc. By clicking on the button labeled with a question mark, the app internal help will be revealed (red circle).



If no user specific input file containing folder was specified, the app will automatically make the example data file available which is included within the package. The following parameter choices would be appropriate.

file type  
 csv  fastq

choose file

choose known BCs file  
 No file selected

choose backbone

mismatches

min. reads

maxHD EC

quality filtering

After starting the analysis by clicking the go button, a progress-bar will appear, unsurprisingly indicating the progress made so far. Then a dropdown menu with a variety of different plot types to choose from, an empty plot area and a table containing the most basic meta data will be visible.

plot type:

- Kirchenplot
- Read Frequencies
- HD Graph
- interactive HD Graph
- Tree
- SeqLogo
- SeqLogo - NGS reads

overview [barcode list](#) [barcode list \(EC\)](#) [source code](#)

Show  entries Search:

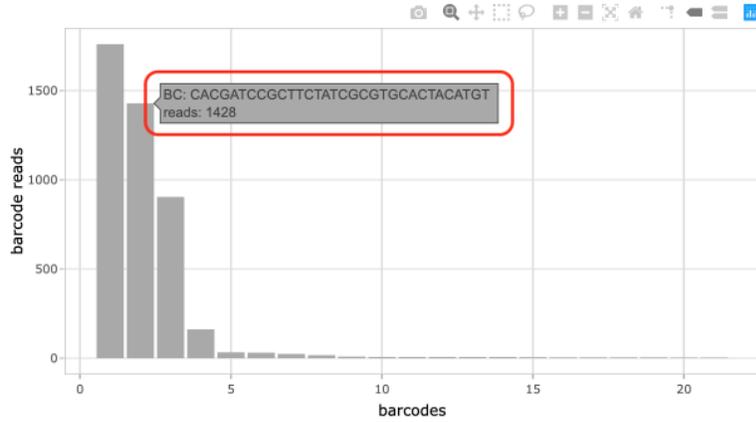
feature	data
number of barcodes	21
number of barcodes (EC)	8
read count min	4
read count median	7
read count mean	211
read count max	1760
read count min (EC)	17
read count median (EC)	98
read count mean (EC)	555
read count max (EC)	1790
feature	data

After choosing a particular plot, the plot will be created and can instantaneously be modified. You can hover over certain parts of the plot to reveal additional informations and modify the displayed data, e.g. displaying the raw or error corrected data or change the scaling of axes.

plot type:  
Kirchenplot

error correction  
 log values

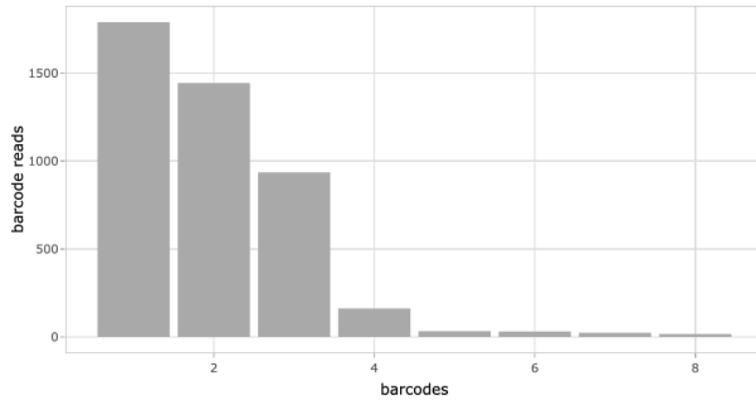
New Exit ?



plot type:  
Kirchenplot

error correction  
 log values

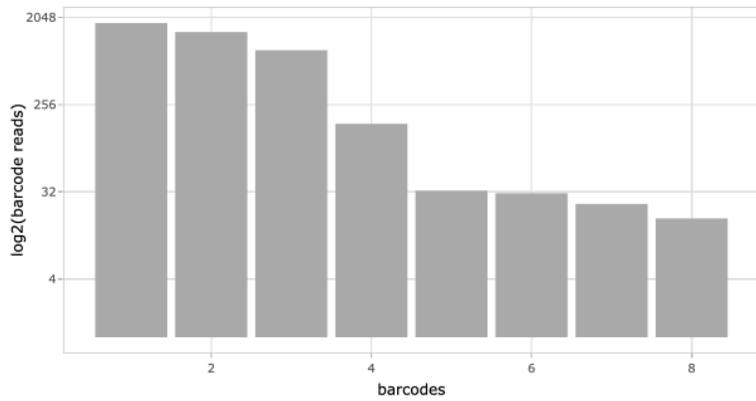
New Exit ?



plot type:  
Kirchenplot

error correction  
 log values

New Exit ?

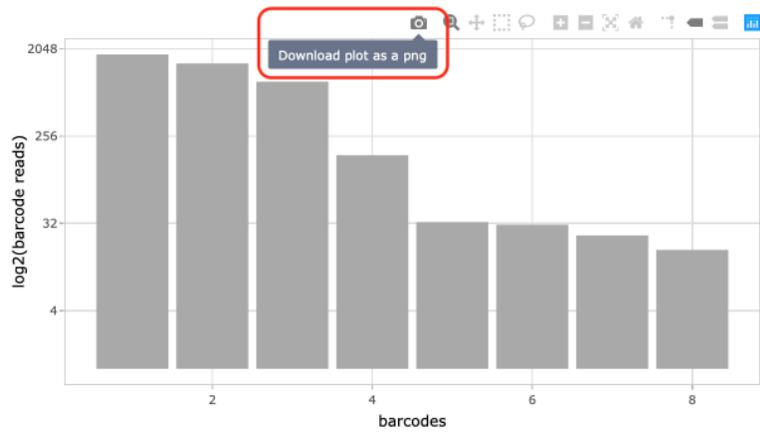


Additionally, since the `ggplotly` package was used there are a lot of further options available like zooming in and out, saving the entire plot as a `png` file or to box-select certain parts of the plot.

plot type:  
Kirchenplot

error correction  
 log values

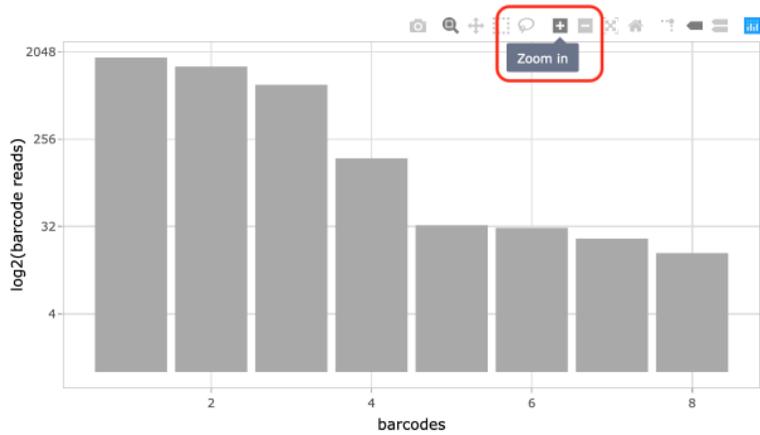
New Exit ?



plot type:  
Kirchenplot

error correction  
 log values

New Exit ?

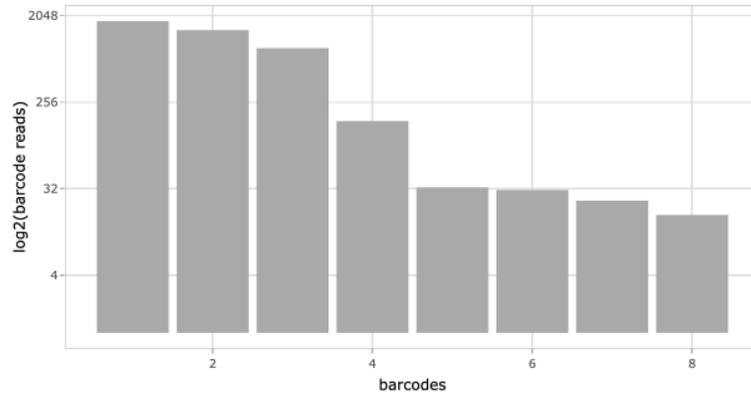


If there are questions regarding the already chosen plot type, there is also a button labeled with a question mark available, explaining all the necessary details regarding the specific plot.

plot type:  
 Kirchenplot

error correction  
 log values

New Exit ?



generateKirchenplot
R Documentation

## Plotting a Kirchenplot

### Description

Generates a barplot based on read counts. If `ori_BC`s is provided the bar color reflects the distance between a particular barcode to one of the provided barcode sequences.

### Usage

```
generateKirchenplot(BC_dat, ori_BC = NULL, ori_BC2 = NULL, loga = TRUE, col_type = NULL, m = "hamming",
  setLabels = c("BC-Set 1", "Rest", "BC-Set 2"))
```

### Arguments

- BC\_dat** a BCdat object.
- ori\_BC** a vector of character strings containing known barcode sequences (without the fixed positions of the barcode construct).
- ori\_BC2** a vector of character strings containing a 2nd set of known barcode sequences (also without the fixed positions).
- loga** a logical value, indicating the use or non-use of logarithmic read count values.
- col\_type** character string, choosing one of the available color palettes ("rainbow", "heat.colors", "topo.colors", "greens", "wild" - see package "grDevices")
- m** a character string, Method for distance calculation, default value is Hamming distance. Possible values are "osa", "lv", "di", "hamming", "lcs", "qgram", "cosine", "jaccard", "jw", "soundex" (see stringdist function of the stringdist-package for more information). If neither 'ori\_BC' nor 'ori\_BC2' are provided with input the choice of 'm' does not matter.
- setLabels** a character vector, containing three strings serving as plot labels.

### Value

a ggplot2 object

Dismiss

read count median (EC)	98
read count mean (EC)	555
read count max (EC)	1790
feature	data

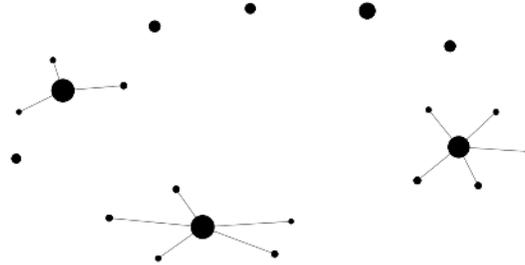
The included tables on the lower right side contain the meta-data, the barcode sequences, their read-counts and the raw source code necessary to redo all of the analysis steps done within the app directly within the R console. Here you can see the exemplary barcode list before the error correction and the corresponding source code.

plot type:  
 HD Graph

graph layout:  
 fruchtermanreingold

complete graph

New Exit ?



overview **barcode list** barcode list (EC) source code

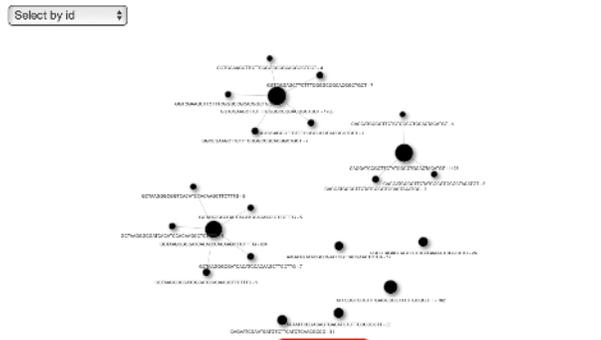
Show 25 entries Search:

read_count	barcode
1760	GGTCGAAGCTCTTTCGGGCCGCACGGCTGCT
1426	CACGATCCGCTTTCATCGCGTGCACTACATGT
904	GCTAAGGGCGATCACATCCACAAGCTTCTTTG
162	ATTGGGTCGGTCTGAGGGGTTTCTGCGCCTT
33	AGTATTCGACAGTGACATGTCTCCCGGCTT
31	CAGAATCGAATGATGCTTCATCTCAACGCCG
24	GGCCTAGAGTAGTTGTGCGGAAAGTCGGCCTC
17	AAGAAGTAACCGGATCGTTACGAACCTCA
9	GCTAAGGGCGATCGCATCCACAAGCTTCTTTG
7	CACGATCCGCTTTCATCGCGTGCACTACATGC
7	GCTAAGGGCGATCACATCCACAAGCTTCTTTG

plot type:  
 Interactive HD Graph

complete graph

New Save Exit ?



overview barcode list **barcode list (EC)** source code

Show 25 entries Search:

```

BC_dat <- processingRawData(file_name = 'test_data.fastq', source_dir =
'/Library/Frameworks/R.framework/Versions/3.5/Resources/library/genBaRcode/extdata', results_dir =
'/Library/Frameworks/R.framework/Versions/3.5/Resources/library/genBaRcode/extdata', mismatch =
1, bc_backbone = '', min_score = 30, min_reads = 3, seqLogo = TRUE)

generateKirchenplot(BC_dat, loga = FALSE, col_type = NULL)

generateKirchenplot(BC_dat_EC, loga = FALSE, col_type = NULL)

BC_dat_EC <- errorCorrection(BC_dat, maxDist = 8)

ggplotDistanceGraph(BC_dat, minDist = 1, loga = FALSE, lay = 'fruchtermanreingold', complete =
FALSE)

plotSeqLogo(BC_dat_EC)

BC_dat_EC <- errorCorrection(BC_dat, maxDist = 8)

plotReadFrequencies(BC_dat, b = 30, show_t = FALSE, log = FALSE)

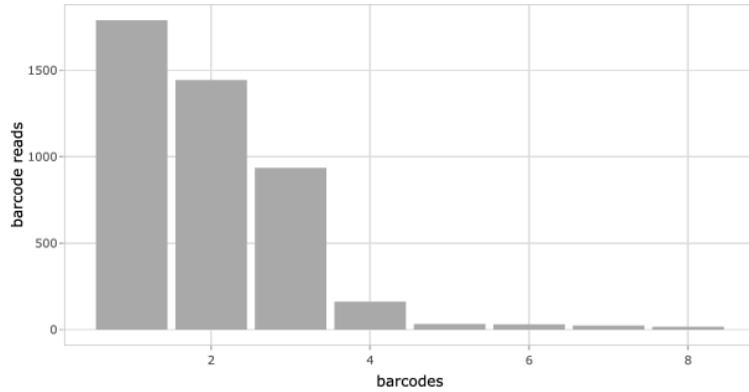
BC_dat_EC <- errorCorrection(BC_dat, maxDist = 8)
  
```

Finally, if you decide to start another analysis or to exit the app entirely, there are the appropriate buttons available.

**plot type:**  
Kirchenplot

error correction  
 log values

New Exit ?



overview barcode list barcode list (EC) source code

Show 25 entries Search:

```
BC_dat <- processingRawData(file_name = 'test_data.fastq', source_dir =  
'/Library/Frameworks/R.framework/Versions/3.5/Resources/library/genBaRcode/extdata/', results_dir =  
'/Library/Frameworks/R.framework/Versions/3.5/Resources/library/genBaRcode/extdata/', mismatch =  
1, bc_backbone = '', min_score = 30, min_reads = 3, seqLogo = TRUE)  
  
generateKirchenplot(BC_dat, loga = FALSE, col_type = NULL)  
  
generateKirchenplot(BC_dat_EC, loga = FALSE, col_type = NULL)  
  
BC_dat_EC <- errorCorrection(BC_dat, maxDist = 8)  
  
ggplotDistanceGraph(BC_dat, minDist = 1, loga = FALSE, lay = 'fruchtermanreingold', complete =  
FALSE)  
  
plotSeqLogo(BC_dat_EC)  
  
BC_dat_EC <- errorCorrection(BC_dat, maxDist = 8)  
  
plotReadFrequencies(BC_dat, b = 30, show_it = FALSE, log = FALSE)  
  
BC_dat_EC <- errorCorrection(BC_dat, maxDist = 8)
```