

# pickpeak User Manual

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## 1 Introduction

### 1.1 Description

Pickpeak is a R software package that makes use of the shiny package developed by Rstudio. While some of its functions might be used outside the shiny application, pickpeak is not intended to be used in other ways than through the graphical interface.

The main tools for the analysis of capillary electrophoresis results are GeneMapper and PeakScanner, developed by Life Technologies. Pickpeak is a free open source graphical tool, which, even if not as complete as pre-existing tools contains some of their most common features.

### 1.2 Disclaimer

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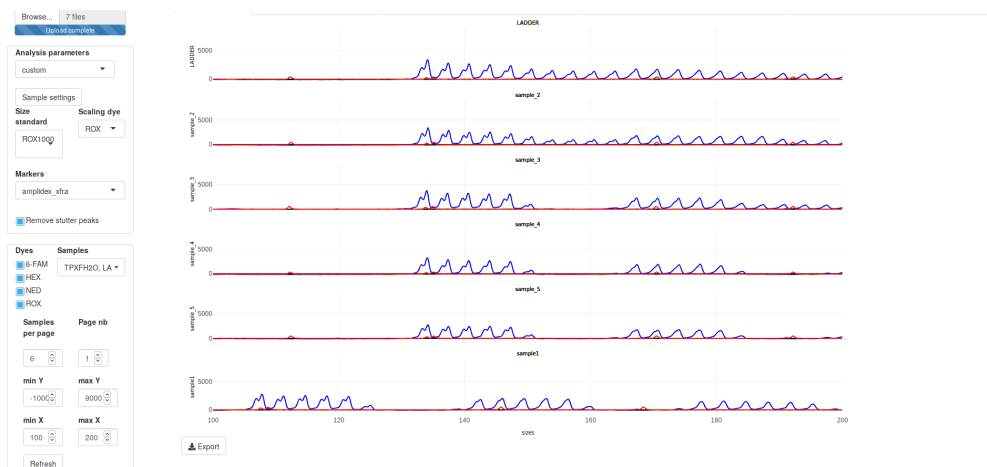


Figure 1: Pickpeak multiexperiment view

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### 1.3 Capillary electrophoresis

Capillary electrophoresis is an alternative to conventional lab gel electrophoresis for the separation of DNA fragments. It offers a number of advantages over slab gel separations in terms of speed, resolution, sensitivity, and data handling. Separation times are generally only a few minutes and the DNA is detected either by UV absorption or by fluorescent labeling. The quantity of DNA required for separation is in the nanogram range. Single-base resolution can be obtained on fragments up to several hundred base pairs. In the presence of appropriate standards, fragments can be accurately sized based on relative electrophoretic mobility [Smith2003].

Pickpeak has been applied to data that were produced using two capillary electrophoresis sequencers, i.e.;

- Applied Biosystems 3730 DNA Analyzer
- Applied Biosystems 3130 Genetic Analyzer

### 1.4 Short presentation of the tool

Starting from capillary electrophoresis result files (FSA files), pickpeak can display, scale, discover and annotate the peaks (Figures 1 and 2).

## 2 Before running pickpeak

Pickpeak presents some configuration features, i.e., flat files are needed to make it work. When no file is provided at startup, Pickpeak will run with only the minimal parameters. As it is not aware of the scale or system, only the raw data can be visualized.

### 2.1 Configuration files

Examples of the configuration files are available in the package.

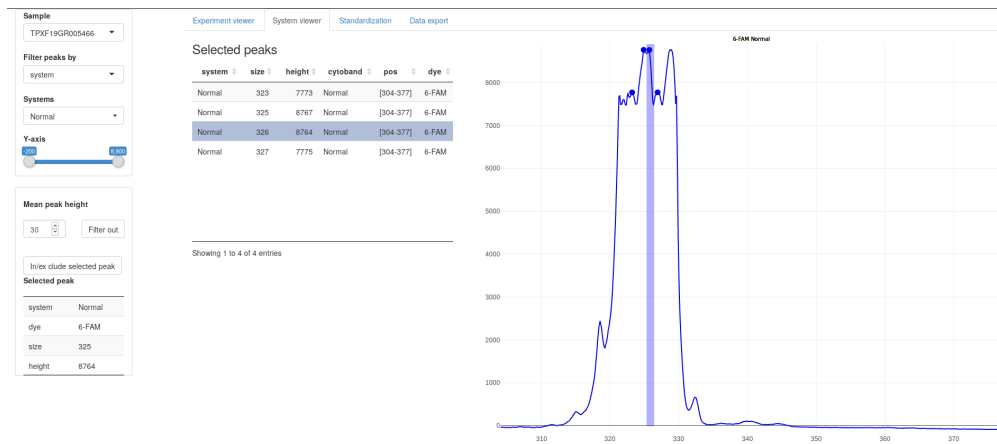


Figure 2: Representation of the values for one single sample over a short range of fragment lengths

```
system.file( "configuration_files", package = "pickpeak")
```

### 2.1.1 Main configuration file

This file is called as a parameter when starting pickpeak from an interactive R session. Its role is to describe the paths to the other configuration files or directories. It is json formatted.

```
{
  "predefined_parameters":"/path/to/predefined_configuration_file",
  "datadir":"/path/to/external_data_dir"
}
```

The demo file is available here:

```
system.file( "configuration_files",'pp_localConfigShiny.json', package = 'pickpeak')
```

### 2.1.2 Predefined configuration file (predefined\_parameters)

pickpeak allows users to define the configuration criteria. According to the experiment type, the set of analysis criteria can be different. The file is tab-delimited and must be formatted according to hereafter. This file can also be edited via the user interface (see below).

id	standard.dye	Dye1	Dye2	Dye3	Dye4	Dye5	analysis_type	ladder
paternity	LIZ	900	900	900	900	500	paternity_v17	ILS500
xfra	ROX	5000	100	100	100	100	amplidex_xfra	ROX1000
HNPCC	ROX	900	900	900	300	500	None	LIZ500

```
system.file( "configuration_files",'config','predef.tab', package = 'pickpeak')
```

### 2.1.3 External data directory

The data directory contains two directories which in turn contains files

```
| -data
|   |-dyes
|     |-colors.json
|     |-scales.json
|   |-markers
|     |-markers.tab
|     |-markers_kit1.tab
|     |-markers_kit2.tab
|     |-markers_kit1_kit2.tab
```

```

    "color": "#0101DF",
    "cval": "blue"
  },
  "VIC": {
    "color": "#31B404",
    "cval": "green"
  },
  "NED": {
    "color": "#000000",
    "cval": "yellow"
  },
  "PET": {
    "color": "#FF0000",
    "cval": "red"
  },
  "LIZ": {
    "color": "#FFBF00",
    "cval": "orange"
  },
  "ROX": {
    "color": "#FF0000",
    "cval": "red"
  },
  "HEX": {
    "color": "#00FF00",
    "cval": "green"
  }
}

system.file( "configuration_files", 'dyes', 'colors.json', package = 'pickpeak')

```

### 2.1.3.1.2 scales.json

This file defines the position of the scaling peaks that will be used to convert the migration time into fragment lengths.

```

{
  "LIZ500":
    [35, 50, 75, 100, 139, 150, 160, 200, 250, 300, 340, 350, 400, 450, 490, 500],
  "ILS500":
    [60, 65, 80, 100, 120, 140, 160, 180, 200, 225, 250, 275, 300, 325,
    350, 375, 400, 425, 450, 475, 500],
  "LIZ120":
    [15, 20, 25, 35, 50, 62, 80, 110, 120],
  "LIZ600":
    [20, 40, 60, 80, 100, 114, 120, 140, 160, 180, 200, 214, 220, 240, 250, 260, 280, 300, 314, 320,
    340, 360, 380, 400, 414, 420, 440, 460, 480, 500, 514, 520, 540, 560, 580 ,600],
  "ROX1000":
    [79,90,105,131,151,182,201,254,306,337,362,425,486,509,560,598,674,739,799,902,1007],
  "CFEU2":
    [100, 114, 120, 140, 160, 180, 200, 214, 220, 240, 250, 260, 280,
    300, 314, 320, 340, 360, 380, 400, 414, 420, 440, 460, 480, 500, 514, 520, 540, 560, 580]
}

```

```
system.file( "configuration_files",'dyes','scales.json', package = 'pickpeak')
```

### 2.1.3.2 The data folder

The files that we are going to describe hereafter are not mandatory for pickpeak to run (only visualisation of the sample raw data). However, they allow a precise analysis and annotation of the peaks.

```
system.file( "configuration_files",'data',package = 'pickpeak')
```

#### 2.1.3.2.1 markers.tab

The markers folder contains a markers.tab file that describes the other files within the directory.

analysis	marker.file	bin.file	runName
aneuploidies	markers_qstr_elucigene.tab	NA	Aneu
paternity_v16	markers_PowerPlex_ESX_16_v16.tab	PowerPlex_ESX_Bins_IDX_Pa3.0_16.txt	Pa3.0_16
paternity_v17	markers_PowerPlex_ESX_17_v17.tab	PowerPlex_ESX_Bins_IDX_Pa3.0_17.txt	Pa3.0_17
amplidex_xfra	markers_Amplidex_FMR1.tab	NA	Xfra
elucigene_muco	markers_Elucigene_MUCO50.tab	NA	Muco

The first column (analysis) contains the name of an analysis type. For a given analysis type there is an associated file containing a list of markers / systems (see hereafter) and potentially a file containing a list of bins (hereafter). If there is no bin defined for an analysis, NA is used instead of a file name. A short name (runName) can be specified for a given type of analysis.

```
system.file( "configuration_files",'data','markers.tab',package = 'pickpeak')
```

#### 2.1.3.2.2 marker file (tab delimited)

This file contains for each dye, the position of the systems (regions targetted) together with their molecular size.

system	cytoband	start.pos	end.pos	color	dye
system1	Xp22.22	68	112	blue	6-FAM
system2	3p20.15	96.01	145.25	blue	6-FAM
DXS3337	2q35	172.01	255	green	VIC

...

```
system.file( "configuration_files",'data','markers_example.tab',package = 'pickpeak')
```

#### 2.1.3.2.3 bin file

The bin file (generally available from the kit supplier website) is a text file file that is made available by the kit manufacturer for kits that also contain a ladder sample. This allows to name each annotated peak. The file format is the same as the one those can be used in the GeneMapper idx tool. The bin file is not of any use if the user does not want to name the exact bin with a ladder sample.

```
Version GMID-X v 1.0
Chemistry Kit XXXXXX
BinSet Name XXXXXXX
Panel Name XXXXXXX
```

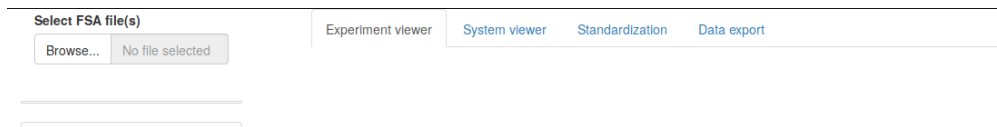


Figure 3: Pickpeak opening screen

```
Marker Name system1
X   77.02   0.5 0.5
Y   83.24   0.5 0.5
Marker Name system2
8   90.21   0.5 0.5 virtual
9   94.5    0.5 0.5
10  98.79   0.5 0.5
11  103.14  0.5 0.5
12  107.52  0.5 0.5
13  111.87  0.5 0.5
14  116.22  0.5 0.5
14.3 119.47 0.5 0.4 virtual
15  120.55  0.4 0.4
...
```

```
system.file( "configuration_files",'data','markers_bin_example.tab',package = 'pickpeak')
```

## 3 Running pickpeak

### 3.1 Console command

```
library(pickpeak)
runShinyPackageApp("/path/to/configfile.json")
```

When running the instruction `runShinyPackageApp` without arguments, the minimal options of pickpeak will be available (only visualization of the raw data).

Provided the configuration files are correct and correspond to the data that are loaded, the following image appears (Figure 3).

### 3.2 Loading, visualizing and formatting the samples

To load the samples, click on the “Browse...” button in section “Select FSA file(s)”. There are demonstration files within the directory `system.file( "data","xfra",package = 'pickpeak')`. These files were gener-

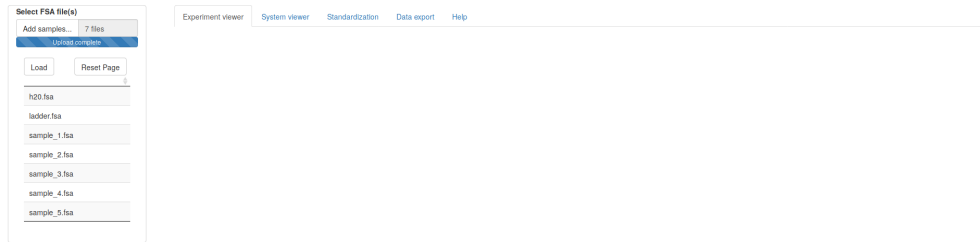


Figure 4: File selection

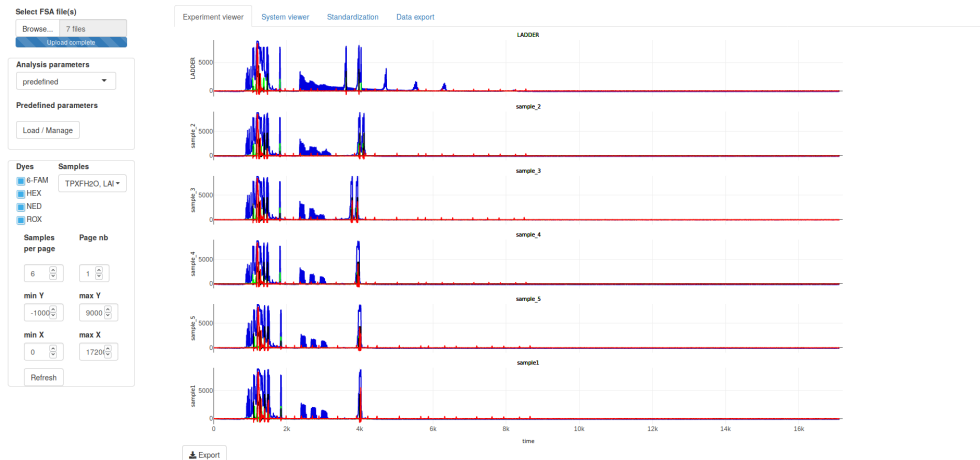


Figure 5: Representation of the values for demo samples

ated on capillary electrophoresis sequencers with the Amplidex FMR1 kit (Asuragen Genetics) for diagnostics of the X-fragile syndrom.

Once the files has been selected, the user has the possibility to add files (e.g. from another directory). Once the files have been selected, one must click on Load and to visualize the samples (raw non standardized electrophoregrams) (Figure 4, one must then click on the “Refresh” button. The screen should look like Figure 5.

Beware, after each parameter change, one must hit the Refresh button in order to visualize the changes.

In the left panel, there are two main windows :

- Above, the analysis parameters which allow the users to specify the way the data should be processed
- Below, the visualization parameters which allow the users to modify the main window view.

Note that, as all figures in pickpeak are drawn using the plotly library library. All the features that are generally associated with it are also made available to plotly (zoom, pan, figure export, etc). Those features are available by using the small icons on top of each plotly figure (Figure 6).

Beware, to visualize any of the changes brought to the visualization window, the user must not forget to click on the refresh button.

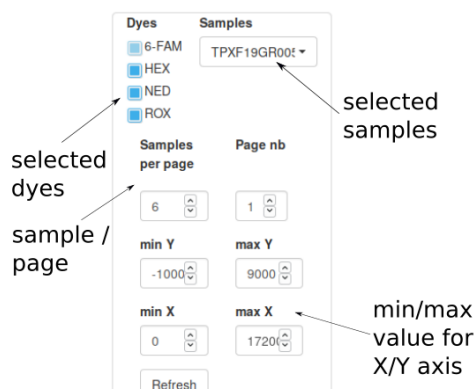


Figure 6: Visualization parameters

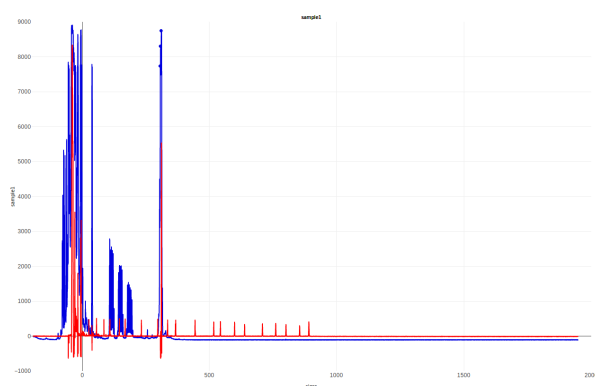


Figure 7: Migration time of the fragments labelled with a red (ROX) and a blue (6-FAM) dye. Red labelled DNA fragments correspond to the scaling fragments of known sizes (here ROX100 scale)

### 3.3 Scaling the migration time of the samples and peaks annotation

Pickpeak is able to convert raw capillary electrophoresis measurements into re-scaled data. Scaling of the data is the first main step as it consists in converting the migration times to fragment lengths according to a set of nucleotides of known lengths labelled with a specific dye (Figure 7).

To scale the samples, the following steps must be followed.

- Select analysis parameters
- Select custom sample settings

In the new windows that pops up, for each sample select the minimum peak height. If the limit is too high or too low the number of detected peaks for the scaling fragments will not correspond to the expected number of peaks and scaling will become impossible (Figure 8).

In this menu, you can also specify whether a given sample should always be on the top of each plot page (always above checkbox).

The clone value button allows users to specify the same value for all dyes and all samples (Clone value button).

That being done, the user can now select the scale as well as the scaling dye. In our example, the scaling



Sample analysis parameters

sample\_2

Default min peak

2000

6-FAM

2000

All samples

HEX

2000

All samples

NED

2000

All samples

ROX

2000

All samples

☐ ladder sample
 ☐ Always above

Submit

Standard

This sample

Clone value

Figure 8: Minimal peak value detection threshold selection .

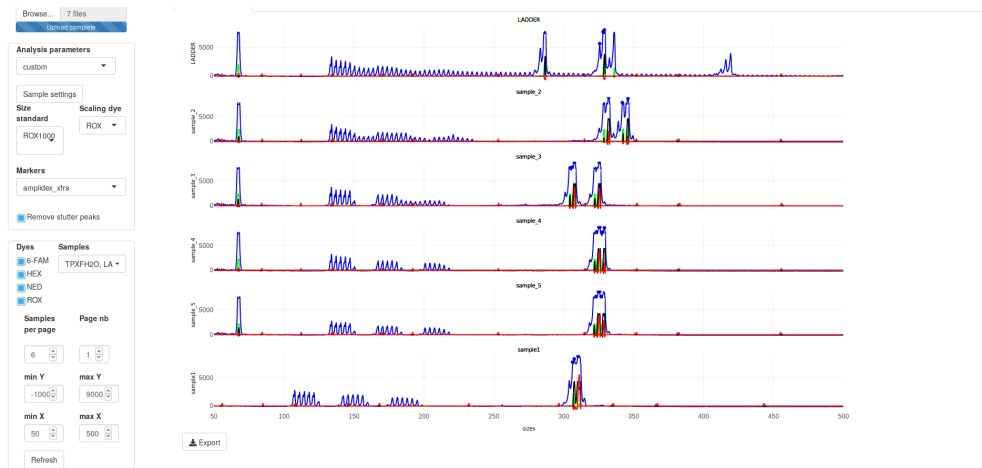


Figure 9: Inferring the fragment lengths according to the migration time of the scaling fragments of known sizes (red)

fragments are ROX1000 and the scaling dye is ROX. The viewer should then display the intensity values using the fragment lengths instead of the migration time (Figure 9).

Converting migration time into fragment lengths is achieved via a linear regression. To check whether the relation between lengths and time is linear, one can check the “Standardization” tab (Figure 12).

One can see on Figures 9 and 12 that there is one sample for which the length/time correlation is not optimal (sample\_1). Indeed, figure 9 shows that the red peaks (corresponding to the fragments on known sizes) of sample\_1 are not well aligned with those of the other samples. Moreover, Figure 12 shows a different correlation pattern. This is due to the fact that sample\_1 presents a parasitic peak with a somewhat large intensity (above our 100 intensity threshold). As this peak is taken into account to set up the linear regression model for the estimation of the fragment length, we must get rid of it, e.g., by increasing the threshold to 200 for peak detection for sample\_1. Doing this, you can observe on Figure X that all correlations seem more similar .

Optionally, now that the lengths have been estimated, the peaks of each sample can be categorized into different systems. The type of experiment analyzed can be selected via the left menu (markers). However, for this menu to contain analyses, the configuration files described above (markers.tab and the marker file) must be available.

Peaks for all samples are also inferred during this last step. When a peak is discovered, a big dot is displayed

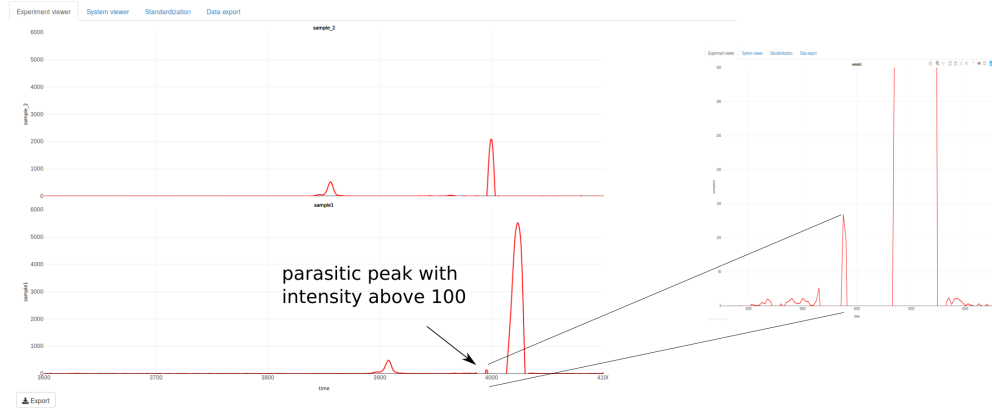


Figure 10: Comparison of the peak intensity between sample\_1 and sample\_2. Supplementary peak wrongly taken into account to compute the linear regression model to convert the migration time into DNA fragment lengths

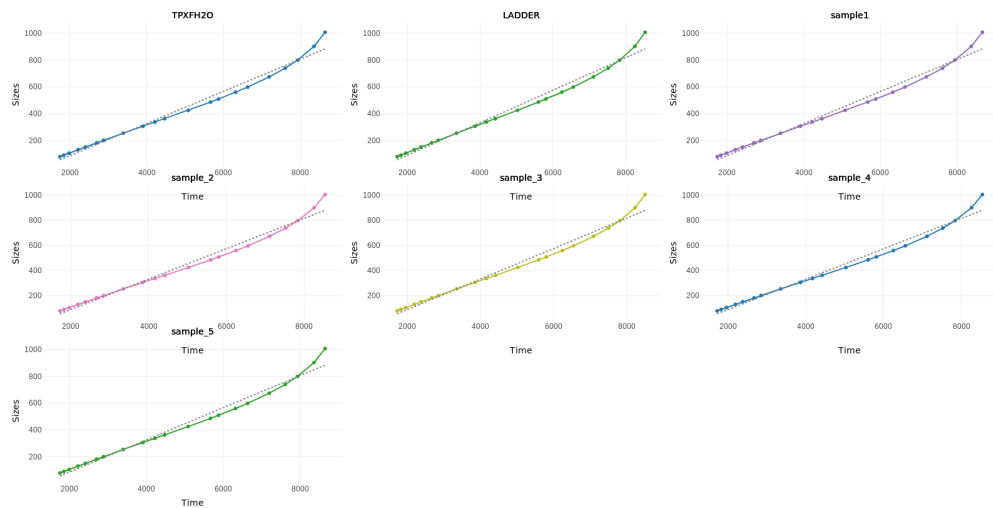


Figure 11: Computation of the linear regression after discarding the parasitic peak

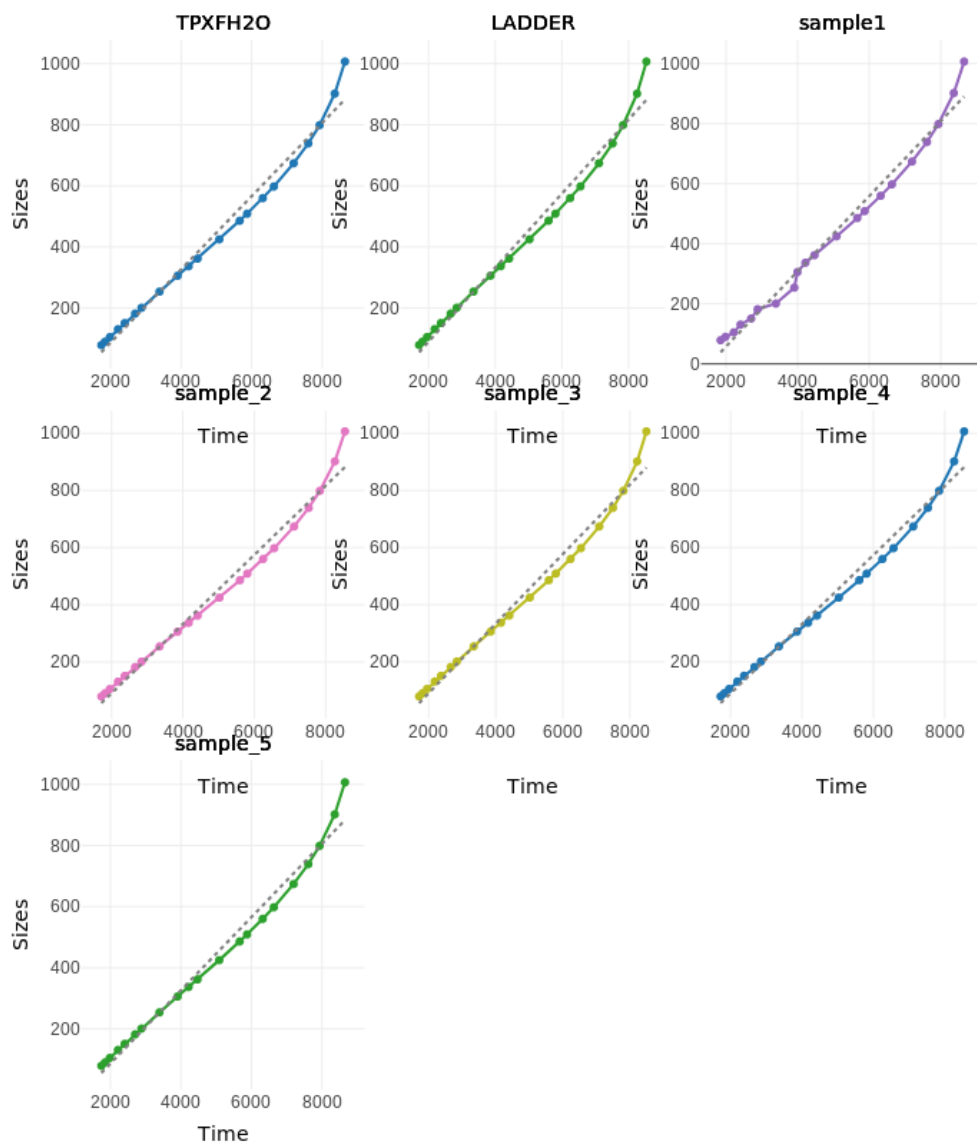


Figure 12: Standardization tab showing the linear regression estimation used from correlating the migration time with the known fragment lengths

Figure 13: Defition of new predefined analysis parameters

on top of it.

### 3.4 Predefined parameters

To save time, pickpeak allows to specify a set of parameters that should work for a given type of experiment. To this, the file `predef.tab` must be present, the user must select Analysis parameters “predefined” and Predefined parameters “Load / Manage”. If the experiment is already predefined, one must just select it and click on Submit button (Figure 13).

If the experiment is not specified, one must define it by clicking on Edit/Create. This opens a windows where you can specify :

- the name of the experiment type
- the minimum threshold value for peak detection for every dye.
- standard dye and standard scale
- the list of systems for a given experiment

You must then click on save after the data have been entered.

### 3.5 Single experiment viewer

#### 3.5.1 Introduction

The single experiment viewer tab allows to focus on individual systems or peaks that have been detected (manually or automatically). It can remove non relevant peaks as well or add peaks that were missed in the previous peak detection steps. Beware, the single experiment viewer is only working if the raw data were scaled and if the detected peaks were matched with systems in the previous steps.

The examples that will be depected on the following figures were not obtained using the example dataset as it does only contains one system and is less illustrative. Here, we make use of data generated using

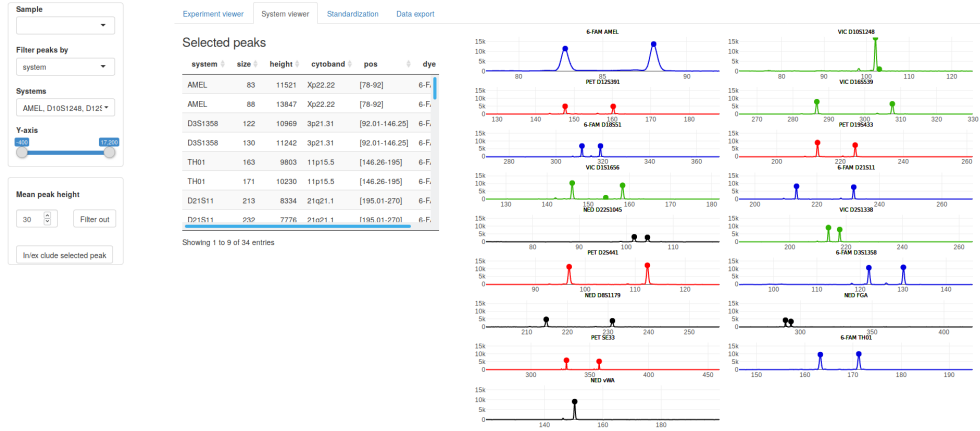


Figure 14: Single experiment viewer

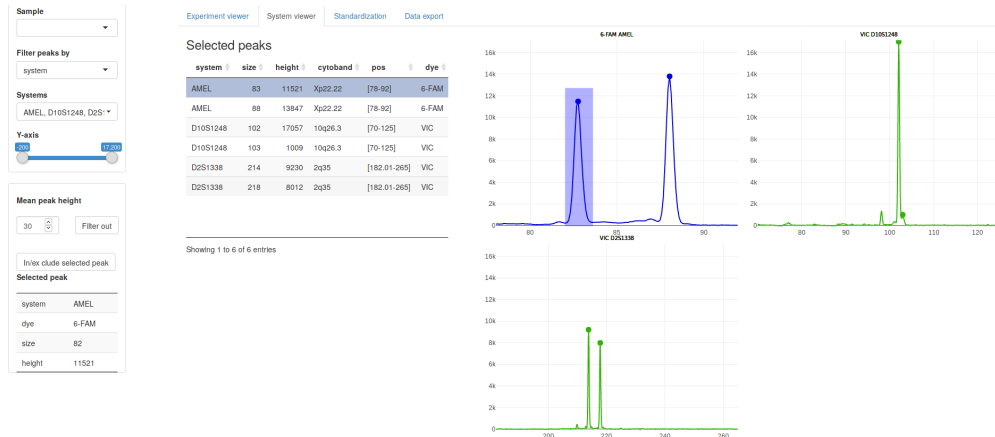


Figure 15: Single experiment viewer : peak selection

the PowerPlex ESX 17 kit for paternity testing developed by Promega. Those file are available within the pickpeak R package (`system.file("data","paternity",package = 'pickpeak')`)

### 3.5.2 Single experiment viewer description.

The Figure 14 shows the main screen of the single experiment viewer. The left part of the screen can be used to modify the view on the right side of the screen. Notably, one can select the system or the dyes that should be on the right side. The table in the middle contains the list of peaks that are to be seen on the right part. A click on one row in this table highlights the corresponds peaks in the view on the right (Figure 15). A peak can also be selected by clicking on the dot on top of it. Information about the peak will then be available in a table on the left of the screen.

### 3.5.3 Peak exclusion

There are two ways to remove a peak that has been detected. You can either select it by clicking on it or by clicking on its corresponding row in the middle table. When selected, you can remove it by clicking on In/Ex-clude peak (it is then moved to a second table below which is called excluded peaks). You can also

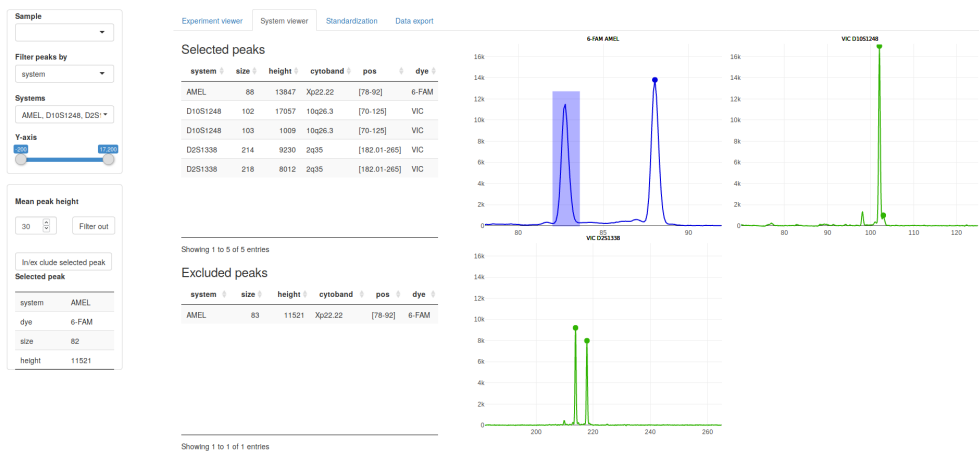


Figure 16: Peak removal with the single experiment viewer

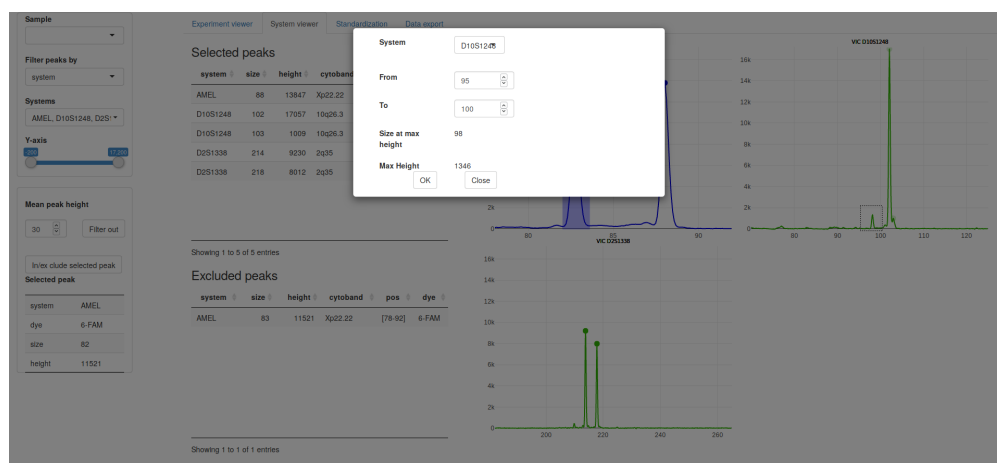


Figure 17: Single experiment viewer : peak addition

reintegrate it in the list of selected peaks by selecting it in the table and click again on In/Ex-clude peak (Figure 16).

In case the detection method has been too sensitive, you can also exclude all the peaks below a given intensity value. To this, simply indicate the threshold value (in the min peak height field on the left) and click on filter out.

### 3.5.4 Peak addition

If a peak has not been automatically detected, one can still add it to the list of selected peak. To this, select the small plotly icon **box select** on top of the figure with the peaks. Draw a box around the peak that you want to add. A window will open where you will have the possibility to precise the coordinates and the intensity of the peak as well as the system to which it belongs (Figure 17).

## 3.6 Data export

Data can be exported to be analyzed with other tools (tab Data Export). The export can be done for all samples together or for a subset of samples. Several formats such as tab-delimited or Excel are available.

Sample analysis parameters

ladder

Default min peak

2000

6-FAM

2000

All samples

VIC

2000

All samples

NED

2000

All samples

PET

2000

All samples

LIZ

2000

All samples

Standard

This sample

Clone value

☒ ladder sample

☐ Always above

Submit

Figure 18: Specification of the type of sample for a ladder sample

There are four types of output.

- Raw data : Table of data with intensities for each dye for each time migration value
- Standardized data : Table of data with intensities for each dye at each migration time point which are converted to fragment lengths.
- Peaks : List of all detected peaks. If it corresponds to a given system, it is indicated.
- Systems : List of all peaks detected within a system (one system per line) (Figure 21).

### 3.7 Analysis of data presenting ladder samples

In some capillary electrophoresis experiments, one or more ladder sample(s) are included. These samples contain a set of named peaks (bin) that may or may not correspond to actual peaks in the sample of interest. Ladder samples must be specified in the menu where custom analysis parameters were defined. A bin file must be specified in the `markers.tab` file (see above). As for the scaling fragments, the number of peaks must correspond to the number bins that are specified in the bin file.

#### 3.7.1 Loading samples

For this example, we will load the samples within the paternity directory of the package (`system.file("data", "paternity", package = 'pickpeak')`). These were generated using the PowerPlex ESX 17 kit for paternity testing developed by Promega.

On top of the other parameters (described above) however, we must indicate to the program that the sample called ladder is the ladder sample.

To this, we must select **Custom** analysis parameters and click **Sample settings**. In the window that opened, we must then select the ladder sample and click on the **ladder sample** box at the bottom of the window, then we can click on submit (Figure 18).

We can now run the scaling as shown above.

If we apply the standard parameters values (minimal peak detection at 900), there might be systems for which the number of annotated bins and the number of bins is not the same (Figure 19). The minimum intensity value for peak detection can be changed in the **sample settings** dialogox box. Here, when setting the minimum peak height to 2000 fot the PET (red) dye, we can already fix some of the ladder issues.

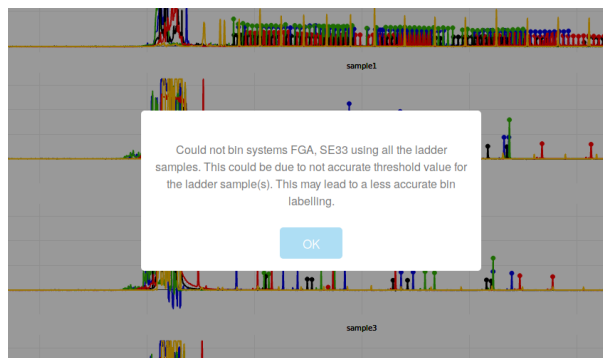


Figure 19: Number of detected bins in the ladder samples and of annotated bins does not correspond for systems FGA and SE33

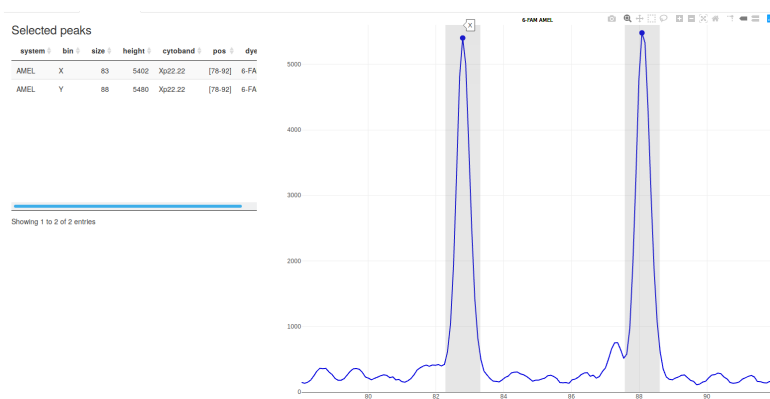


Figure 20: Example of peak naming using the ladder sample (system AMEL)

In the single experiment viewer, having defined the ladder sample allows to name the peaks. The bins are greyed zone on each of the plots. Hover the mouse over the top of the grey zone displays the name of the bin.



Experiment viewer


System viewer

Standardization

Data export

dye	system	cytoband	start_pos	end_pos	color	peak.height	peak.maxpos.time	peak.startpos.time	peak.endpos.time	id	maxpos.size	startpos.size	endpos.size	key
6-FAM						5235	932	923	946	sample_2	-39	-40	-38	tru
6-FAM						5503	975	963	985	sample_2	-34	-36	-33	tru
6-FAM						6043	1026	1004	1038	sample_2	-28	-31	-26	tru
6-FAM						7817	1096	1093	1100	sample_2	-19	-20	-19	tru
6-FAM						5597	1117	1109	1135	sample_2	-17	-18	-15	tru
6-FAM						7805	1169	1138	1174	sample_2	-11	-14	-10	tru
6-FAM						8945	1195	1187	1209	sample_2	-7	-8	-6	tru
6-FAM						8900	1226	1223	1229	sample_2	-4	-4	-3	tru
6-FAM						8607	1232	1229	1237	sample_2	-3	-3	-2	tru
6-FAM						8051	1242	1237	1246	sample_2	-2	-2	-1	tru
6-FAM						7977	1257	1249	1262	sample_2	0	-1	1	tru
6-FAM						5832	1275	1272	1278	sample_2	2	2	3	tru
6-FAM						7872	1296	1292	1302	sample_2	5	4	6	tru
6-FAM						7866	1305	1302	1308	sample_2	6	6	6	tru
6-FAM						8467	1386	1377	1397	sample_2	16	15	17	tru
6-FAM						7827	1400	1397	1421	sample_2	17	17	20	tru

Showing 1 to 17 of 100 entries



Export

Figure 21: Data export