1 Example Site

2 Citation
  2.1 Install .............................................................. 5
  2.2 Example Workflow .................................................. 6
  2.3 Groups .............................................................. 11
  2.4 Configuration File ................................................... 12
  2.5 Plot Tabs ............................................................ 13
  2.6 Area Range .......................................................... 13
  2.7 Bar ................................................................. 16
  2.8 Heatmap ............................................................. 18
  2.9 Histogram ........................................................... 20
  2.10 Line ................................................................. 22
  2.11 Plate Heatmap ....................................................... 25
  2.12 Table ............................................................... 27
FQC is designed to better group FastQC result data across groups where each group is comprised of FASTQs related to an experiment or sequencing batch. Individual samples are grouped into paired-end sets when available and the dashboard’s extensibility allows a user to add plots or tables as desired.
Example Site

https://pnnl.github.io/fqc/

2.1 Install

2.1.1 Requires

Parsing the table and running FastQC is performed with code written for Python 3. We recommend using Anaconda (https://www.continuum.io/downloads) to install the FastQC dependency.

**Set Up BIOCONDA channels**

```bash
conda config --add channels conda-forge
conda config --add channels defaults
conda config --add channels bioconda
```

**Install Dependency**

```bash
conda install fastqc
```

2.1.2 Install

The dashboard reads local files, so install where you will eventually be serving the site:

```bash
git clone https://github.com/pnnl/fqc.git
cd fqc
python setup.py install
```
This installs \texttt{fqc} command-line tool to process FASTQs and create the dashboard. Then to deploy a local copy from within the \texttt{fqc} directory, you can run:

\begin{verbatim}
python -m http.server --bind localhost 8000
\end{verbatim}

And navigate to \texttt{localhost:8000} in your browser.

By default, this will show the test data QC as determined by the data directory in \texttt{js/fqc.js}:

\begin{verbatim}
var filePath = "/example/plot_data/"
\end{verbatim}

Edit \texttt{fqc.js} to your local path \textbf{within} the \texttt{fqc} directory tree.

\section*{2.2 Example Workflow}

Using the example data set provided in the repo, let’s walk through creating the example site with paired-end data and some custom plots.

In our example, we’re looking at highly replicated 16S amplicon data, so we will be omitting non-informative plots from our display using \texttt{--exclude}.

\subsection*{2.2.1 Running QC}

After installation, run QC over the first sample and generate the dashboard from within \texttt{fqc} repository:

\begin{verbatim}
$ cd example
$ fqc qc -t 8 -e 'Basic Statistics' \\n- e 'Overrepresented Sequences' \\
- e 'Count by Length' \\
- e 'Kmer Content' \\
2016 160912_M03018 data/fastqs/160912_M03018_R1.fastq.gz
\end{verbatim}
2.2.2 Adding Custom Plots

Next, add the Lorenz curve which gives us an idea of how equitably the sequences were distributed among barcodes. This plot will be added as the top tab using \(--prepend\):

```
$ fqc add --prepend --x-value FractionOfSamples --y-value Equal \\
--y-value Actual --x-label 'Fraction of Samples' \\
--y-label 'Fraction of On Target Reads' \\
plot_data/2016/160912_M03018/config.json \\
'Read Distribution' \\
line \\
data/tables/160912_lorenz.csv
```

The JSON entry in the output above is just for confirmation as it has already been added to this run’s configuration. Our display now shows the new tab in the first position:
Tip: Based on the distribution of barcodes, the user could have specified a fail or warning condition on using the Gini Coefficient and set a tab icon using `--status fail` in the previous command. For more information see Tab Status.

To add the sequence summary table, we need to append another tab:

```bash
$ fqc add --prepend plot_data/2016/160912_M03018/config.json 'Run Stats' table data/tables/160912_summary.csv
```
Another plot we typically add shows read abundance across primer plates. This is valuable to observe positive and negative control wells in addition to seeing the effects on neighboring wells. Run 160912 did not have any controls, so we’ll just add abundance for its plate:

```bash
$ fqc add --x-value WELL_COL --y-value WELL_ROW \
 --value TOTAL_PAIRED_READS --label LABEL \
 --label-color LABEL_COLOR \
 plot_data/2016/160912_M03018/config.json \
 'Abundance by Plate' \
 plateheatmap \
 data/tables/160912_plate_1.csv
```
And finally, sometimes things go wrong and barcode plates get mixed up, so we display the top barcodes and their counts. Usually we simply add it as a table, but let's display it as a bar plot:

```
$ fqc add --x-value Barcode --y-value Count \
   plot_data/2016/160912_M03018/config.json \
   "Barcode Counts" \
   bar \
   data/tables/160912_top50barcodes.csv
```
The remainder of the example site iterates over these steps for the remainder of the samples.

### 2.3 Groups

Located within the `plot_data` directory, this holds metadata for each group and samples within the groups:

```
[
  {
    "group_id": "group_01",
    "uids": [
      "test_01"
    ]
  },
  {
    "group_id": "group_00",
    "uids": [
      "test_00"
    ]
  }
]
```

Renders as:
The sample ID and group ID must match the underlying directory tree that is built by `fqc qc` and maintained when using `fqc batch-qc` and `fqc add`.

The directory tree of this simple example:

```
plot_data/
    group_00
        test_00
            R1
            R2
            config.json
    group_01
        test_01
            R1
            R2
            config.json
    groups.json
```

For a more detailed example, see the `groups.json` file located in the example data directory.

### 2.4 Configuration File

Each FASTQ or FASTQ pair will have an associated `config.json` file that holds information like which plots to draw into which tabs and where the associated data files reside. Each entry must have a `tab_name`, `filename`, and `chart_properties` specific to the chart type. For more information on individual plots and their requirements, see their respective pages.

#### 2.4.1 Tab Status

This is an optional icon for page tabs and supports values of `pass`, `fail`, or `warn`. It's rendered as:

- Basic Statistics
- Quality by Position
- Quality by Tile

#### 2.4.2 Plot Options

The configuration of plots themselves occurs within the `chart_properties` key. Individual plot options are defined in the docs under each plot type.

#### 2.4.3 Manual Editing

Plots can edited and plot data can be added manually to a particular sample’s `config.json`. If you’re adding a new sample manually, you will have to add it to `groups.json`. 

---

Chapter 2. Citation
2.5 Plot Tabs

Tabs can be added to the plot area using a list of lists for the `filename` attribute. The first position is the name of the tab while the second is the file path. An example JSON entry for this in a sample’s `config.json` looks like:

```json
"filename": [
    [
        "Plate 1",
        "plt1_counts.csv"
    ],
    [
        "Plate 2",
        "plt2_counts.csv"
    ]
]
```

Which will render as:

![Plot Tabs](image)

2.6 Area Range

The area range plot is automatically generated from FastQC output for inspecting read quality as a function of position along the sequence.

2.6.1 Example Data

An example table after parsing output from FastQC looks like:

<table>
<thead>
<tr>
<th>Base</th>
<th>Mean</th>
<th>Lower Quartile</th>
<th>Upper Quartile</th>
</tr>
</thead>
<tbody>
<tr>
<td>1</td>
<td>32.193</td>
<td>32.0</td>
<td>33.0</td>
</tr>
<tr>
<td>2</td>
<td>32.365</td>
<td>32.0</td>
<td>33.0</td>
</tr>
<tr>
<td>3</td>
<td>32.570</td>
<td>32.0</td>
<td>33.0</td>
</tr>
</tbody>
</table>
2.6.2 Plot Options

<table>
<thead>
<tr>
<th>Option</th>
<th>Value</th>
</tr>
</thead>
<tbody>
<tr>
<td>filename</td>
<td>supports either a single file path or list of lists with [plot tab name, file path] pairs (see Plot Tabs)</td>
</tr>
<tr>
<td>tab_name</td>
<td>left main menu entry</td>
</tr>
<tr>
<td>status</td>
<td>left main menu icon – supports ‘pass’, ‘fail’, ‘warn’, or alternatively, omitted (see Tab Status)</td>
</tr>
<tr>
<td>chart_properties</td>
<td>See table below</td>
</tr>
</tbody>
</table>

2.6.3 Chart Properties

<table>
<thead>
<tr>
<th>Option</th>
<th>Value</th>
</tr>
</thead>
<tbody>
<tr>
<td>type</td>
<td>the required entry is ‘arearange’</td>
</tr>
<tr>
<td>x_label</td>
<td>x-axis label</td>
</tr>
<tr>
<td>x_value</td>
<td>the header label defined in filename corresponding to x-values</td>
</tr>
<tr>
<td>y_label</td>
<td>y-axis label</td>
</tr>
<tr>
<td>lower_quartile</td>
<td>the header label defined in filename corresponding to lower quartile values</td>
</tr>
<tr>
<td>upper_quartile</td>
<td>the header label defined in filename corresponding to upper quartile values</td>
</tr>
<tr>
<td>mean</td>
<td>the header label defined in filename corresponding to mean values</td>
</tr>
<tr>
<td>zones</td>
<td>defined as ‘value’:'color’ with an initial ‘color’ as the base; see example below</td>
</tr>
</tbody>
</table>

Example JSON entry:

```
{
    "filename": "R1/Per_base_sequence_quality.csv",
    "tab_name": "Quality by Position",
    "status": "pass",
    "chart_properties": {
        "type": "arearange",
        "x_label": "Position",
        "x_value": "Base",
        "y_label": "Quality (Phred score)",
        "lower_quartile": "Lower Quartile",
        "upper_quartile": "Upper Quartile",
        "mean": "Mean"
    }
}
```
There is support for adding zones as well, if you’re going for the classic FastQC look and feel:

```json
{
    "filename": [
        ["R1", "R1/Per_base_sequence_quality.csv"],
        ["R2", "R2/Per_base_sequence_quality.csv"]
    ],
    "tab_name": "Quality by Position",
    "status": "warn",
    "chart_properties": {
        "type": "arearange",
        "x_label": "Position",
        "x_value": "Base",
        "y_label": "Quality (Phred score)",
        "lower_quartile": "Lower Quartile",
        "upper_quartile": "Upper Quartile",
        "mean": "Mean",
        "zones": [
            {
                "value": 30, "color": "#e5afb0"
            },
            {
                "value": 34, "color": "#e6d6b1"
            },
            {"color": "#b0e5b1"}
        ]
    }
}
```

2.6. Area Range
2.7 Bar

No bar plots are automatically generated from FastQC output, but can optionally be added for custom data tables.

2.7.1 Example Data

<table>
<thead>
<tr>
<th>Barcode</th>
<th>Count</th>
</tr>
</thead>
<tbody>
<tr>
<td>TCACGGGAGTTG</td>
<td>579558</td>
</tr>
<tr>
<td>AGTTCAGACGCT</td>
<td>250808</td>
</tr>
<tr>
<td>ATTTCGACATGC</td>
<td>245063</td>
</tr>
<tr>
<td>TAATGACCAGGC</td>
<td>230339</td>
</tr>
<tr>
<td>CGATCCGTATTA</td>
<td>215466</td>
</tr>
</tbody>
</table>

2.7.2 Usage to Add

Given the example data for barcode counts:

```
$ fqc add --x-value Barcode --y-value Count \
  plot_data/2016/160912_M03018/config.json \
  "Barcode Counts" \
  bar \
  example/data/tables/160912_top50barcodes.csv
```
2.7.3 Plot Options

<table>
<thead>
<tr>
<th>Option</th>
<th>Value</th>
</tr>
</thead>
<tbody>
<tr>
<td>filename</td>
<td>supports either a single file path or list of lists with [plot tab name, file path] pairs (see Plot Tabs)</td>
</tr>
<tr>
<td>tab_name</td>
<td>left main menu entry</td>
</tr>
<tr>
<td>status</td>
<td>left main menu icon – supports ‘pass’, ‘fail’, ‘warn’, or alternatively, omitted (see Tab Status)</td>
</tr>
<tr>
<td>chart_properties</td>
<td>See table below</td>
</tr>
</tbody>
</table>

2.7.4 Chart Properties

<table>
<thead>
<tr>
<th>Option</th>
<th>Value</th>
</tr>
</thead>
<tbody>
<tr>
<td>type</td>
<td>the required entry is ‘bar’</td>
</tr>
<tr>
<td>subtitle</td>
<td>an optional subtitle for the plot</td>
</tr>
<tr>
<td>x_label</td>
<td>x-axis label</td>
</tr>
<tr>
<td>x_value</td>
<td>the header label defined in filename corresponding to x-values</td>
</tr>
<tr>
<td>y_label</td>
<td>y-axis label</td>
</tr>
<tr>
<td>y_value</td>
<td>the header label defined in filename corresponding to y-values</td>
</tr>
</tbody>
</table>

Example JSON entry:

```json
{
    "filename": "bar_plot_example.csv",
    "tab_name": "Barcode Counts",
    "chart_properties": {
        "type": "bar",
        "x_value": "Barcode",
        "x_label": "Barcode",
        "y_value": [ "Count" ],
        "y_label": "Count"
    }
}
```
2.8 Heatmap

A heatmap is generated using tile quality data from FastQC, but a custom one can be generated using data with an \( x \), an \( y \), and a value associated with the coordinate.

### 2.8.1 Example Data

<table>
<thead>
<tr>
<th>Tile</th>
<th>Base</th>
<th>Mean</th>
</tr>
</thead>
<tbody>
<tr>
<td>1101</td>
<td>1</td>
<td>0.4305</td>
</tr>
<tr>
<td>1101</td>
<td>2</td>
<td>0.1525</td>
</tr>
<tr>
<td>1101</td>
<td>3</td>
<td>0.0202</td>
</tr>
</tbody>
</table>

### 2.8.2 Usage to Add

Tile example data from FastQC can be added manually using:

```
$ fqc add --x-value Barcode --y-value Count --min-value -10 --max-value 10 plot_data/2016/160912_M03018/config.json "Barcode Counts" bar example/data/tables/160912_top50barcodes.csv
```
### 2.8.3 Plot Options

<table>
<thead>
<tr>
<th>Option</th>
<th>Value</th>
</tr>
</thead>
<tbody>
<tr>
<td>filename</td>
<td>supports either a single file path or list of lists with [plot tab name, file path] pairs (see <em>Plot Tabs</em>)</td>
</tr>
<tr>
<td>tab_name</td>
<td>left main menu entry</td>
</tr>
<tr>
<td>status</td>
<td>left main menu icon – supports ‘pass’, ‘fail’, ‘warn’, or alternatively, omitted (see <em>Tab Status</em>)</td>
</tr>
<tr>
<td>chart_properties</td>
<td>See table below</td>
</tr>
</tbody>
</table>

### 2.8.4 Chart Properties

<table>
<thead>
<tr>
<th>Option</th>
<th>Value</th>
</tr>
</thead>
<tbody>
<tr>
<td>type</td>
<td>the required entry is ‘heatmap’</td>
</tr>
<tr>
<td>subtitle</td>
<td>an optional subtitle for the plot</td>
</tr>
<tr>
<td>x_label</td>
<td>x-axis label</td>
</tr>
<tr>
<td>x_value</td>
<td>the header label defined in filename corresponding to x-values</td>
</tr>
<tr>
<td>y_label</td>
<td>y-axis label</td>
</tr>
<tr>
<td>y_value</td>
<td>the header label defined in filename corresponding to y-values</td>
</tr>
<tr>
<td>value</td>
<td>the header label defined in filename corresponding to heatmap values</td>
</tr>
<tr>
<td>min_color</td>
<td>the minimum color used in the heatmap color map</td>
</tr>
<tr>
<td>mid_color</td>
<td>the middle color used in the heatmap color map</td>
</tr>
<tr>
<td>max_color</td>
<td>the maximum color used in the heatmap color map</td>
</tr>
<tr>
<td>min</td>
<td>the minimum value defined for the heatmap color map</td>
</tr>
<tr>
<td>max</td>
<td>the maximum value defined for the heatmap color map</td>
</tr>
</tbody>
</table>

Example JSON entry:

```json
{
    "filename": "R1/Per_tile_sequence_quality.csv",
    "tab_name": "Quality by Tile",
    "status": "pass",
    "chart_properties": {
        "type": "heatmap",
        "subtitle": "Per Tile Average Quality Deviation",
        "x_label": "Position",
        "x_value": "Base",
        "y_label": "Tile",
        "y_value": "Tile",
        "shape": "square",
        "value": "Mean",
        "min": "-10",
        "max": "10",
        "min_color": "#36c",
        "mid_color": "#ffffff",
        "max_color": "#dc3912"
    }
}
```
2.9 Histogram

This plot is useful in the context of 16S amplicon sequencing after we’ve quality trimmed reads then joined paired-end reads. Tabulating observed read lengths and their respective counts can give insights into the quality of the sequence ends.

2.9.1 Example Data

<table>
<thead>
<tr>
<th>Length</th>
</tr>
</thead>
<tbody>
<tr>
<td>153</td>
</tr>
<tr>
<td>179</td>
</tr>
<tr>
<td>177</td>
</tr>
<tr>
<td>191</td>
</tr>
<tr>
<td>198</td>
</tr>
</tbody>
</table>

2.9.2 Usage to Add

Given the example data for read length counts:

```bash
$ fqc add -x Length -Y "Read Count" --step 10 \
   plot_data/2016/160912_M03018/config.json \
   "Joined Read Lengths" \
   histogram \
   data/tables/histogram_example.csv
```
### 2.9.3 Plot Options

<table>
<thead>
<tr>
<th>Option</th>
<th>Value</th>
</tr>
</thead>
<tbody>
<tr>
<td>filename</td>
<td>supports either a single file path or list of lists with [plot tab name, file path] pairs (see Plot Tabs)</td>
</tr>
<tr>
<td>tab_name</td>
<td>left main menu entry</td>
</tr>
<tr>
<td>status</td>
<td>left main menu icon – supports 'pass', 'fail', 'warn', or alternatively, omitted (see Tab Status)</td>
</tr>
<tr>
<td>chart_properties</td>
<td>See table below</td>
</tr>
</tbody>
</table>

### 2.9.4 Chart Properties

<table>
<thead>
<tr>
<th>Option</th>
<th>Value</th>
</tr>
</thead>
<tbody>
<tr>
<td>type</td>
<td>the required entry is 'histogram'</td>
</tr>
<tr>
<td>subtitle</td>
<td>an optional subtitle for the plot</td>
</tr>
<tr>
<td>x_label</td>
<td>x-axis label</td>
</tr>
<tr>
<td>x_value</td>
<td>the header label defined in filename corresponding to values</td>
</tr>
<tr>
<td>y_label</td>
<td>y-axis label</td>
</tr>
<tr>
<td>step</td>
<td>histogram bin size</td>
</tr>
</tbody>
</table>

Example JSON entry:

```
{
    "filename": "histogram_example.csv",
    "tab_name": "Joined Read Lengths",
    "chart_properties": {
        "type": "histogram",
        "x_value": "Length",
        "x_label": "Length",
        "y_label": "Read Count",
        "step": 10
    }
}
```
2.10 Line

2.10.1 Example Data

<table>
<thead>
<tr>
<th>Quality</th>
<th>Count</th>
</tr>
</thead>
<tbody>
<tr>
<td>18</td>
<td>1.0</td>
</tr>
<tr>
<td>19</td>
<td>14.0</td>
</tr>
<tr>
<td>20</td>
<td>46.0</td>
</tr>
<tr>
<td>21</td>
<td>111.0</td>
</tr>
<tr>
<td>22</td>
<td>141.0</td>
</tr>
</tbody>
</table>

2.10.2 Usage to Add

Given quality data across read positions, we can add this plot using:

```
$ fqc add --x-value Barcode --y-value Count \
  plot_data/2016/160912_M03018/config.json \
  "Barcode Counts" \
  bar \
  example/data/tables/160912_top50barcodes.csv
```
### 2.10.3 Plot Options

<table>
<thead>
<tr>
<th>Option</th>
<th>Value</th>
</tr>
</thead>
<tbody>
<tr>
<td>filename</td>
<td>supports either a single file path or list of lists with [plot tab name, file path] pairs (see Plot Tabs)</td>
</tr>
<tr>
<td>tab_name</td>
<td>left main menu entry</td>
</tr>
<tr>
<td>status</td>
<td>left main menu icon – supports ‘pass’, ‘fail’, ‘warn’, or alternatively, omitted (see Tab Status)</td>
</tr>
<tr>
<td>chart_properties</td>
<td>See table below</td>
</tr>
</tbody>
</table>

### 2.10.4 Chart Properties

<table>
<thead>
<tr>
<th>Option</th>
<th>Value</th>
</tr>
</thead>
<tbody>
<tr>
<td>type</td>
<td>the required entry is ‘bar’</td>
</tr>
<tr>
<td>subtitle</td>
<td>an optional subtitle for the plot</td>
</tr>
<tr>
<td>x_label</td>
<td>x-axis label</td>
</tr>
<tr>
<td>x_value</td>
<td>the header label defined in filename corresponding to x-values</td>
</tr>
<tr>
<td>y_label</td>
<td>y-axis label</td>
</tr>
<tr>
<td>y_value</td>
<td>the header label defined in filename corresponding to y-values</td>
</tr>
</tbody>
</table>

Example JSON entry:

```json
{
   "filename": "simple_line.csv",
   "tab_name": "Quality by Position",
   "chart_properties": {
      "type": "line",
      "x_value": "Quality",
      "x_label": "Quality",
      "y_value": ["Count"],
      "y_label": "Count"
   }
}
```
2.10.5 Multi-line Plots

When multiple y-values are being plotted:

<table>
<thead>
<tr>
<th>Base</th>
<th>G</th>
<th>A</th>
<th>T</th>
<th>C</th>
</tr>
</thead>
<tbody>
<tr>
<td>1</td>
<td>45.96</td>
<td>51.62</td>
<td>1.38</td>
<td>1.04</td>
</tr>
<tr>
<td>2</td>
<td>0.8999999999999999</td>
<td>7.26</td>
<td>1.5</td>
<td>90.34</td>
</tr>
<tr>
<td>3</td>
<td>8.14</td>
<td>79.12</td>
<td>11.72</td>
<td>1.02</td>
</tr>
<tr>
<td>4</td>
<td>1.1199999999999999</td>
<td>5.1</td>
<td>4.5</td>
<td>89.28</td>
</tr>
<tr>
<td>5</td>
<td>1.82</td>
<td>1.0999999999999999</td>
<td>1.32</td>
<td>95.76</td>
</tr>
</tbody>
</table>

These data are added by specifying `-y` multiple times:

```
$ fqc add -x Base -X Position -y G -y A -y C -y T -Y Percent
   plot_data/2016/160912_M03018/config.json "Content by Position" line data/tables/multiple_line.csv
```

Example JSON entry:

```
{
    "filename": "multiple_line.csv",
    "tab_name": "Content by Position",
    "chart_properties": {
        "type": "line",
```

(continues on next page)
2.11 Plate Heatmap

This plot is intended to be a nicely spaced heatmap specifically for showing trends over sample plates. Definitions for colors are optional and will be used to outline their respective coordinates.

An example for this plot type is executed in the workflow at plate-heatmap-example.

2.11.1 Example Data

This is an alternate example from the workflow to show how to deal with multiple label colors.
### 2.11.2 Usage to Add

```
$ fqc add --x-value WELL_COL --y-value WELL_ROW \
   --value TOTAL_PAIRED_READS --label LABEL \
   --label-color LABEL_COLOR \n   plot_data/2016/160912_M03018/config.json \n   'Abundance by Plate' \n   plateheatmap \n   data/tables/160912_plate_1.csv
```

### 2.11.3 Plot Options

<table>
<thead>
<tr>
<th>Option</th>
<th>Value</th>
</tr>
</thead>
<tbody>
<tr>
<td>filename</td>
<td>supports either a single file path or list of lists with [plot tab name, file path] pairs (see Plot Tabs)</td>
</tr>
<tr>
<td>tab_name</td>
<td>left main menu entry</td>
</tr>
<tr>
<td>status</td>
<td>left main menu icon – supports ‘pass’, ‘fail’, ‘warn’, or alternatively, omitted (see Tab Status)</td>
</tr>
<tr>
<td>chart_properties</td>
<td>See table below</td>
</tr>
</tbody>
</table>

### 2.11.4 Chart Properties

<table>
<thead>
<tr>
<th>Option</th>
<th>Value</th>
</tr>
</thead>
<tbody>
<tr>
<td>type</td>
<td>the required entry is ‘plateheatmap’</td>
</tr>
<tr>
<td>subtitle</td>
<td>an optional subtitle for the plot</td>
</tr>
<tr>
<td>x_label</td>
<td>x-axis label</td>
</tr>
<tr>
<td>x_value</td>
<td>the header label defined in filename corresponding to x-values</td>
</tr>
<tr>
<td>y_label</td>
<td>y-axis label</td>
</tr>
<tr>
<td>y_value</td>
<td>the header label defined in filename corresponding to y-values</td>
</tr>
<tr>
<td>label</td>
<td>the header label defined in filename corresponding to point labels; displayed on hover when specified</td>
</tr>
<tr>
<td>label_color</td>
<td>header of column containing colors; acts to color surrounding point to highlight</td>
</tr>
</tbody>
</table>

Example JSON entry:

```json
{
   "filename": "160912_plate_1.csv",
   "tab_name": "Abundance by Plate",
   "chart_properties": {
      "type": "plateheatmap",
      "x_value": "WELL_COL",
      "x_label": "WELL_COL",
      "y_value": ["WELL_ROW"],
      "y_label": "WELL_ROW",
      ...
   }
}
```

(continues on next page)
2.12 Table

2.12.1 Example Data

<table>
<thead>
<tr>
<th>Measure</th>
<th>Value</th>
</tr>
</thead>
<tbody>
<tr>
<td>Total Reads</td>
<td>15752091</td>
</tr>
<tr>
<td>Fraction On Target</td>
<td>0.67042235853</td>
</tr>
<tr>
<td>Fraction Off Target</td>
<td>1.0284348916e-05</td>
</tr>
<tr>
<td>Fraction Unmatched</td>
<td>0.329567357121</td>
</tr>
<tr>
<td>Coefficient of Distribution (G)</td>
<td>0.260394791718</td>
</tr>
</tbody>
</table>
2.12.2 Usage to Add

```
$ fqc add --prepend 
   plot_data/2016/160912_M03018/config.json 
   'Run Stats' 
   table 
   data/tables/160912_summary.csv
```

2.12.3 Plot Options

<table>
<thead>
<tr>
<th>Option</th>
<th>Value</th>
</tr>
</thead>
<tbody>
<tr>
<td>filename</td>
<td>supports either a single file path or list of lists with [plot tab name, file path] pairs (see Plot Tabs)</td>
</tr>
<tr>
<td>tab_name</td>
<td>left main menu entry</td>
</tr>
<tr>
<td>status</td>
<td>left main menu icon – supports ‘pass’, ‘fail’, ‘warn’, or alternatively, omitted (see Tab Status)</td>
</tr>
</tbody>
</table>

Example JSON entry:

```
{
   "filename": "160912_summary.csv",
   "chart_properties": {
      "type": "table"
   },
   "tab_name": "Run Stats"
}
```