Growth curve analysis | data: 08/17/2013

This script does some data plotting and quality check for my first Bioscreen-C experiment
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17 auot 2013

Read data

Notes:

- change the working directory
- replace the filename with the appropriate name

```
raw <- read.csv("BioscreenExperiment20130816.csv")
# note: each column is temporal data for one well
data <- as.matrix(raw[, -1])
```

Design matrix

- define the strains
- define all factors involved
- setup the design matrix

```
## Strains
```

```
## [1] "wt"            "pho80-1"       "pho80-2"        "pho4"
## [5] "pho80.scPho4-1" "pho80.scPho4-2" "empty"
```

```
## Each strain is tested in the following 10 conditions
```

```
##    Glucose    Pi Rapamycin
## 1      2%  10mM    0ng/ml
## 2      2%   1mM    0ng/ml
## 3      2% 0.1mM    0ng/ml
## 4      2%   0mM    0ng/ml
## 5    0.5%  10mM    0ng/ml
## 6    0.5%   1mM    0ng/ml
## 7    0.5% 0.1mM    0ng/ml
## 8      2%  10mM   10ng/ml
## 9      2%  10mM   50ng/ml
## 10     2%   1mM   10ng/ml
```

Functions

1. Subfunction to summarize the data by calculating the mean and sd of tech. repl.

2. A function to visualize the time course for any given strain at a particular condition

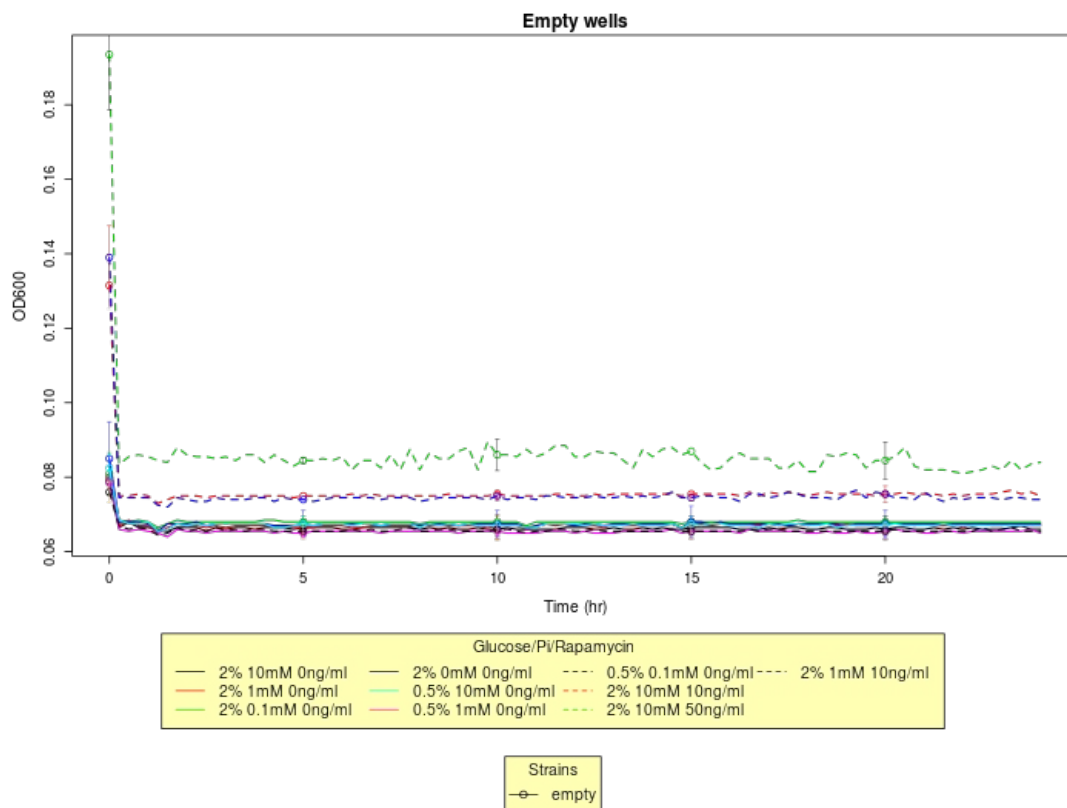3. Based on plotTrace, but plot the mean of tech. repl.

Analyses

1. Quality check

Negative controls

The last well of each column has no cells in it. Plotting the OD of the 20 empty wells should be background.

```
x = myMeanSD(data, design.mat)
plotMeanTrace(x, "empty", 1:10, title = "Empty wells", lwd = 1.5)
```


But something is wrong with the first column

Notice the flat line including the wt, the two pho80 strain, all of which are in the first column Also notice that the rest three strains shared a similar pattern, i.e. there is a peak at ~6h, then a drop, followed by a recovery. In the case of pho80.scPHO4, there is a subsequent drop. The *pho4* strain seems to do particularly well in this condition. By the end it still doesn't seem to saturate.

```
plotMeanTrace(x, "all", 1, lwd = 1.5, title = "First column problem")
```
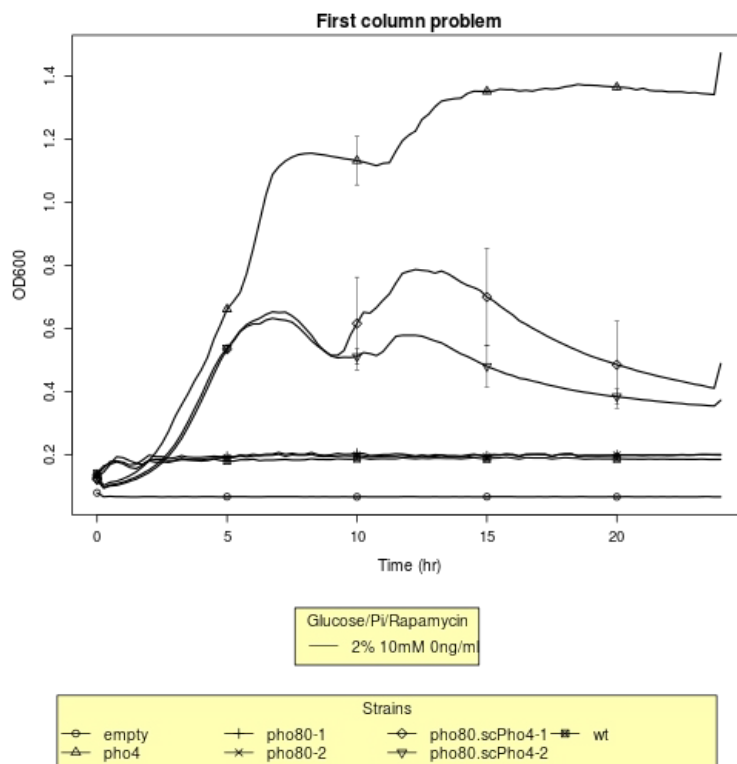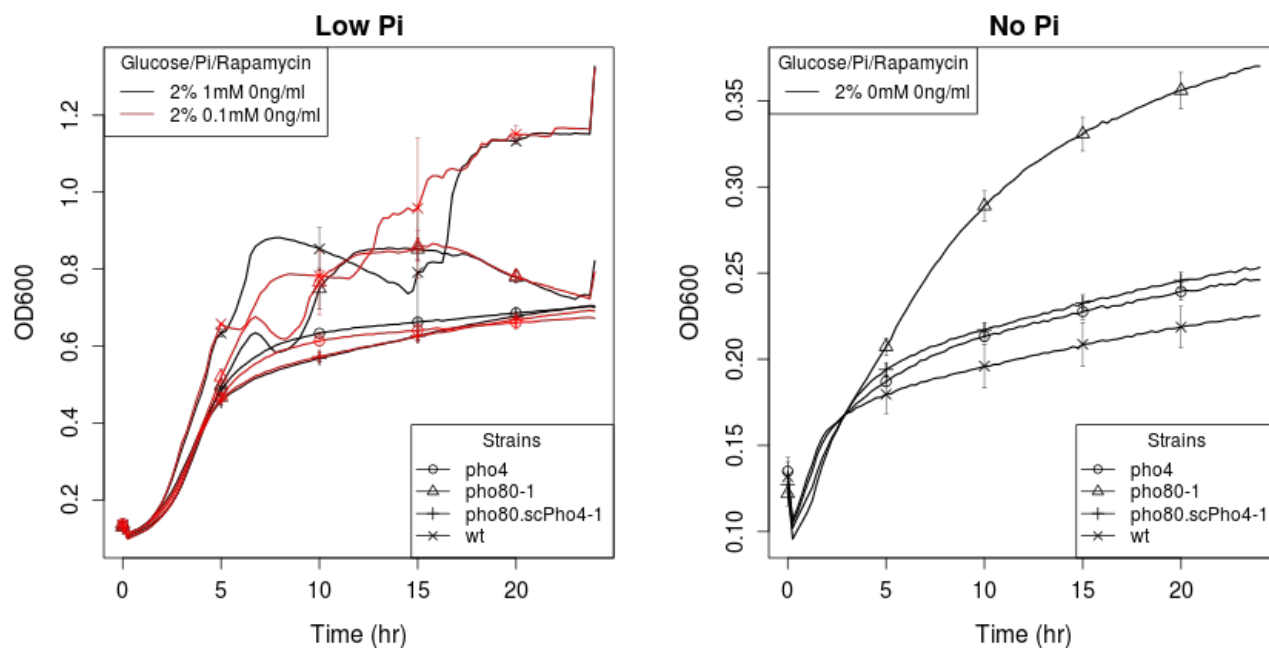

Starved for Pi

The biological replicates (pho80 and pho80.scPHO4) are quite similar. From now on I just plot one of them

```
st.use <- c("wt", "pho80-1", "pho4", "pho80.scPho4-1")
layout(matrix(c(1, 2), ncol = 2))
plainMeanTrace(x, st.use, c(2:3), lwd = 1.5, title = "Low Pi")
plainMeanTrace(x, st.use, 4, lwd = 1.5, title = "No Pi")
```


Starved for Glucose (and Pi)

```
layout(matrix(c(1, 2), ncol = 2))
plainMeanTrace(x, st.use, 5, lwd = 1.5, ylim = c(0.06, 1.2), title = "Low Glucose")
plainMeanTrace(x, st.use, c(6, 7), lwd = 1.5, ylim = c(0.06, 1.2), title = "Low
Glucose + Low Pi")
```
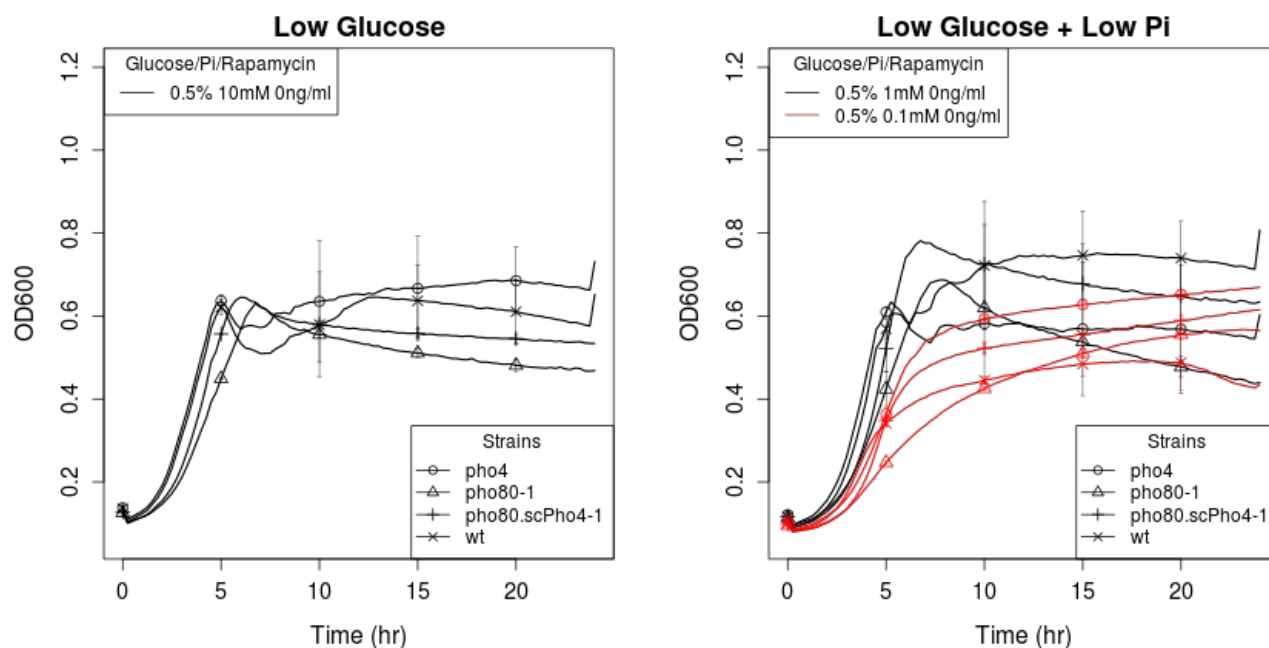

Comparison grouped by strains, not conditions

```
layout(matrix(c(1:4), byrow = TRUE, ncol = 2))
plainMeanTrace(x, "wt", 1:7, lwd = 1.5, ylim = c(0.06, 1.2), title = "wt")
plainMeanTrace(x, "pho80-1", 1:7, lwd = 1.5, ylim = c(0.06, 1.2), title = "pho80")
```

```
plainMeanTrace(x, "pho80.scPho4-1", 1:7, lwd = 1.5, ylim = c(0.06, 1.2), title =
"pho80.scPho4")
plainMeanTrace(x, "pho4", 1:7, lwd = 1.5, ylim = c(0.06, 1.2), title = "pho4")
```