Exercises

In the Exercises folder you will find following folders and files:

Folder	File(s)	Description
ddpcr_data	.qlp, .qlr, .csv, .log, .qlp, error.log, .txt	ddpcr reader output files
/	2014-11-18 Dilutions serie mistakes.csv	Head file with mistakes
/	template_headfile.xlsx	Empty head file template
/	template_headfile_testdata.xslx	Solution head file template

Exercises Part1:

1. **Perform the demo analysis (set to qx100!)**
2. **Use the demo dataset and set the threshold to a manual defined threshold for assay RNA**
    - Download the plots, summary table and summary parameters

Exercises Part2:

1. **Perform demo analysis for RU5: Quantasoft analysis in following folder ddpcr_data**
    - Open in Quantasoft (qlp)
    - Go to Analyze (left side panel)
        1. Select all samples (*) + sort on target + select all RU5 + update
        2. Go to 1-D Amplitude
        3. Auto Analyze with individual and combined wells => What is wrong?
            1. Individual => No calls + negative droplets are blue = positive
            2. Combined wells => negative droplets are positive (NTC + samples)
        4. Select wells C01 and E03 and look in ch1 => What is wrong?
            1. Baseline shift
        5. Write down the concentration of C01:
    - Export the amplitudefiles
        6. Go to Setup > options > export amplitude and cluster data
        7. Select folder

2. Upload the amplitudefiles + headfile to ddpcRquant

3. Run analysis with standard settings

- Write down the concentration of sample C01:
- (0.5 vs 0.28) => reason? threshold in quantasoft to close to negative droplet population

4. Run analysis with a 99.99 threshold

- What happens with the threshold and positive droplets? Why?
- Higher CI = higher threshold => captures 99.99% of the extreme events (you allow to miss 1 extreme event in 10000 events)