## Case study: Investigating C. reinhardtii’s capability as a cell factory

### TAG production

1. Intuition and transcriptome data from Goodenough 2014 (<https://doi.org/10.1128/EC.00013-14>). Transcriptomic data of 16 time series were taken.
2. PC-model is set up, so ammonia uptake is zero and growth rate is zero. Acetate uptake is opened to -1000.
3. 16 data sets were clustered into 4 groups for nonconvex QP. The best r vector is estimated for 4 groups.
4. R vector is used to update the model. A convex QP is conducted for each data set to interpret the metabolic flux network. The quadratic objective function needs to be weighted to prevent the solver from overlooking lowly transcribed genes.