

# Explanation of Information and Parameters for GCAF - Goodwin Gibbins

## 1 Meta-Information Sections

These sections make up the columns in the database information files and the `$Info` portion of class `gAnalysis` objects.

**Initials** The initials of the experimenter. Part of the unique identification of a growth curve.

- FYL - Fang Yin Lo
- ST - Serdar Turkarslan
- LP - Lee Pang
- KB - Karlyn Beer

**Date** The date the experiment was carried out or a consecutive day if multiple experiments occurred at the same time. Part of the unique identification of a growth curve.

- YYYYMMDD - for example, April 15, 2010 would be 20100415

**Well.Number** The well number for a bioscreen experiment, matching the well number on the results file and extracted from the labels file. Part of the unique identification of a growth curve.

**Well.Name** The label-file entry for a given well number, to be translated to fill in columns of information file.

**Media** A description of the media use.

- CM - complete media
- CDM -
- NA - no media in well
- More...

**Background** The strain of bacteria used for the experiment.

- NRC-1 - wild type
- ura3 - d-ura3, means bacteria were grown with uracil
- NA - no bacteria in well

**Knockout** A gene or list of genes removed. Multiple knockouts separated by & (need to develop search method for this). Naming is based on the ORF Name from the annotated genome search on the Baliga lab website.

- more....
- NA - no knockout

**Overexpression** A gene or list of genes overexpressed. Multiple knockouts separated by & (need to develop search method for this). Naming is based on the ORF Name from the annotated genome search on the Baliga lab website.

- more....
- NA - no overexpression

**Biological.Replicate** The number of a biological replicate

- NA - not listed or only one biological replicate.

**Temp** The temperature the experiment is run at.

- NA - unspecified - probably 37°.

**pH** The pH of the media.

- NA - unspecified/unperturbed.

**Culture.OD** the OD of the culture before dilution for growth curve run.

- NA - not recorded

**NaCl.Concentration** The molarity of salt in the media.

- NA - XX M

**XX.Concentration** The  $\text{Cu}^{2+}$  (Cu2p), Fe, Mn, Ni, Co, or Zn concentration in mM.

- NA - no metal.

## 2 Parameters

The parameters are based on mathematical algorithms which can be found in the `gSplineFit.r` or `gFitXXX.r` functions.

**A** - the maximum growth (often just the final recorded growth since maximum not achieved.)

**time.A** - the time which A occurs at.

**mu** - the maximum growth rate (sometimes of first hump, sometimes second. Based on derivative of spline fit)

**time.mu** - the time which the maximum growth rate occurs.

**y.mu** - the cell density at the maximum growth rate.

**lambda** - the lag time - the intercept of the maximum growth rate with the spline initial growth level. (Subject to errors capturing the wrong maximum growth rate).

**integral** - the area under the growth curve.

**initial.od** - the initial cell density, extrapolated from the spline fit to avoid noise.

**time.max** - the length of the experiment.

**trajectory** - the slope at the end of the curve (more positive would mean that the actual A was much higher than the measured A)

**max.secderv** - the maximum of the spline-interpolated second derivative.

**max.secderv.time** - time at which the maximum of the second derivative occurs.

**max.secderv.index** - index location of the maximum of the second derivative.