

# Package: PEcAn.photosynthesis (via r-universe)

September 18, 2024

**Type** Package

**Title** PEcAn functions used for leaf-level photosynthesis calculations

**Version** 1.7.3.9000

**Description** The Predictive Ecosystem Carbon Analyzer (PEcAn) is a scientific workflow management tool that is designed to simplify the management of model parameterization, execution, and analysis. The goal of PEcAn is to streamline the interaction between data and models, and to improve the efficacy of scientific investigation. The PEcAn.photosynthesis package contains functions used in the Hierarchical Bayesian calibration of the Farquhar et al 1980 model.

**Depends** rjags

**Imports** coda (>= 0.18), utils, graphics, stats

**Suggests** knitr (>= 1.42), rmarkdown (>= 2.19), markdown

**SystemRequirements** JAGS (>=2.2.0)

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**LazyLoad** yes

**LazyData** FALSE

**Collate** fitA.R Licor.QC.R plots.R

**Encoding** UTF-8

**RoxygenNote** 7.3.2

**VignetteBuilder** knitr

**Repository** <https://pecanproject.r-universe.dev>

**RemoteUrl** <https://github.com/PecanProject/pecan>

**RemoteRef** HEAD

**RemoteSha** f22a7c4bbc532e4551f7bc9624cef649da317ac1

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estimate_mode	<i>estimate_mode</i>
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### Description

estimate\_mode

### Usage

```
estimate_mode(x, adjust = 0.1)
```

### Arguments

x	numeric values
adjust	passed to stats::density

### Author(s)

Mike Dietze  
Xiaohui Feng

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fitA	<i>fitA</i>
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### Description

fitA

### Usage

```
fitA(flux.data, cov.data = NULL, model = NULL)
```

**Arguments**

flux.data	data.frame of Licor data, concatenated by rows, and with a leading column 'fname' that is used to count the number of curves and match to covariates
cov.data	data.frame of covariate data. Column names used in formulas
model	list including at least 6 components: the fixed effects model for alpha (a.fixed) and Vcmax (V.fixed), the random effects for these (a.random, V.random), the variable used to match the gas-exchange and covariate data (match), and the number of MCMC iterations (n.iter). Additional optional arguments: TPU = TRUE turns on TPU limitation; Temp == 'Bernacchi01' turns on the Bernacchi et al 2001 temperature correction. If this is turned on all parameters are estimated for 25C, otherwise no temperature correction is applied. Setting Temp = 'June2004' will turn on the June et al 2004 Funct Plant Biol temperature correction to Jmax. Note: these two corrections are not mutually exclusive, you can set Temp = c('June2004','Bernacchi2001')

Right now the fixed effects are specified as a string using the standard R lm formula syntax, but without the LHS variable (e.g. '~ SLA + chl + SLA:chl'). The tilde is optional. For random effects, the two options right now are just 'leaf' for leaf-level random effects and NULL. 'model' has a default that sets all effects to NULL (fit one curve to all data) and n.iter=1000.

**Author(s)**

Mike Dietze  
Xiaohui Feng

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Licor\_QC

*Licor\_QC*

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**Description**

Licor\_QC

**Usage**

```
Licor_QC(dat, curve = c("ACi", "AQ"), tol = 0.05)
```

**Arguments**

dat	data frame
curve	Whether to do Quality Control by examining the 'ACi' curve, the 'AQ' curve, or both
tol	Code automatically tries to separate ACi and AQ curves in the same dataset by detecting the 'reference' condition for light and CO2 respectively. This is the relative error around the mode in that detection.

**Author(s)**

Mike Dietze

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plot_photo	<i>plot_photo</i>
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**Description**

plot\_photo

**Usage**

```
plot_photo(data, out, curve = c("ACi", "AQ"), tol = 0.05, byLeaf = TRUE)
```

**Arguments**

data	input data
out	fitted model output from <a href="#">fitA</a>
curve	Whether to do Quality Control by examining the 'ACi' curve, the 'AQ' curve, or both
tol	Code automatically tries to separate ACi and AQ curves in the same dataset by detecting the 'reference' condition for light and CO2 respectively. This is the relative error around the mode in that detection.
byLeaf	whether to plot fits on a leaf-by-leaf basis

**Author(s)**

Mike Dietze

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read_Licor	<i>read_Licor</i>
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**Description**

read\_Licor

**Usage**

```
read_Licor(filename, sep = "\t", ...)
```

**Arguments**

filename	name of the file to read
sep	file delimiter. defaults to tab
...	optional arguments forwarded to read.table

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**Author(s)**

Mike Dietze

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