



REGGAE

Regression Generator  
& Analyzer

How-to-reggae at Coding Camp  
By Liliana Gallegos

# What is REGGAE?



Compiled data  
(csv format)



Select analysis  
Run regression



✓ Analysis report  
✓ Regression plot



## Aims:

*Statistical reproducibility  
open-source  
user-friendly  
quick analysis*

# Setup

☐ Create r environment and install r-essentials:

```
conda create -n r_env r-essentials r-base
```

☐ Activate environment:

```
conda activate r_env
```

☐ Install packages required:

```
conda install --yes --file R-requirements.txt
```

☐ Confirm by running reggae help options:

```
Rscript reggae.r -h
```

# Statistical analysis options

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Regression analysis: Multivariate Linear or Random Forest (*quick not opt*)

-m , --model

- o Feature selection: *full, stepwise, dredge, mincorr*

-b , --buildmodel

- o Build a model:  $x_1, x_2, x_n$

-y , --yresponse

- o Define y-response
- o Split into Train/ Test datasets: [Default = 1 full dataset]

-r , --randsample

- o (a) ratio between 0 and 1 or (b) 0 = predefined test/train

-p , --pca

- o Principal Component analysis with kmeans clustering.
- o Build scaled/unscaled train and test sets random or universal training set.

-c , --corrplot

- o Pairwise Correlation

-q , --crossvalidation

- o Cross Validation  $q^2$  values from leave-one-out, K-fold, and external.

-d , --diagnostics

- o Diagnostics QSAR criteria for an acceptable model, F-value comparisons, collinearity, *outlier testing*.

- o ANOVA analysis.

-v , --verbose

- o Plots for selected analysis.

# Other options

`-i , --inputfile`

Requires csv file name.

`-o , --outputfile`

Optional: output file name (default = REGGAE-analysis-output.txt)

`-x , --extdata`

To validate model using external csv data set. Requires the name of csv data file.

`-e , --exportdata`

Export data sets. Select from option: scaled, unscaled, predicted.

`-s , --seed`

Optional: specify the seed for random sample split. (default seed = 42)

`-k , --kfoldvalue`

Optional: To adjust k-value for K-fold cross validation. (default = 5)

`-v , --verbose`

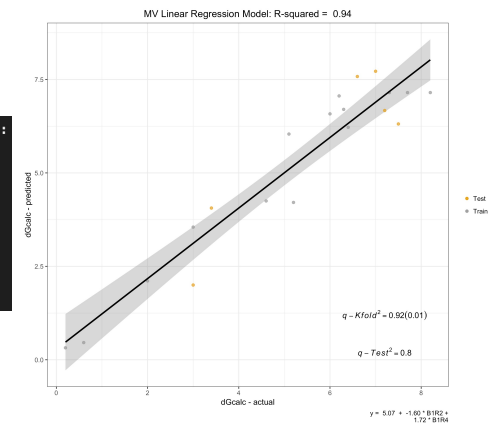
Optional: To print extra output and plots. (default = FALSE)

`-h , --help`

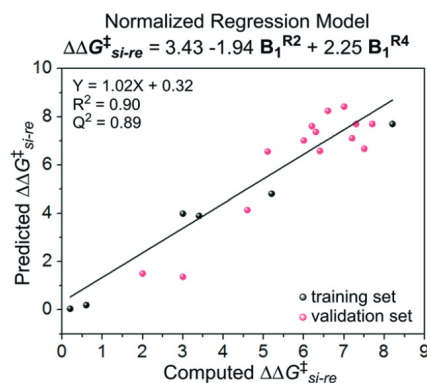
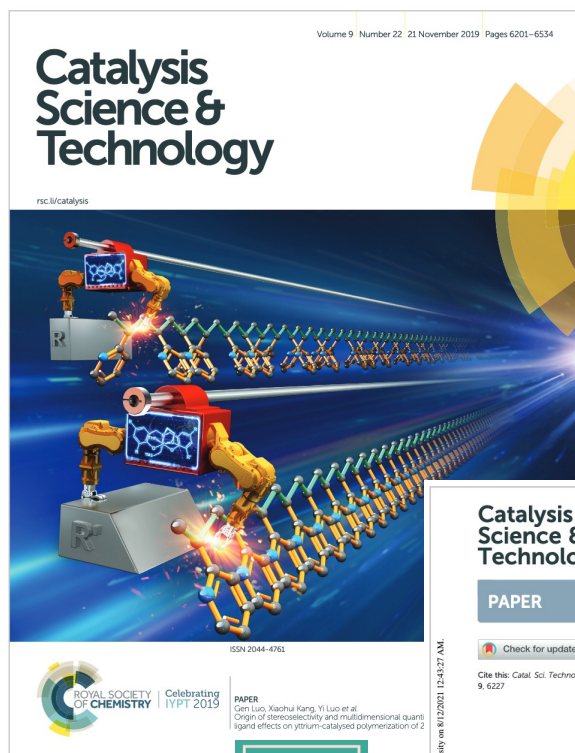
```
Rscript reggae.r -i data.csv -m stepwise -y dG -r 0.8 -q -d -v
```

## Predictive Model & Report

```
o Linear regression model with SELECTED features:  
  Number of features (including response): 3  
a) scaled coefficients:  
  y = 5.073 + -1.602 * B1R2 + 1.720 * B1R4  
b) unscaled:  
  y = 4.23 + -2.92 * B1R2 + 1.61 * B1R4  
R2-train = 0.94  
adj R2-train = 0.93  
RMSE-train = 0.58
```



# Example: Quantitative Structure–Selectivity Relationships



Total of 21 catalysts

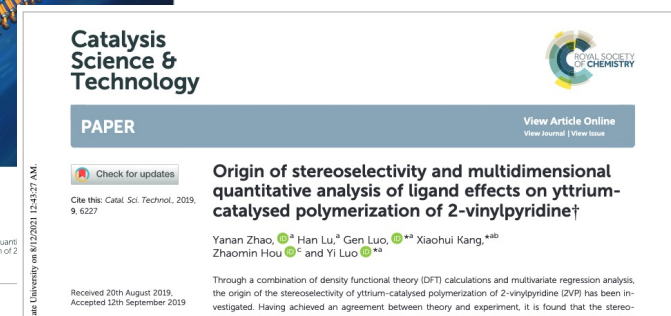
Steric and electronic features:

- Sterimol descriptors:  
B<sub>1</sub>, B<sub>5</sub>, L and %Vbur
- Natural Population Analysis (NPA) charges

For statistical reproducibility:

- Available dataset (ESI: .xlsx, .csv, table)
- Available code
- Labeled split datasets or methods used

	R <sup>2</sup>			R <sup>4</sup>			NPA Charge			%V <sub>Bur</sub>	$\Delta G_{DFT}^{\ddagger}$	$\Delta G_{predicted}^{\ddagger}$
	L <sup>2</sup>	B <sub>1</sub> R <sup>2</sup>	B <sub>5</sub> R <sup>2</sup>	L <sup>4</sup>	B <sub>1</sub> R <sup>4</sup>	B <sub>5</sub> R <sup>4</sup>	Q <sub>Y</sub>	Q <sub>O1</sub>	Q <sub>O2</sub>			
A	4.62	2.98	6.07	4.62	2.98	6.07	1.92	-0.92	-0.92	89.7	0.2	0.0
B	4.41	2.93	3.35	4.62	2.98	6.07	1.91	-0.92	-0.92	89.7	0.6	0.2
C	3.09	1.70	2.19	4.62	2.98	6.07	1.93	-0.91	-0.90	88.7	3.4	3.9



```
Rscript reggae.r -i 2vp-labeled.csv -b B1R2,B1R4 -y dGcalc -r 0 -q -d -v
```

Zhao, Y.; Lu, H.; Luo, G.; Kang, X.; Hou, Z.; Luo, Y. *Catal. Sci. Technol.*, **2019**, 9, 6227–6233.

Kraczyk, M. S.; Shi, A.; Bhaskar, A.; Marinov, D. Stodden, V. *Phil. Trans. R. Soc. A* **2021**, 379.