Sources

GMDHreg: Regression using GMDH Algorithms

<https://rdrr.io/cran/GMDHreg/>

(Tilve, 2021a)

GMDHreg: an R Package for GMDH Regression

<https://cran.r-project.org/web/packages/GMDHreg/vignettes/GMDHreg.html>

(Tilve, 2021b)

Package ‘GMDHreg’

<https://cran.r-project.org/web//packages//GMDHreg/GMDHreg.pdf>

Generalized Iterative Algorithm GIA GMDH

<http://www.mgua.irtc.org.ua/attach/ICIM-IWIM/2013/2.6%20.pdf#:~:text=Iterative%20methods%20are%20similar%20to%20a%20class%20of,stops%20when%20a%20criterion%20CR%20starts%20to%20grow>.

(Stepashko et al., 2013)

UCI Protein Dataset

<https://archive.ics.uci.edu/ml/datasets/Protein+Data>

(*UCI Machine Learning Repository: Protein Data Data Set*, n.d.)

Pairwise Structure Alignment

<https://www.rcsb.org/docs/tools/pairwise-structure-alignment>

(Bank, n.d.)

CASP5 Website

<https://predictioncenter.org/decoysets2019/description.cgi?casp=CASP5>

(*- DECOYSETS2019*, n.d.)

Harvard: Protein Folding, the good the bad the ugly

<https://sitn.hms.harvard.edu/flash/2010/issue65/>

(Admin, 2014)

Shrake Ripley Algorithm

<https://www.ncbi.nlm.nih.gov/pmc/articles/PMC6748739/>

(Ribeiro et al., 2019)

Protein Folding

<https://chemistrytalk.org/protein-folding/>

Kabsch

Kabsch, W. (1976). A solution for the best rotation to relate two sets of vectors. Acta Cryst. A32, 922–923.

(Kabsch, 1976)

Secondary Structure Penalty F8

<https://www.researchgate.net/publication/41426170_Effects_of_side-chain_packing_on_the_formation_of_secondary_structures_in_protein_folding#:~:text=At%20the%20same%20time%2C%20the%20dehydration%20penalty%20%28i.e.%2C,formed%20as%20much%20as%20possible%20in%20protein%20folding>.

(Yasuda et al., 2010)

Admin. (2014, January 9). *Protein Folding: The Good, the Bad, and the Ugly - Science in the News*. Science in the News. https://sitn.hms.harvard.edu/flash/2010/issue65/

Bank, R. P. D. (n.d.). *Pairwise Structure Alignment*. https://www.rcsb.org/docs/tools/pairwise-structure-alignment

*- DECOYSETS2019*. (n.d.). https://predictioncenter.org/decoysets2019/description.cgi?casp=CASP5

Gloyd, J. (2023). Protein Folding. *ChemTalk*. https://chemistrytalk.org/protein-folding/

Kabsch, W. (1976). A solution for the best rotation to relate two sets of vectors. Acta Cryst. A32,

922–923.

Ribeiro, J., Ríos-Vera, C., Melo, F. S., & Schüller, A. (2019). Calculation of accurate interatomic contact surface areas for the quantitative analysis of non-bonded molecular interactions. *Bioinformatics*, *35*(18), 3499–3501. https://doi.org/10.1093/bioinformatics/btz062

Stepashko, V., Bulgakova, O., & International Research and Training Centre for Information Technologies and Systems of the NAS and MES of Ukraine. (2013). *Generalized Iterative Algorithm GIA GMDH*. International Conference in Inductive Modelling ICIM’.

Tilve, M. V. (2021a, July 5). *GMDHreg: an R Package for GMDH Regression*. https://cran.r-project.org/web/packages/GMDHreg/vignettes/GMDHreg.html

Tilve, M. V. (2021b). GMDHreg: Regression using GMDH Algorithms. *rdrr.io*. https://rdrr.io/cran/GMDHreg/

*UCI Machine Learning Repository: Protein Data Data Set*. (n.d.). https://archive.ics.uci.edu/ml/datasets/Protein+Data

Yasuda, S., Yoshidome, T., Oshima, H., Kodama, R., Harano, Y., & Kinoshita, M. (2010). Effects of side-chain packing on the formation of secondary structures in protein folding. *Journal of Chemical Physics*, *132*(6), 065105. https://doi.org/10.1063/1.3319509