Sources

GMDHreg: Regression using GMDH Algorithms

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

GMDHreg: an R Package for GMDH Regression

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

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>.

UCI Protein Dataset

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

Pairwise Structure Alignment

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

CASP5 Website

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

Harvard: Protein Folding, the good the bad the ugly

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

Shrake Ripley Algorithm

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