# Inconsistency about the pathway information from various databases

Since two decades hundreds of databases are being developed and maintained for pathway. The choice of database can significantly influence the results of enrichment analysis of expression studies (Mubeen et al. 2019) . The databases tend to differ in various aspects, such as, the number of pathways, the number of genes in a pathway, the type of biochemical interactions and their mining approaches(Mubeen et al. 2019).

Plethora of enrichment tools are available causing i) difficulty to comprehend the features and algorithms of tool; ii) redundant efforts in developing similar tools that are already present, because researchers unable to understand the in depth idea of algorithms; iii) out of date ideas being used in new tools; and iv) confusion in users due to overwhelming choices.(Huang, Sherman & Lempicki 2008)

# Databases

# KEGG (Kyoto Encyclopaedia of Genes and Genomes)

KEGG is the consolidated database of 16 databases, which all are manually curated from published literature (Kanehisa et al. 2016). [ last updated in Nov1, 2022 ]

Data base is influenced by:

1. How frequently database is updated ?
2. How the mining is done, is it manually or computationally?
3. Also, vast amount of literature and research papers produced every day, many of them has contrasting and controversial information and often their approach of producing the data and analysing is doubtful ( imp of papers published do not have followed a correct technique of enrichment analysis (Wijesooriya et al. 2022)

# References

Kanehisa, M., Furumichi, M., Tanabe, M., Sato, Y., Morishima, K. (2016). KEGG: new perspectives on genomes, pathways, diseases and drugs. *Nucleic Acids Res.* 45 (D1), D353–D361. doi: 10.1093/nar/gkw1092

Huang, DW, Sherman, BT & Lempicki, RA 2008, 'Bioinformatics enrichment tools: paths toward the comprehensive functional analysis of large gene lists', *Nucleic acids research*, vol. 37, no. 1, pp. 1-13.

Kanehisa, M, Furumichi, M, Tanabe, M, Sato, Y & Morishima, K 2016, 'KEGG: new perspectives on genomes, pathways, diseases and drugs', *Nucleic acids research*, vol. 45, no. D1, pp. D353-D361.

Mubeen, S, Hoyt, CT, Gemünd, A, Hofmann-Apitius, M, Fröhlich, H & Domingo-Fernández, D 2019, 'The Impact of Pathway Database Choice on Statistical Enrichment Analysis and Predictive Modeling', *Frontiers in Genetics*, vol. 10.

Wijesooriya, K, Jadaan, SA, Perera, KL, Kaur, T & Ziemann, M 2022, 'Urgent need for consistent standards in functional enrichment analysis', *PLOS Computational Biology*, vol. 18, no. 3, p. e1009935.