WikiPathways: Pathway Models for Network Analysis

Martina Kutmon^{1,2}, Anders Riutta³, Denise Slenter¹, Egon Willighagen¹, Kristina Hanspers³, Chris T Evelo^{1,2}, Alexander R Pico³

Department of Bioinformatics – BiGCaT, NUTRIM, Maastricht University, Maastricht, the Netherlands¹, Maastricht Centre for Systems Biology (MaCSBio), Maastricht University, Maastricht, the Netherlands², Institute of Data Science and Biotechnology, Gladstone Institutes, San Francisco, CA, USA³

WikiPathways (www.wikipathways.org) is a community curated pathway database that enables researchers to capture rich, intuitive models of biological pathways. Importantly, pathway models from WikiPathways are also a valuable source for network analysis and the content is provided in different formats including RDF [1], via dedicated apps like for Cytoscape [2], and on the network data exchange platform, NDEx [3]. This enables simple integration of pathway and interaction data in network analysis as highlighted in recent publications [4-6].

In addition to ongoing curation efforts to grow and maintain the database, we have identified publication figures as a valuable resource. We estimate ~1000 pathway figures are published and indexed by PubMed Central each month [7]. These figures contain novel pathway content not present in the text nor captured in pathway databases. We identified 64,643 pathway figures published over the past 25 years and performed optical character recognition (OCR) to extract over a million gene symbols mapping to 13,464 unique human NCBI Genes [8]. Pathway figure-based gene sets can be used to index and annotate the literature, to perform enrichment analysis, and to prioritize curation of new pathway models for downstream network analysis.

References

- 1. https://doi.org/10.1371/journal.pcbi.1004989
- 2. https://doi.org/10.12688/f1000research.4254.2
- 3. https://dx.doi.org/10.1016%2Fj.cels.2015.10.001
- 4. https://doi.org/10.3389/fgene.2019.00059
- 5. https://doi.org/10.1167/iovs.61.4.24
- 6. https://doi.org/10.1016/j.jsbmb.2019.01.003
- 7. https://doi.org/10.1101/379446
- 8. https://doi.org/10.1101/2020.05.29.124503