# NuGO Bioinformatics Tutorial

# Creating publication-ready figures

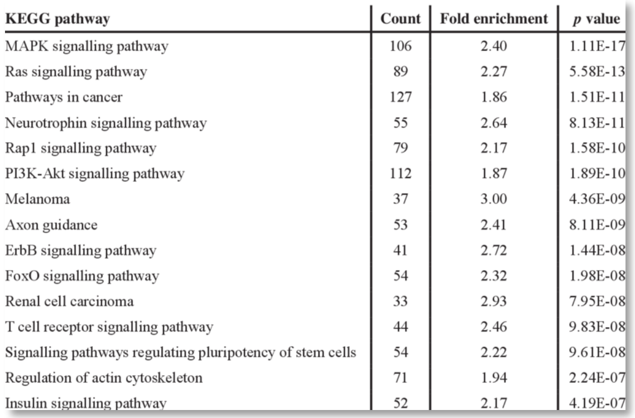
## <u>Afternoon #1</u>

**A**. Visualizing pathway enrichment results

**B**. Visualizing GO enrichment results

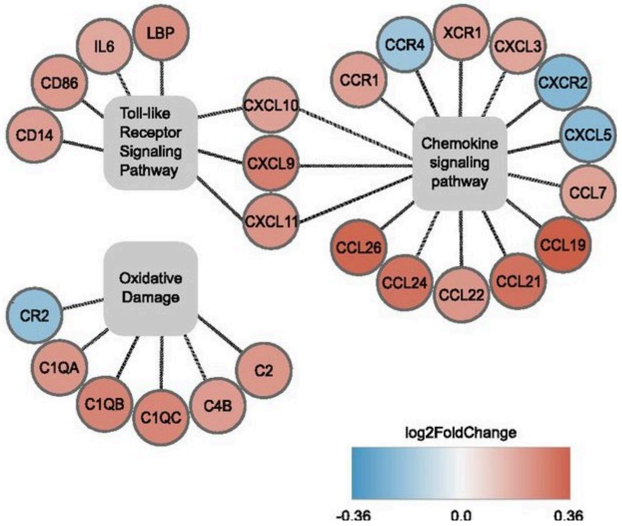
*Omics types:*
*Proteomics*
*Transcriptomics*

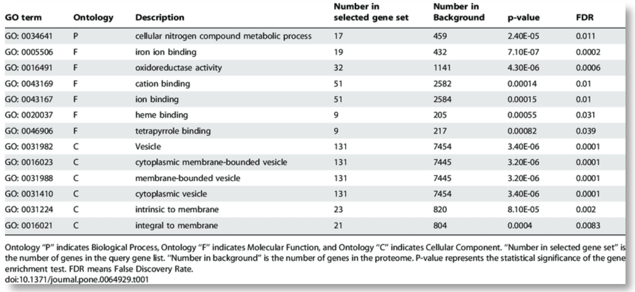
*<u>DEMO Dataset</u>*



| KEGG pathway | Count | Fold enrichment | *p* value |
|---|---|---|---|
| MAPK signalling pathway | 106 | 2.40 | 1.11E-17 |
| Ras signalling pathway | 89 | 2.27 | 5.58E-13 |
| Pathways in cancer | 127 | 1.86 | 1.51E-11 |
| Neurotrophin signalling pathway | 55 | 2.64 | 8.13E-11 |
| Rap1 signalling pathway | 79 | 2.17 | 1.58E-10 |
| PI3K-Akt signalling pathway | 112 | 1.87 | 1.89E-10 |
| Melanoma | 37 | 3.00 | 4.36E-09 |
| Axon guidance | 53 | 2.41 | 8.11E-09 |
| ErbB signalling pathway | 41 | 2.72 | 1.44E-08 |
| FoxO signalling pathway | 54 | 2.32 | 1.98E-08 |
| Renal cell carcinoma | 33 | 2.93 | 7.95E-08 |
| T cell receptor signalling pathway | 44 | 2.46 | 9.83E-08 |
| Signalling pathways regulating pluripotency of stem cells | 54 | 2.22 | 9.61E-08 |
| Regulation of actin cytoskeleton | 71 | 1.94 | 2.24E-07 |
| Insulin signalling pathway | 52 | 2.17 | 4.19E-07 |

**A.**

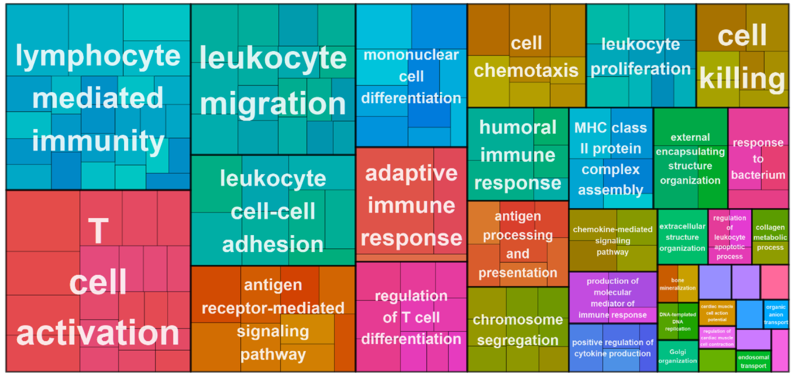




| GO term | Ontology | Description | Number in selected gene set | Number in Background | p-value | FDR |
|---|---|---|---|---|---|---|
| GO: 0034641 | P | cellular nitrogen compound metabolic process | 17 | 459 | 2.40E-05 | 0.011 |
| GO: 0005506 | F | iron ion binding | 19 | 432 | 7.10E-07 | 0.0002 |
| GO: 0016491 | F | oxidoreductase activity | 32 | 1141 | 4.30E-06 | 0.0006 |
| GO: 0043169 | F | cation binding | 51 | 2582 | 0.00014 | 0.01 |
| GO: 0043167 | F | ion binding | 51 | 2584 | 0.00015 | 0.01 |
| GO: 0020037 | F | heme binding | 9 | 205 | 0.00055 | 0.031 |
| GO: 0046906 | F | tetrapyrrole binding | 9 | 217 | 0.00082 | 0.039 |
| GO: 0031982 | C | Vesicle | 131 | 7454 | 3.40E-06 | 0.0001 |
| GO: 0016023 | C | cytoplasmic membrane-bounded vesicle | 131 | 7445 | 3.20E-06 | 0.0001 |
| GO: 0031988 | C | membrane-bounded vesicle | 131 | 7445 | 3.20E-06 | 0.0001 |
| GO: 0031410 | C | cytoplasmic vesicle | 131 | 7454 | 3.40E-06 | 0.0001 |
| GO: 0031224 | C | intrinsic to membrane | 23 | 820 | 8.10E-05 | 0.002 |
| GO: 0016021 | C | integral to membrane | 21 | 804 | 0.0004 | 0.0083 |

Ontology "P" indicates Biological Process, Ontology "F" indicates Molecular Function, and Ontology "C" indicates Cellular Component. "Number in selected gene set" is the number of genes in the query gene list. "Number in background" is the number of genes in the proteome. P-value represents the statistical significance of the gene enrichment test. FDR means False Discovery Rate.
doi:10.1371/journal.pone.0064929.t001

**B.**



# NuGO Bioinformatics Tutorial

# Creating publication-ready figures

Are you an early career scientist in nutrigenomics looking to improve your bioinformatics skills and enhance the impact of your publications? Join our specialized online tutorial sessions where you'll learn to transform your pathway and Gene Ontology (GO) enrichment results into visually appealing, publication-ready figures. Under expert guidance, you'll utilize powerful bioinformatics tools such as R and Cytoscape to clearly communicate your findings. This **online course** emphasizes **hands-on experience**, providing structured demonstrations followed by individual application on your own proteomics or transcriptomics datasets, ensuring immediate applicability to your research.

Due to the hands-on nature, this first edition is **limited to 5 – 10 participants.**
Secure your spot and elevate your research visuals!

**Course organisers:**

- Michiel Adriaens, Maastricht Centre for Systems Biology, Maastricht University, NL*
- Esther Kemper, Department of Human Biology, Maastricht University, NL
- Matthijs Vynck, Integrative Metabolomics Lab, Ghent University, BE

* *michiel.adriaens@maastrichtuniversity.nl*

## NuGO Bioinformatics Tutorial

# Creating publication-ready figures

**Course Dates -> ONLINE in ZOOM:**

- Thursday, May 8th (13.00 - 15.00)
- Thursday, May 22nd (13.00 - 15.00)
- Thursday, June 5th (13.00 - 15.00)

**Prerequisites:**

- Experience with R
- Familiarity with Cytoscape
- Basic knowledge of pathway and GO enrichment analyses
- Your own proteomics or transcriptomics dataset

# NuGO Bioinformatics Tutorial

# Creating publication-ready figures

**Course Outline**

**Afternoon #1:** Getting Started (May 8th)

- Introduction and demonstration using a provided dataset
- Step-by-step guidance on creating impactful visualizations
- Assignment: Apply the methods learned to your own dataset at home

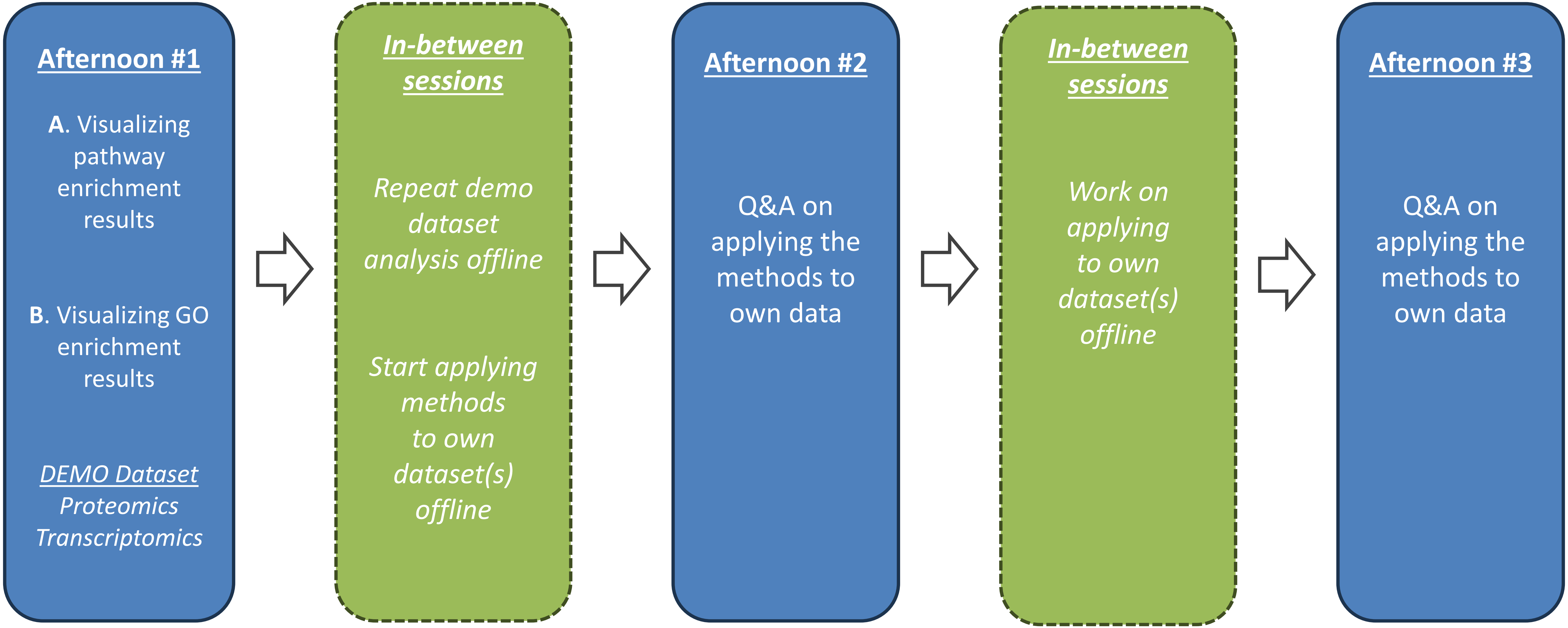
**Afternoon #2:** Hands-On Troubleshooting (May 22nd)

- Discuss experiences and troubleshoot together
- Receive expert support tailored to your data
- Assignment: Continue refining your figures independently

**Afternoon #3:** Final Wrap-Up & Evaluation (June 5th)

- Finalize and review your figures
- Tips on best practices for publication-quality visualizations
- Course feedback and evaluation

# NuGO Bioinformatics Tutorial Setup



### Afternoon #1

**A.** Visualizing pathway enrichment results

**B.** Visualizing GO enrichment results

*DEMO Dataset*
*Proteomics*
*Transcriptomics*

### *In-between sessions*

*Repeat demo dataset analysis offline*

*Start applying methods to own dataset(s) offline*

### Afternoon #2

Q&A on applying the methods to own data

### *In-between sessions*

*Work on applying to own dataset(s) offline*

### Afternoon #3

Q&A on applying the methods to own data

NuGO ONLINE hands-on course

# Creating publication-ready figures

10 seats available, find more information & apply here!

*Deadline is April 16!*

https://forms.gle/H3ggoTxgnnNwFfi87