

# Interactive workshop

## Pathway analysis with cluster Profiler

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Pathway analysis is one of the most widely used technique for interpreting gene lists, genome-wide regions of interest (ROIs) and whole genome expression profile. Although there are a number of software tools exist, most of them are designed for model organisms or specific domains. Non-model organisms and functional annotations other than GO and KEGG are poorly supported. Moreover, an increasing concern upon the quality of gene annotation has raised an alarm in biomedical research. A previous study (Nat. Methods 13, 705 (2016)) reported that about 42% of the tools were outdated by more than five years and functional significance were severely underestimated with only 26% of the biological processes or pathways were captured compare to using up-to-date annotation.

The workshop will introduces pathway analysis using the R package clusterProfiler and its sub-packages, DOSE, ReactomePA and enrichplot. The clusterProfiler package was designed by considering the supports of multiple ontology/pathway annotations, up-to-date gene annotations, multiple organisms, user customized annotation data and comparative analysis. We will go through the reproducible examples for pathway analysis and visualization methods to help interpreting results.

**Date:** 25 January 2019

**Time:** 13:00 — 15:00

**Place:** Amber

**Hosts:** Thomas K. Doktor and Veit Schwämmle, BMB, SDU.