

**XII<sup>th</sup> Annual Congress of the European Proteomics Association**  
**June 16<sup>th</sup> 2018**

**EuPA pre-congress course**

**Analysis and Visualization of Biological Networks with Cytoscape**

**Target Audience:** The course will be aimed to bench-based biologist with no prior knowledge of pathway analysis or computer programming skills.

**Teachers:** Scooter Morris from the University of California, San Francisco (<https://www.cgl.ucsf.edu/home/scooter/>).

**Duration:** 7-8 h (starting at 9:30h).

**Objectives:**

- Basic concepts in network analysis and representation in Cytoscape: the use of visual styles, attributes, filters and apps.
- To build and represent networks in Cytoscape from public resources and experimental results.
- To integrate and make use of quantitative proteomics data in the network.
- To find highly interconnected groups of node, named clusters, using the clusterMaker2 Cytoscape app.
- To find enriched proteins based on the Gene Ontology, KEGG, and other resources.

**The attendants need to bring their own laptops**

If you have any question regarding this course, feel free to contact us:

Prof. Concha Gil: [conchagil@ucm.es](mailto:conchagil@ucm.es)

**Attendance:** limited to 40 people.

**Fee:** 50 € (registration through the congress website).