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Christophe Dessimoz

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Swiss Institute of Bioinformatics

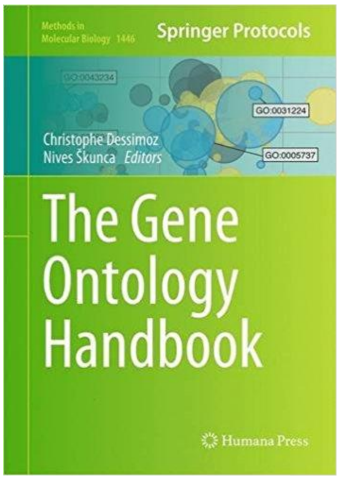
Friday, April 14, 2017
14:30~15:30 Auditorium C1F

Gene Ontology: biases, pitfalls, remedies

Summary

The Gene Ontology (GO) is a formidable resource, but there are several considerations about it that are essential to understand the data and interpret it correctly. In my talk, I will discuss some of the misconceptions and misleading assumptions commonly made about GO, including the effect of data incompleteness, the importance of annotation qualifiers, and the transitivity or lack thereof associated with different ontology relations. I will discuss several biases that can confound aggregate analyses such as gene enrichment analyses. For each of these pitfalls and biases, I will will suggest remedies and best practices.

Reference:


Methods in Molecular Biology 1446
Springer Protocols
GO:0043234
GO:0031224
GO:0005737
Christophe Dessimoz
Nives Škunca Editors
The Gene Ontology Handbook
Humana Press

Methods in Molecular Biology, Springer Protocols
‘The Gene Ontology Handbook’

Editors: Christophe Dessimoz, Nives Škunca

Published in November, 2016

Open access – http://gohandbook.org

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