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:
Editors: Christophe Dessimoz, Nives Škunca
Published in November, 2016
Open access – http://gohandbook.org