

# DETECTING COMMUNITY STRUCTURES IN GENE NETWORKS USING GENE-ONTOLOGY ANNOTATION

LIUHUAN DONG, WINKING Q. YU AND ANDREAS A. W. DRESS

ABSTRACT. In this note, we explore — by means of a specific case study — the potential of a new approach towards identifying gene functional modules in *Gene-Ontology* (or, for short, *GO*) networks, i.e., networks whose nodes are formed by the genes from a given collection of genes under consideration while two such nodes are connected by an edge if and only if they share — according to their *GO annotation* — at least one gene attribute.

We construct such a network for genes from the Zebra-Fish-genome data base. Then, to detect the implied GO-based gene communities, we apply the *FastCommunity* heuristics developed by Aaron Clauset *et al* and, as an alternative, a *Linear-Programming*-based method for community detection recently developed by William Chen *et al*, we discuss the biological significance of the gene communities identified by these methods and, finally, we discuss the potential of community-detection methods as general tools for (i) identifying gene functional modules on the basis of GO data as well as (ii) for deriving insights regarding such modules even if, instead of reliable and comparatively detailed and sophisticated GO annotations, only comparatively primitive “yes-no” data about functional attributes are available, corroborating that community-detection methods may actually be useful for constructing (or checking) GO annotations on the basis of much less sophisticated primary data.

---

THE FIRST-NAMED AUTHOR INITIATED AND DID MOST OF THE ACTUAL WORK, BUT RECEIVED SOME HELP INCLUDING SUGGESTIONS ABOUT HOW TO RUN THE CLPEX SOFTWARE PACKAGE, HOW TO SET UP AND TO INTERPRET THE GO-NETWORK AND ITS COMMUNITY STRUCTURES, AND HOW TO PRESENT THE RESULTS FROM THE OTHER TWO AUTHORS.