Related Work

Newman first studied the structure of scientific collaboration networks in different research fields. He showed that these collaboration networks form “small worlds” [1]. In this paper, many indicators were investigated, including: number of authors, mean papers per author, number of collaborators (node degree), the giant component and average degrees of separation. Then Newman analyzed more detailed statistical properties of scientific co-authorship networks [2], including size of giant component, closeness, betweenness and clustering coefficient.

Many papers were inspired by Newman’s initial work. People started to analyze the co-authorship in different domains. Hou et al. studied the structure of scientific collaboration networks in Scientometrics [3]. Tomassini et al. paid attention to genetic programming collaboration network [4]. Some researchers used countries to separate the network, e.g. collaboration network in Turkey [5].

Some researchers also try to identify how the scientific collaboration networks evolve. Barabsi et al. [6] are the first to infer the dynamic and the structural mechanisms that govern the evolution and topology of this complex system. Tomassini [7] studied the genetic programming network and found that degree distribution tends to stabilize toward an exponentially truncated power-law. Huang et al analyze different fields in computer science and found that major observations are that the database community is the best connected while the AI community is the most assortative. Lara-Cabrera et at [8] chose an interdisciplinary domain in computer science as research objects and also observed sub-linear preferential attachment for new nodes.

我们使用的数据来自[9]

Network [10]

Gephi [11]

Rich club [12]

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