

ABSTRAK

Kanker payudara merupakan salah satu penyebab utama kematian pada wanita di seluruh dunia dengan mekanisme biologis yang kompleks, yang melibatkan mutasi genetik, gangguan regulasi ekspresi gen, serta perubahan jalur molekuler yang memengaruhi proliferasi sel. Untuk memahami kompleksitas tersebut, analisis jaringan *Protein–Protein Interaction* (PPI) menjadi pendekatan yang relevan karena protein membentuk modul fungsional yang saling berinteraksi dalam berbagai proses biologis. Namun, sebagian besar metode deteksi komunitas pada jaringan PPI masih bersifat *non-overlapping*, sehingga kurang mampu merepresentasikan sifat multifungsional protein. Oleh karena itu, penelitian ini menerapkan *Adjacency Propagation Algorithm* (APAL) untuk mendeteksi komunitas overlap pada jaringan PPI kanker payudara. Data protein diperoleh dari IntOGen dan data interaksi dari STRING *Database*, menghasilkan jaringan dengan 99 protein dan 495 interaksi. Algoritma APAL diterapkan melalui tahapan inisialisasi kandidat komunitas, perhitungan intrakonektivitas (α), evaluasi komunitas menggunakan *Jaccard Index*, serta proses deduplikasi. Sistem analisis dan visualisasi dikembangkan menggunakan framework Dash berbasis Python, dan kualitas komunitas dievaluasi menggunakan Normalized Node Cut (ψ). Selain itu, *enrichment analysis* dilakukan menggunakan Metascape untuk mengidentifikasi fungsi biologis komunitas. Hasil penelitian menunjukkan bahwa APAL membentuk 14 komunitas dengan waktu eksekusi 0.709 detik. Sebanyak 60 protein (60.6%) teridentifikasi sebagai protein *overlap*, mencerminkan sifat multifungsional protein dalam jaringan kanker payudara. Analisis biologis menunjukkan keterkaitan komunitas dengan proses penting seperti regulasi ekspresi gen, proliferasi sel, dan jalur molekuler terkait kanker, sehingga menegaskan bahwa APAL efektif dalam mendeteksi struktur komunitas overlap sekaligus memberikan wawasan biologis yang relevan.

Kata Kunci: Kanker Payudara, *Protein–Protein Interaction*, Deteksi Komunitas *Overlap*, APAL, *Normalized Node Cut*.

ABSTRACT

Breast cancer is one of the leading causes of death among women worldwide and is characterized by complex biological mechanisms involving genetic mutations, dysregulation of gene expression, and alterations in molecular pathways that affect cell proliferation. To address this complexity, Protein–Protein Interaction (PPI) network analysis is a relevant approach, as proteins form functional modules that regulate various biological processes. However, most existing community detection methods focus on non-overlapping structures, limiting their ability to represent the multifunctional nature of proteins. This study applies the Adjacency Propagation Algorithm (APAL) to detect overlapping communities in breast cancer PPI networks. Protein data were obtained from IntOGen and interaction data from the STRING Database, resulting in a network consisting of 99 proteins and 495 interactions. APAL was implemented through stages of candidate community initialization, intraconnectivity (α) calculation, community evaluation using the Jaccard Index, and deduplication. A Python-based Dash framework was developed for visualization and analysis, and community quality was evaluated using the Normalized Node Cut (ψ) metric. Functional enrichment analysis was conducted using Metascape to identify biological functions associated with the detected communities. The results show that APAL partitioned the network into 14 communities with an execution time of 0.709. A total of 60 proteins (60.6%) were identified as overlapping proteins, highlighting their multifunctional roles within the breast cancer network. Biological analysis revealed that several communities are associated with key processes such as gene expression regulation, cell proliferation, and cancer-related molecular pathways, demonstrating that APAL is effective in detecting overlapping community structures while providing biologically meaningful insights into breast cancer mechanisms.

Keywords: *Breast Cancer, Protein Interaction Network, Overlapping Community Detection, APAL, Normalized Node Cut.*