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Abstract

In this article we describe a complete method to the layout clustered graph in hierarchical fashion. We have adopted Sugiyama[11] framework for hierarchical layout and modified its phases to produce the clustered graph layout. The algorithm is based on Sanders compound graph layout algorithm. Our main contribution is positioning of nodes with different sizes without any node overlap while maintaining straight lines for long edges. Experimental results show that the executiontime and quality of the produced drawings with respect to commonly accepted layoutcriteria are quite satisfactory. This algorithm is intended to integrate as a part of system biology software Cell-in-Silico, for drawing biological pathways with compartmental constraints and arbitrary nesting of graphs and molecular complexes.

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Computer Science

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Clustered Graph Hierarchical Layout Biological Graphs Node Size Complex Species.