

**Presentation title:** An introduction to graph theory for bioinformatics

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**Abstract:**

One of the simplest yet most useful structures in mathematics is the graph. The essence of a graph is to model pairwise relations between objects by defining a set of vertices or nodes and edges that connect the vertices. They are widely used throughout almost every field of mathematics and have been applied to an extraordinarily wide range of problems such as military communication networks design for robustness in the event of nuclear attack, the structure of language, or who has acted with whom in Hollywood movies. Many classic problems such as the travelling salesman problem and the four colour map problem are at their foundation graph problems. Not surprisingly, graphs arise and are useful throughout bioinformatics. Proteins interaction networks, species trees, metabolic networks, gene regulatory networks and many other areas of bioinformatic interest have benefited from graph analysis and graph algorithms. In this talk the foundational ideas of graph theory will be covered with some examples and applications from bioinformatics.