70. Evolution of microRNA diversity and regulation: Statistical Modeling

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MicroRNAs (miRNAs) are small molecules found in all plants and animals. Despite their relatively small size and limited number, they regulate many cellular processes in healthy and disease states. In the c. 600-million-year history of animal evolution, the number of miRNA-encoding genes has grown from 8 in sponges, to over 1,400 in humans. Despite this overall trend, the number of miRNA genes among species is highly variable, and has no obvious relationship to the age of the species. In our project, we are developing statistical models to evaluate the strength of the association between miRNA number and the following species-specific parameters besides evolutionary age: organism mass, surface area, tissue complexity, genome size and genome complexity. In order to investigate these relationships, we will consider both parametric and non-parametric statistical techniques (implemented using JMP software).