Dfam Web Server

Travis Wheeler

*University of Montana, Missoula*

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Name: Travis Wheeler
Department: Computer Science
Project title: Dfam Web Server

Objective
Establish a new server for my open access web database of transposable element families (Dfam.org), migrate the service to the new server, and upgrade content of the server in preparation for a substantial collaborative R01.

Summary of Results
Funds from the UGP grant were used to offset a portion of the cost of a new 16-core server, which is now home to the Dfam.org web service.

Mammalian and most other eukaryotic genomes contain a large number of interspersed repeats (IRs), most of which are copies of transposable elements (TEs) at varying levels of decay. Their presence complicates many genome sequence analyses, but their accurate identification in an early analysis stage can reduce these complications. In addition to their pervasiveness, it is increasingly clear that they have enormous impact on genome activity and evolution.

Accurate annotation of TEs enables research into their biology and can shed light on the evolutionary processes that shape genomes. Dfam represents a collection of alignments and HMMs of such transposable elements and other repetitive DNA elements. The Dfam website gives information about each model, and provides genome annotations for a collection of core genomes.

Following server purchase and migration, we substantially upgraded Dfam, adding several new features and increasing data volume 4-fold. The result was a publication in Nucleic Acids Research. Following that publication, we submitted a $4M NIH R01 proposal ($1.2M earmarked for Montana). Though the proposal was not funded, we will resubmit in October 2016.