# Research and Education at the Virginia Bioinformatics Institute at Virginia Tech

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Virginia Tech, the largest research university in the Commonwealth of Virginia, has developed over the last 15 years resources essential for high throughput biological and computational research. Using these resources, VT has become a leader in computational and bioinformatics research. Several major groundbreaking results were produced by researchers at VT in the last decade including the sequencing of the turkey genome and the Phytophthora genome.

Virginia Tech scientists at the internationally reputed Virginia Bioinformatics Institute, for example, have developed web based software to help Tuberculous researchers track and curate their genetic data. They've made detailed models of synthetic populations located in Washington, DC, to study the spread of contagious diseases like influenza on high traffic tourist destinations, and they create and analyze computational models of H. pylori, a bacteria in the gut that causes ulcers and possibly cancer. Experiences in these projects and their associated resources provide unique opportunities for partnering with Howard and its faculty and others in the region for research and education activities. In addition to these computational and bioinformatics resources, VT is also home to competitively funded successful R25 and T32 NIH training grants that could provide training opportunities for students interested in computational biology. Recent programs in neuroscience and translational biology at the Carillion Research Institute, further enhance VT as a strong potential collaborator with Howard and others in our region.

Whole genome sequencing
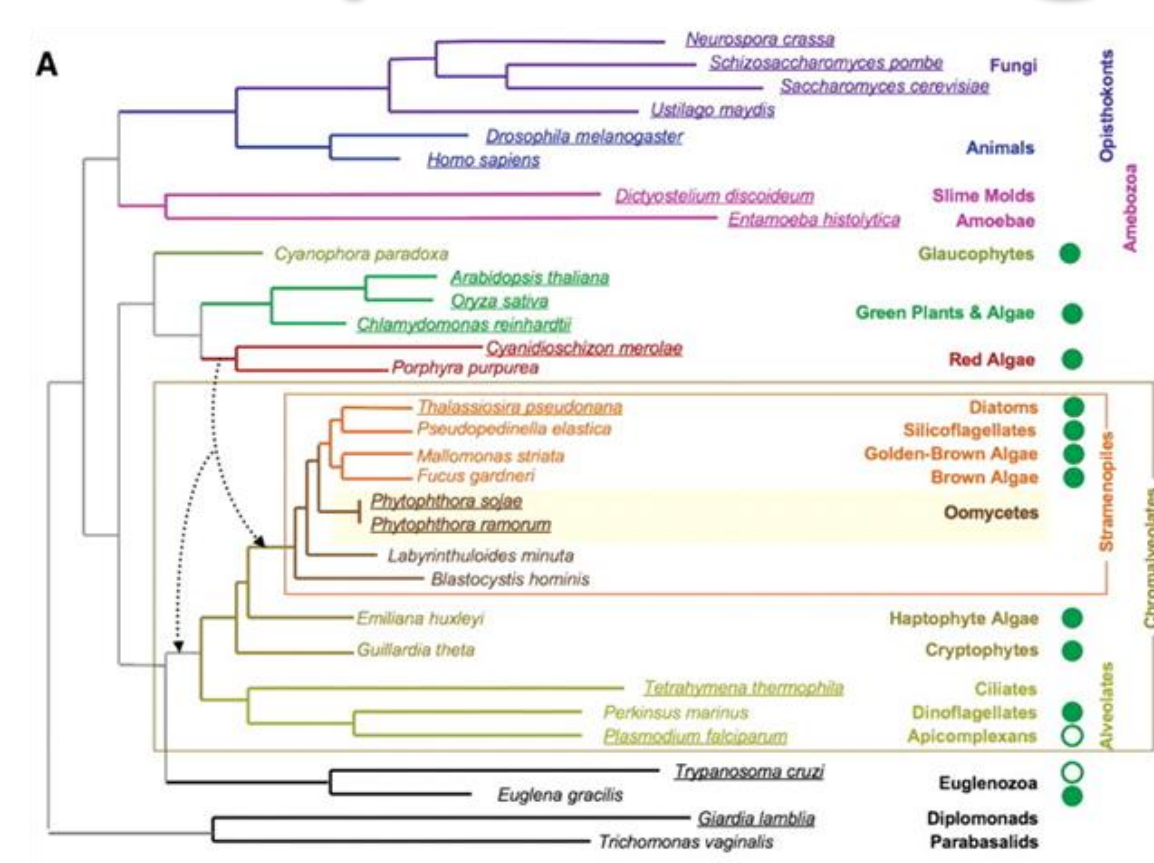
Schematic phylogenetic tree of the eukaryotes. The tree is adapted from that of Baldauf *et al* which is based on a concatenation of six highly conserved proteins.

Proteomics Analysis
EvoCor
Please type a gene ID (e.g. MuSK).

[Search]

Computational Immunology
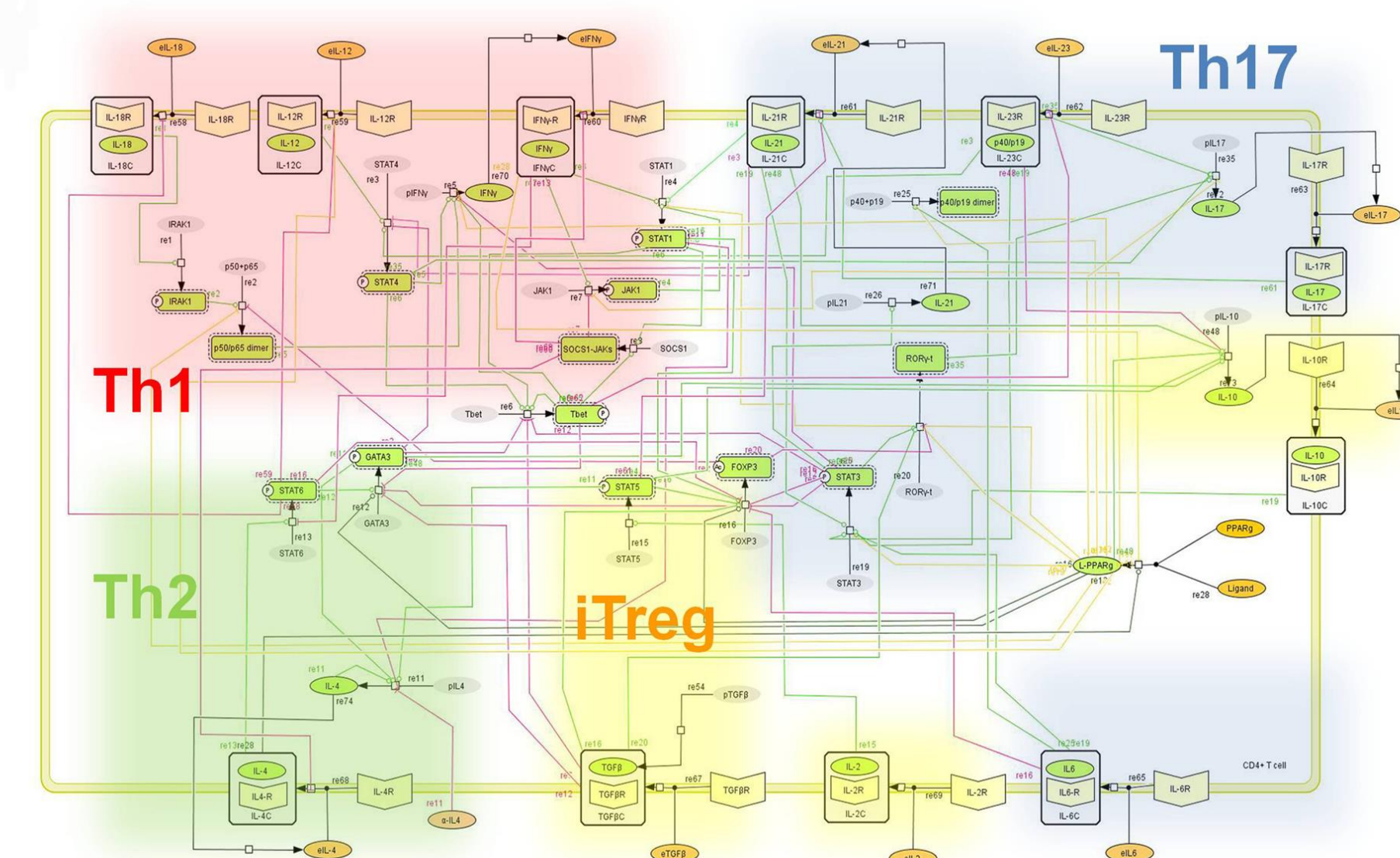
Network model illustrating signaling pathways and transcriptional factors controlling the CD4+ T cell differentiation process.

Social and Public Policy

Genomics-Centric Resources: PATRIC
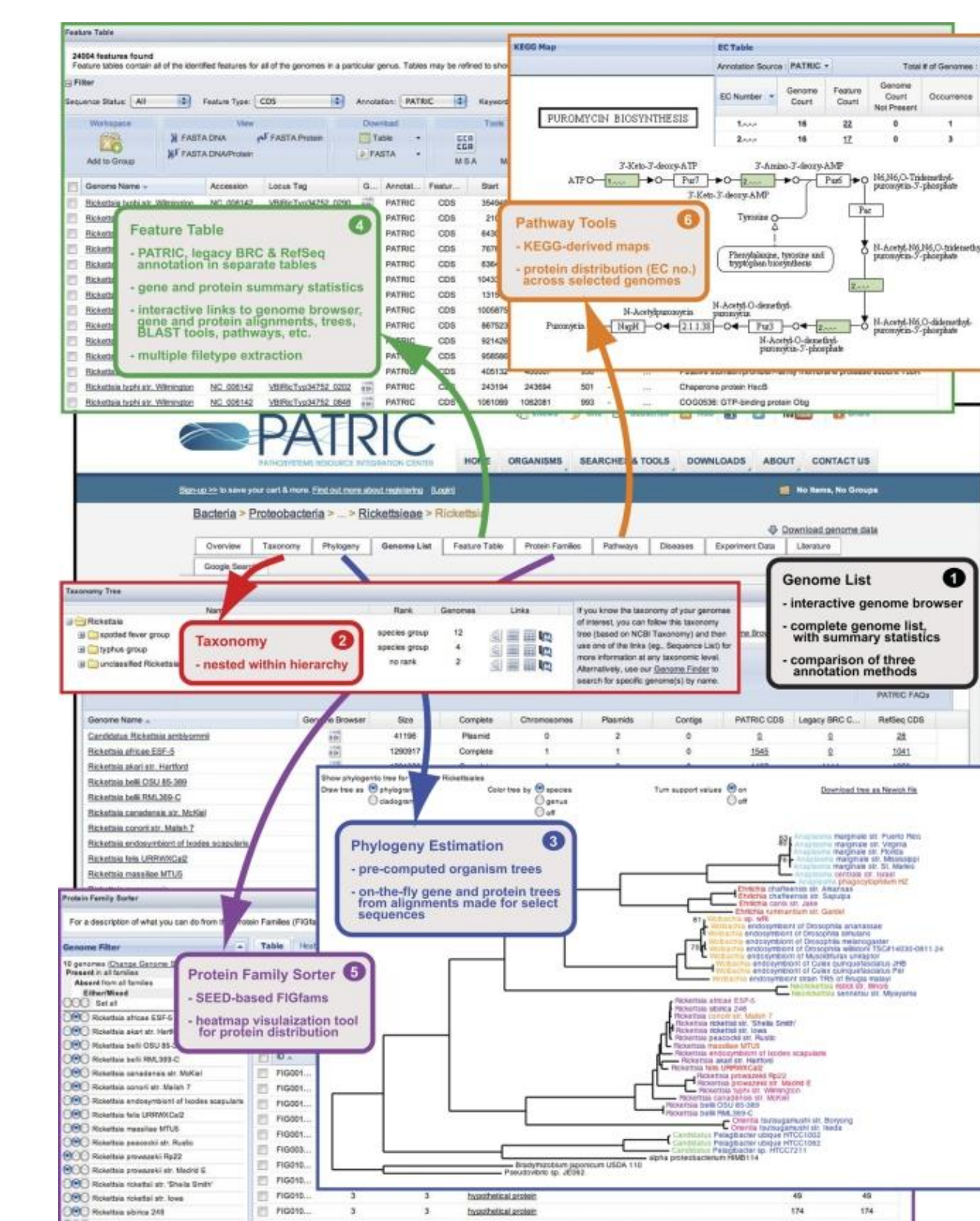
Schema depicting major genomic and comparative genomic tools available from an organism "Overview" homepage.

VirginiaTech
Virginia Bioinformatics Institute

VT- INITIATIVE TO MAXIMIZE STUDENT DIVERSITY

VIRGINIA TECH VT PREP PREP PROGRAM