Poster C-26

3D Phylogeny Explorer: Distinguishing paralogs, lateral transfer, and violations of the "molecular clock" assumption with 3D visualization

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Short Abstract: 3D Phylogeny Explorer projects trees onto three axes: species (X); paralogs (Z); evolutionary distance (Y), enabling one to distinguish speciation, gene duplication and lateral gene transfer at a glance. Live 3D views (VRML2) of microbial gene phylogenies (COGS) at http://bioinfo.mbi.ucla.edu/3DPhylogenyExplorer.

Long Abstract:
We have developed 3D Phylogeny Explorer, a novel phylogeny tree viewer that maps trees onto three spatial axes (species on the X-axis; paralogs on Z; evolutionary distance on Y), enabling one to distinguish at a glance evolutionary features such as speciation; gene duplication and paralog evolution; lateral gene transfer; and violations of the "molecular clock" assumption. To illustrate the value of this visualization approach for microbial genomes, we generated 3D Phylogeny data for all clusters from COG, made available as "live" 3D views using VRML2 at http://bioinfo.mbi.ucla.edu/3DPhylogenyExplorer. We constructed tree views using well-established phylogeny methods and graph algorithms. We used CLUSTALW/PHYLIP to generate traditional 1D phylogeny. 3D Tree layout is generated on the fly based on user queries: after finding best hit relationship from 1D phylogeny tree, orthologous groups were identified as fully connected cliques of reciprocal best hits. Trees are then reoriented by evolutionary order, recent events first and old events last. While walking tree in POSTORDER traversal, 2D gene layout - species and orthologous group - is generated by order of appearance. We used Scientific Python to generate VRML2 3D views viewable in any web browser. Views can be scrolled, rotated, rescaled, and explored interactively, make it easy to see all evolutionary events such as speciation, gene duplication and lateral gene transfer. All objects in 3D Phylogeny Explorer are clickable to display subtrees, connectivity path highlighting, sequence alignments, and gene summary views, etc.