Identifying single copy orthologs in Metazoa

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Family problems

Reconstruction

Species Tree

Gene Tree

Methodology

Eukaryotic guide trees construction

- wgNOC
- 40 universal genes
- Alignment with Muscle
- GBlocks
- Phylogenetic
- Phylogenetic
- Coelomata tree
- Ecdysozoa tree
Assessing datasets

Conclusions

• Our approach increased by 35% the number of single-copy orthologs identified in gene-family datasets (despite being very strict).

• These orthologs represented a wide range of functional categories, expression profiles and levels of divergences.

• Using 1,126 identified in Metazoa: We found that the vast majority of the 62 EST datasets and low coverage genomes assessed are far from complete and probably do not accurately represent the actual genomic complement of the organisms.