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Ortholog identification in genera of high genetic diversity and evolution

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In the era of high-throughput sequencing, comparative genomics is vastly used in the discovery of genetic diversity between species, but also in defining the core and pan genome of single species to whole genera. Current comparative approaches are implementing ortholog identification to establish genome annotations, gene or protein evolutions or defining functional features in individual species and groups.

In this project we aim to compare the genomes of 300 species from the genus of the filamentous fungi - *Aspergillus*, which represent evolutionary changes over 200 million years [1]. Present-day's gene orthology prediction software combine genetic diversity with evolutionary distance. However, when the genetic variation within this genus is higher than the variation between fish and humans [2], identifying true orthologs becomes problematic. The cause of this high genetic diversity within such closely related species might be due to genetic events such as gene duplication and horizontal gene transfer. Here we tackle this problem by stringent the alignment parameters and loosen the linkage criteria. The approach is based on BLAST alignments with optimized cut-offs considering identity and coverage and clustering using single linkage.

The result of this procedure is a large number of orthologous protein families, that will allow for guilt-by-association-based detailed investigation into mapping of genotype to phenotype. The data will highlight the genomic and functional features defining the pan and core genome of individual strains, species, clades and the genus of *Aspergillus*.

[1] Galagan et al. (2005). *Nature*, 438:1105–1115.

[2] Fedorova et al. (2008). *PLoS Genetics*, 4(4), e1000046.