Master project in bioinformatics:
Adaptive evolution in birds

at Stockholm Bioinformatics Centre, Science for Life Laboratory

Background: With the recent sequencing of the zebrafinch, two different bird genomes are available, allowing us to try to find evidence on how their differing lifestyles have affected their genomes. Chicken, the other available bird, has been domesticated since the dawn of civilization and is effectively a flightless bird living in packs. Zebrafinches, on the other hand, are songbirds, and have been used as a model organism for learning and memory, because of how the males learn songs from their fathers during chickhood.

Goals: This project will involve acquiring the latest versions of the chicken and zebrafinch genomes, as well as the corresponding protein sequences and what functional annotation is available for them, particularly within the Gene Ontology framework. After filtering out sequences that cannot be reliably assigned to a chromosome region, or that are pseudogenes, orthology clusters should be reconstructed for chicken and zebrafinch using the InParanoid algorithm, with a proper outgroup species chosen to maximize accuracy and resolution. For each ortholog group, gene phylogenies should be reconstructed, and any disagreements between InParanoid orthology inferences and these phylogenies should be inspected to ensure all families studied are of sufficient data quality. Next, some tool like PAML should be applied to search for branches in these gene family trees where there is statistically significant support for adaptive evolution. Both significantly relaxed selective pressure in either lineage or positive selection are of interest, as indicators of how the lifestyle of the respective species may have impacted which genes were needed as well as may have caused a need for novel functions. Assuming that a set of genes is found which have evolved adaptively in either species, these should then be investigated with respect to their likely functions. Are some functional categories subject to adaptive evolution in chicken or in zebrafinch more often than others? If so, can this be connected to differences in species lifestyle? Moreover, gene family expansions in either lineage should also be functionally characterized, and the study should test if such expansion through gene duplication changes the likelihood of the various forms of adaptive evolution. If the analysis yields results, we anticipate that the project will lead to a publication in a peer-reviewed scientific journal.

Requirements: This project will require a student with relatively high bioinformatics skills, or a strong capacity for learning. Ideally, the applicant should be familiar with phylogenetic methods for analysing adaptive evolution. The applicant must be capable of working semi-independently, although tutoring will be available when requested. Experience in Linux/UNIX and programming/scripting is important. Please apply be sending your CV and the email address of a reference person to:

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