

Biology Seminar

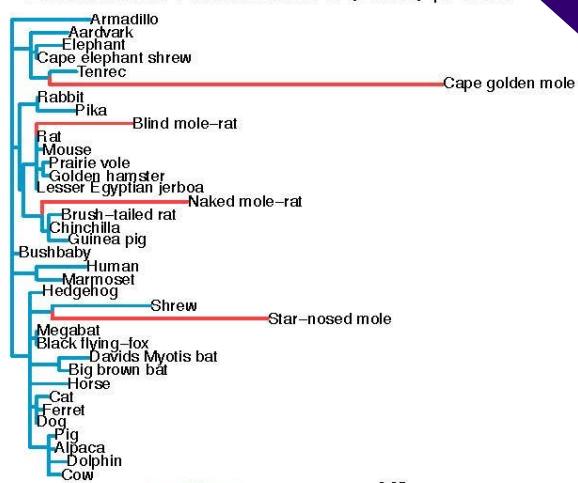
By: Dr. Nathan Clark

University of Pittsburgh | Assistant Professor, Department of Computational and Systems Biology

<http://www.csb.pitt.edu/faculty/Clark/>

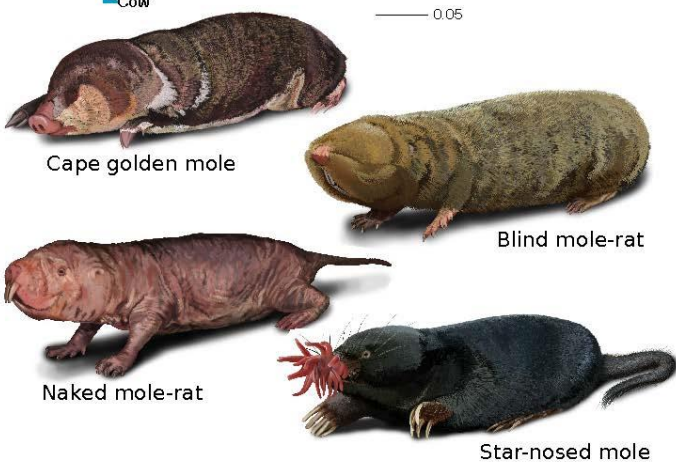
History repeats itself: Using evolutionary convergence to reveal adaptations and genome-wide functional networks

Lens intrinsic membrane 2 (Lim2) protein



Monday, April 10, 2017 | 12:00pm
HCK 132 Refreshments at 11:45am

Life is in a constant state of revision in response to evolutionary pressures such as environmental change. In the Clark lab we seek to understand these adaptive changes by studying evolutionary signatures in genes and regulatory sequences. Our computational methods leverage convergent evolution, in which independent phylogenetic lineages evolve the same phenotype, to discover the genetic changes underlying specific adaptations. In the case of marine mammals, we identified a large set of genes that responded to the environmental transition from land to water in similar ways for all three unrelated lineages: cetaceans, pinnipeds, and sirens. Evolution in these genes underlies many of the adaptive changes known for marine mammals. Furthermore, other genes exhibited convergent loss of function, thereby altering marine mammal sensory systems, and in one case leaving them vulnerable to man-made pesticides. I will also demonstrate how studying blind, subterranean mammals yielded a wealth of previously unknown vision-related genes and cis-regulatory regions, which in turn are proving to be clinically valuable. Finally, an extension of our



methods, named Evolutionary Rate Covariation (ERC), allows us to infer novel functional relationships between genes throughout the genomes of mammals, insects, nematodes and fungi. I will discuss specific applications of ERC to infer new protein-protein interactions for alpha-arrestin proteins in yeast and humans as well as in *Drosophila* reproductive protein pathways, all of which we have validated experimentally. Overall, molecular patterns left by adaptation and convergence can be exploited to reveal important phenotypic changes in many biological systems. Accordingly, my group has developed an R package so that any biologist can apply these techniques to their system of interest.

Seminar Speaker Host: Barbara Wakimoto, Professor