Eran Segal: Computing Expression

Eran Segal followed a meandering route to the field of computational biology. He began by earning a bachelor's degree in computer science from Tel-Aviv University in 1998, and went on to study in Stanford University's computer science department under Daphne Koller. He also studied genetics at Stanford, where he began to explore how probabilistic models can answer biologic questions.
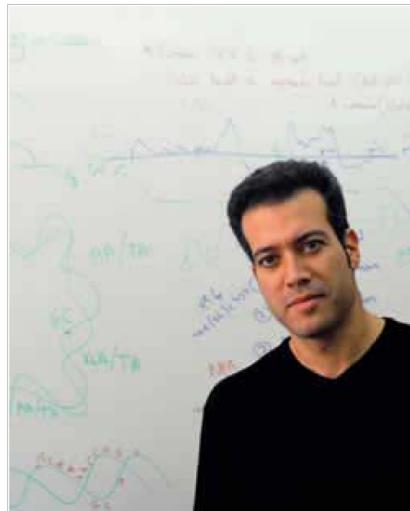

Photo: Ahikam Seri

As a graduate student Segal focused on designing computational models of gene expression. One included a method for identifying groups of coregulated genes and their regulators. [1] He tested this method on yeast gene data and then applied it to transcription factor Ypl230w, protein kinase Kin82, and the phosphatase Ppt1, to predict regulation functions, targets, and conditions, which he experimentally verified. Koller says that this research joined a relatively new movement to produce testable hypotheses about regulatory relationships that could be worked out in the lab.

Segal also worked on a model that identified 22,163 pairs of genes that are coexpressed in the DNA of humans, flies, worms, and yeast. [2] Segal showed that these genes often have a shared function, which would allow researchers to predict the unknown functions of genes based on their coexpressed partners. While comparative genomics has been around for a while, says Koller, "we were the first to do this for gene-expression data across species."