Kinase annotation for helminths

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John Martin
Mitreva Lab (MGI, Washington University in St. Louis)
jmartin@wustl.edu*Corresponding Author*

Makedonka Mitreva
MGI, Washington University in St. Louis

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Abstract

A method to annotate kinase domains in nematodes and platyhelminths by using dynamic thresholds for different kinase groups.

Introduction

Kinases are one of the most common types of targets for existing drugs for human diseases[1] and are considered strong candidates for the development of new ones. This method was developed to annotate kinase domains in the gene sets of nematodes and platyhelminths by aligning to the Kinomer profile database[2] using carefully considered scoring thresholds specific to each kinase group.

Reagents

1. kinase domain models from kinomer
2. installation of HMMER v2.3.2

Procedure

1. Download the Kinase domain models file from the Kinomer website ("http://www.compbio.dundee.ac.uk/kinomer/allPK.hmm":http://www.compbio.dundee.ac.uk/kinomer/allPK.hmm).
2. Kinase class specific score thresholds are determined by starting with those used in the Kinomer paper[3] and then adjusting them until an hmmpfam search (HMMER v2.3.2) comes as close as possible to identifying all known *C. elegans* kinases using the Kinomer allPK.hmm profile database. e.g. The final cutoffs used for the associated publication were: TK, 5.5e-03; CAMK, 9.6e-07; CK1, 1.1e-02; CMGC, 6.7e-03; AGC, 1.1e-14; STE, 3.4e-03; RGC, 4.8e-05; TKL, 8.7e-03; PDHK, 4.7e-160; PIKK, 1.4e-06; Alpha, 8.5e-66; and RIO, 7.5e-10.
3. Hmmpfam is used with default settings to map the user provided gene protein sequences against the Kinomer models.
4. Genes with hmmpfam 'hits' meeting the kinase class specific custom cutoffs are then annotated as a putative kinase of the given class.

Anticipated Results

A set of annotated kinase genes with the corresponding domain annotations

References

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2. Kinomer URL: "http://www.compbio.dundee.ac.uk/kinomer/allPK.hmm":http://www.compbio.dundee.ac.uk/kinomer/allPK.hmm
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