Targeting Unique Pathogen Signatures
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Determining where a unique region of DNA can be found within a genome can be a long and tedious process. Signature Target was developed to allow users to compare any number of genomes and signatures to determine where and how these unique regions are represented within the genome.

1) Introduction:
A DNA signature is a region of DNA that is conserved in all strains of the pathogen and is unique when compared with all other organisms. Each signature consists of a forward, internal and reverse probe. These unique regions can be exploited by a variety of detection chemistries and approaches. The goal with each pathogen is to find multiple unique regions with in each organism. The problem is determining where in a genome a signature will be found and if that signature will also be found in the genomes of any other organisms.

2) Methods:
Signature Target was designed to address the before mentioned problems. The user can enter any number of genome ids, either by Genbank GI or Kpath ID numbers. The user can then upload a file that contains any number of signature candidates and “compare each genome with each signature”. Depending on what options were set the user can also specify a number of allowable mismatches so that signatures do not have to be exact matches. The user can also specify to check all primer orientations which can detect if there is a possibility of the signature to react with genome in an unexpected way.

3) Results:
The results page displays information for each comparison including the title of the genome and signature, sequence of primers searched and well as a visual display of any signature match within the genome that displays the start and stop coordinates of each of the primers. If there is any available annotation information, (such as genes hit by the signature) a link will be given to that database.

4) Discussion:
Signature Target provides a fast method for determining which signatures are found in which genomes. Future plans include integrating TaqSim, an exhaustive signature searching tool, into Signature Target to allow the user to compare any given signature against every sequenced genome instead of having to specify which genomes to compare.