Licensable Technologies

SEQUEDEX: Classify Phylogeny & Function of Short DNA Sequences

Applications:

- Rapid ID of viruses and bacteria (medical, biodefense)

- Microbiome characterization (medical, pharmaceutical, consumer)

- Metagenome characterization (ecology, manufacturing)

- Transcriptome characterization (medical, pharmaceutical, algal biofuels)

- Epidemiology (public health, product safety)

- Enzyme mining (chemical manufacturing, biofuels)

- Cancer genomics (medical, pharmaceutical)

Benefits:

- Extremely rapid (~6 Gbp/hr on a desktop, ~250,000X faster than BLAST)

- High sensitivity, selectivity even for short reads (as short as 30 bp)

- Produces searchable database of classified reads

- Works for novel and known organisms, including eukaryotes and viruses

- Characterizes sample complexity (biodiversity)

- Characterizes similarities among samples (beta diversity)

- Built-in evolutionary theory simplifies bioinformatics

- Drops bioinformatics costs

Contact:

David Hadley
(505) 667-7539, dhadley@lanl.gov

sequedex@lanl.gov

Technology Transfer Division

Los Alamos
NATIONAL LABORATORY
ESTABLISHED 1943

Summary:

Sequedex is bioinformatics redesigned from the ground up to make use of the wealth of genomic data that has become available in the 20 years since the most commonly used algorithms like BLAST were written. The result is a remarkable increase in speed and sensitivity: Sequedex can chew through one human genome's worth of DNA analysis in 30 minutes on a laptop, getting usable results from reads as short as 30 base-pairs.

Sequedex employs a science-of-signatures approach that combines a foundation in evolutionary theory with well-developed informatics technology taken from web search engines. Unlike conventional approaches that rely on "mapping" reads of DNA to a large and growing database of genomes, Sequedex uses evolutionary signatures to place reads directly on the Tree of Life. LANL scientists have constructed a Tree of Life that spans plants, animals, bacteria, archaea, and viruses, thus allowing Sequedex to accurately classify DNA sequences from organisms which have no close relatives in databases.

Development Stage:

A demo version of Sequedex will be available for free public download at http://sequedex.lanl.gov pending copyright and publication issues. Features beyond those in the demo version, such as writing a database of classified reads, can be enabled by purchase of a software license from Los Alamos. Contact sequedex@lanl.gov for details.

Patent Status:

A patent application on the underlying algorithm is pending. The software package is copyright-protected.

Licensing Status:

Los Alamos is seeking commercial partners for licensing and distribution. Exclusive licenses in limited markets are possible.

www.lanl.gov/partnerships/license/technologies/
An Equal Opportunity Employer / Operated by Los Alamos National Security LLC for DOE/NNSA

06/12