SeqNFind™
facilitating discovery

REVOLUTIONIZE YOUR BIOINFORMATICS!

Introducing SeqNFind™ — a revolutionary genomic sequence analysis toolset for facilitating bioinformatics research in Next Generation Sequencing, Pipelined Microarray Analysis and Genomic Comparisons. This powerful system provides the ability to compute complete solutions by pairing massively parallel commodity hardware with optimized algorithms to increase throughput with the goal of handling genomic comparison across thousands of genomes.

A unique hardware-software solution tool, **SeqNFind™** offers extreme speed, space and energy-savings by leveraging GPU technology (Graphic Processing Unit), which utilizes hundreds of cores, resulting in a 112-fold increase in the number of processors over a traditional CPU (Computer Processing Unit).

SeqNFind™ is a powerful, flexible system that can be easily and affordably scaled to outperform clusters, resulting in significant time and electrical energy-savings, and — most importantly — dramatically improved accuracy.

SeqNFind™ can be used for:

- SeqNFind™ Reference Assembly
- BLAST
- Smith-Waterman
- HMM
- De novo Assembly
- RNA-Seq

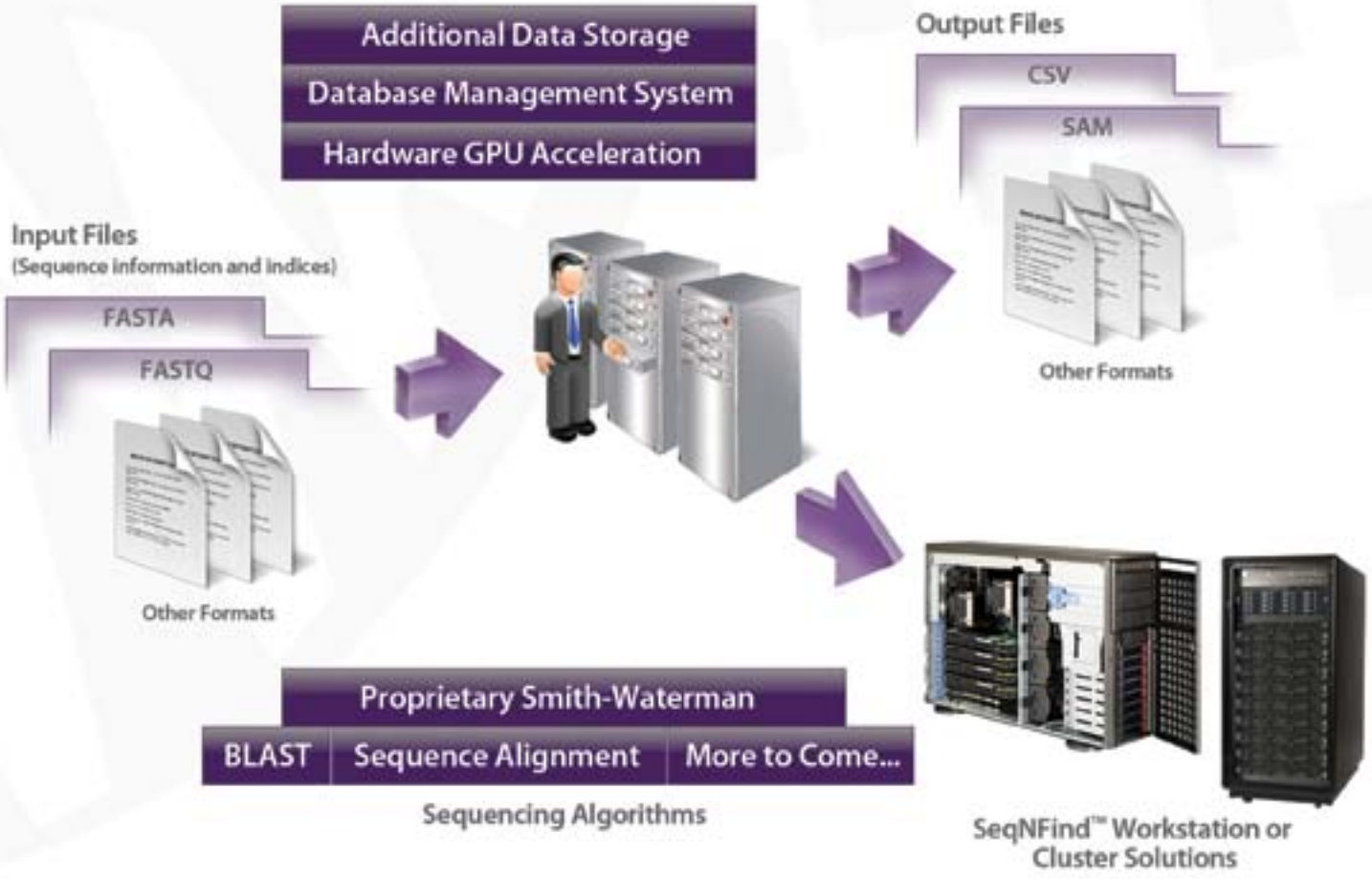
ACCELERATE YOUR BIOINFORMATICS RESEARCH

Contact us today for more information on this industry-changing solution!

800.565.5467 or ***910.673.8165***
(outside the US and Canada)

www.**atlab**.com

SeqNFind™ *Bioinformatics Software Solution*



336 cores =
$300/day electric

versus

448 cores =
$7/day electric

powered by

SeqNFind™ processes fast and complete short-read genomic sequence alignments.

Utilizing a unique hardware/software cluster system and multi-processing environment, this powerful system addresses the need for accurate alignments of many small sequences against entire genomes while requiring a fraction of the power other systems need.

SeqNFind™ leverages a cross-platform, graphical user interface-based toolset for facilitating bioinformatics research in Next Generation Sequencing, Pipelined Microarray Analysis and Genomic Comparisons. Unlike many algorithms and implementations such as BLAST, which is heuristic, or other proprietary systems that use large tiled sequences, **SeqNFind™** examines every genomic base as an individual affine gap alignment. The system uses a modified Smith-Waterman to examine short-read local alignments, returning a filtered set of viable patterns and locations.

In addition, **SeqNFind™** provides job-tracking functionality with robust database and data-storage solutions.

SeqNFind™ is the first comprehensive genomic data-management solution of its kind. Harness the power in your laboratory today!

For more information or to contact an ATL Sales Representative, please call **800.565.5467** or **910.673.8165** or visit us on the Web at **www.atlab.com.** European Customers, please contact Dr. Peter Maier of iCD in Europe at Pmaier@icd.eu or call: **+49 173 5303 706**.

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