PatternHunter
general purpose homology search software

PatternHunter is a revolutionary general-purpose homology search tool based on well-recognized, innovative and proprietary technologies. It provides all the tools necessary for fast and sensitive homology search in all flavors, including: DNA-DNA, Protein-Protein, translated DNA-protein, and translated DNA-DNA searches. PatternHunter saves you time and money by delivering sequence comparisons with astonishing speed and accuracy.

Speed

PatternHunter, run on a normal desktop computer, is 100 times faster than BLAST (at similar sensitivities). Even when PatternHunter is run at full sensitivity, it is as fast or faster than BLAST.

PatternHunter is even faster than Mega BLAST. With PatternHunter?, you can spend your valuable time (and CPU time) more effectively.
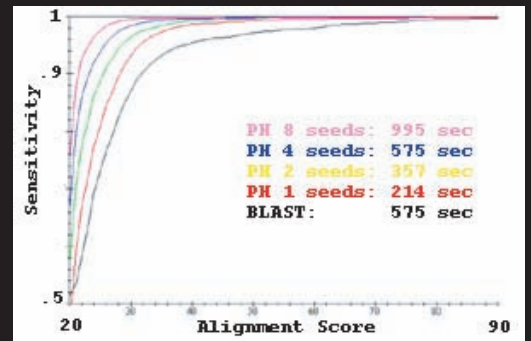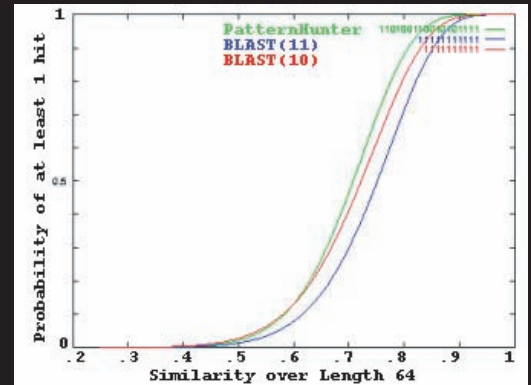

Sensitivity

PatternHunter can approach 100% sensitivity while still running as fast as a standard BLAST search – that's 3000 times faster than the Smith-Waterman algorithm. With PatternHunter, you can trust your results.

The PatternHunter Approach

PatternHunter is the only homology search software that can use multiple optimized spaced seeds, a BSI proprietary technology.
- A seeded search is fast because it will only look for a homology where it finds a hit with a small search string – a seed.
- Spaced seeds increase the sensitivity of the search
- Increasing the number of simultaneously used seeds increases sensitivity without sacrificing speed.
- Optimizing seeds lets them work more efficiently and work well together.

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homology search software

Types of Searches

PatternHunter's comprehensive search package replaces all BLAST functionalities (BLASTn, BLASTp, BLASTx, tBLASTx, tBLASTn) and all full sensitivity search methods. It can compare single sequences and large databases of sequences. PatternHunter? is the only tool you need.
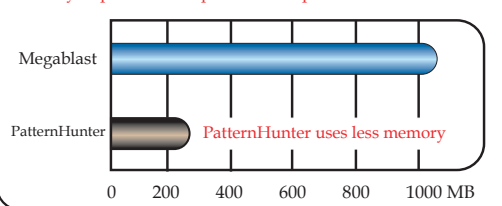
Result Quality

PatternHunter provides more sensitive searching and fewer false positive hits than does BLAST. Also, PatternHunter intelligent programming accounts for frame shift errors and non-coding regions in their respective searches. You can rely on PatternHunter.
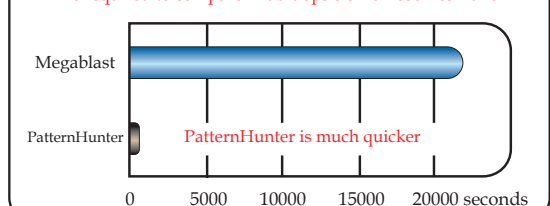
System Compatibility

Java based programming allows portability and scalability:
 • PatternHunter will run in any Java 1.4 environment.
 • PatternHunter is memory friendly even when performing intensive comparisons.

Memory required to compare Arabidopsis chromosomes 2 and 4

Megablast

PatternHunter — PatternHunter uses less memory

0   200   400   600   800   1000 MB

Time required to compare Arabidopsis chromosomes 2 and 4

Megablast

PatternHunter — PatternHunter is much quicker

0   5000   10000   15000   20000 seconds

PatternHunter published results from Li et al. in Nature Publishing, Bioinformatics Journal & GIW.

Customized Searching

You have control. PatternHunter searches the way you want it to with customizable scoring, custom search parameters, and Custom seeding. With custom seeding you set number of seeds, seed weight and seed shape to:
 • Ensure 100% success when searching for small/specialized sequences
 • Optimize your search for speed and sensitivity

"The birth of PatternHunter is an absolutely revolutionary change in sequence comparison. For me, it's a lifesaver for my project."
- Chunyu Liu PhD.,
Dept. of Psychiatry
University of Chicago

"The PatternHunter program has taken the science of genomic research and analysis a quantum leap forward."
- Java.Sun.Com

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