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Solutions For Bioinformatics and Genomic Data Analysis

Is Next-Generation Sequencing in Your Future?

With the price of sequencing dropping dramatically, new applications for the latest high-throughput technologies are creating impressively large data sets. The ability to generate a microbial genome in a week or two, or to resequence patient samples to identify variation has now become within reach for many research laboratories.

But what technology to choose? ABI/Solid, Illumina/Solexa, or Roche/454? Each has its strengths and weaknesses. To learn more about each technology, we've made this material [available on our website](#).

Having the ability to generate these data enables many researchers to ask questions that were previously either too expensive or complex for their small to moderate sized budgets. After years of flat or decreasing NIH budgets, it is a welcome change to see the current increase in funding, along with the (good luck!) promise of ARRA challenge grants and supplements.

But what does a lab do with all of this data? Depending on the technology, they could be managing and analyzing hundreds of gigabytes to over a terabyte of raw data. Comparative genome analysis, *de novo* assembly or framework-based assembly, SNP discovery, CNV, and SAGE are capable of generating large and complex data sets.

Is it in your lab's best interest to manage and analyze the primary data internally? Probably not, especially if your focus is understanding the molecular mechanisms in a model system, disease state, or biological process. Working with a third party (and guess who I'd recommend!) frees up

About the Company:

B-Tech, Ltd. provides contract research and analytical services in bioinformatics. We have worked extensively on the identification of differentially regulated genes using the Affymetrix and Illumina platforms, high-throughput DNA sequencing, SAGE and pathway analysis. We are also highly skilled in data integration, statistical analysis, and data presentation and visualization.

We are able to accommodate both large scale long-term projects as well as an individual experiment. All work is tailored to the needs of the researcher, and is a highly interactive process. In this way we ensure that the analytical methods will provide the best answer to the scientific questions being asked.

A typical analysis is completed within 2 weeks from receipt of data. If you have special needs, such as grant or meeting deadlines, we will do our best to accommodate your requests. Our work is affordable, professional, and presented in a format designed for the bench scientist.

We currently perform contract research and support for several major universities, and we welcome reference checks. We have also worked closely with several top-tier pharmaceutical companies, which can also

resources to focus on integrating those data into your research program, developing new hypotheses, and wet-lab validation of predictions.

In a nutshell, next-generation sequencing technologies are powerful tool for discovery. Which platform you choose depends on your needs, budget, and other factors. Roche/454 is an excellent platform for whole genome and *de novo* sequencing due to the longer read length. On the other hand, if you have a reference genome, Illumina Solexa and ABI Solid can be faster and more cost effective. Shorter read length means deeper depth of coverage, something to consider if you're interested in SNP discovery.

Paper of the Month:

I find miRNA's fascinating from both a biological and computational perspective. Identification of genomic regions which code for miRNA's, and the identification of targets for miRNA binding are both hot topics in bioinformatics. What interests me lately is the identification of miRNA's in plasma, and their potential as biomarkers. [In this article](#), the ratio of miR-92/miR-638 in plasma was able to distinguish between leukemia patients from health individuals.

- Brian

provide references.

About the Founder:

Brian Moldover, Ph.D. I have worked in bioinformatics since 1993, where I was a Research Fellow at NIH working in the Human Genome Project. Since then I spent 15 years working in the pharmaceutical industry for companies such as Warner-Lambert , Pfizer, Aventis, and Schering AG. I have held positions from Sr. Scientist through Vice-President of Global Research Computing. I have extensive knowledge of genomics and bioinformatics research, as well as significant business experience.

Because of my long industry experience, you can expect any work we perform to be done professionally, securely, and timely.

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