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Executive Summary

The completed sequencing of the entire human genome has provided the world with an abundance of valuable information. The availability of this immense resource holds significant potential. To unravel the secrets contained in the sequences of human DNA, researchers must rely on computers to analyze this data. Computers are essential in the analysis of this data in many ways, from basic sequence similarity searches to advanced predictions of gene function.

However, advances in computing power and speed are not fully utilized unless they are coupled with similar advances in programming techniques and software algorithms. Advances in computer technology mean that hardware is ready to answer the computational challenges of the post-genomics era. However, advances in software to model biological systems, discover the pathways in systems biology, and find novel correlations within the data have lagged behind. Both industry and academia are pursuing improved algorithms and high-performance computational techniques in order to take advantage of the opportunities within genomics and genetics.

Bio::Neos, Inc. has the experience and support to provide industry and the research community with exciting and effective software applications. Bio::Neos, Inc. works with some of the foremost mutation identification researchers in the nation from the Center for Bioinformatics and Computational Biology (CBCB) in the University of Iowa. Through this collaboration, Bio::Neos has developed a Laboratory Information Management System (LIMS) focused on mutation detection and discovery, called Bio::WebLab. Using the Prioritization of Annotated Regions (PAR) algorithm, unique to Bio::Neos, the software provides a visualization of genomic data, including gene structure and associated annotation, and predicts the regions that are most likely to contain disease-causing mutations.

By altering the data gathering and management process into automated tasks, researchers can spend more time performing their research rather than managing their immense collections of data. In Bio::WebLab, users can incorporate and integrate publicly available data and privately generated data. Using the PAR algorithm, the system provides users with a prioritized order in which to screen regions within their candidates for mutations. The flexibility of the system augments this prioritization by combining it with other custom prioritization techniques in order to best suit the needs of each individual researcher. Because of the relationship with scientists at The University of Iowa, Bio::Neos, Inc. has a competitive advantage on cutting edge scientific developments as well as customer feedback including specific research requirements for bioinformatics software in an academic setting.

Pharmaceutical companies spent \$275 million dollars in 2002 on LIMS software in order to discover drug targets and develop possible drugs. Additionally, academic research labs that collaborate with pharmaceuticals purchase LIMS software as well. To increase their efficiency, these research groups increasingly rely on efficient

software and novel data analyses. Bio::Neos, Inc. provides the innovative software that these companies are seeking. Furthermore, providing an academic release tailored to the capabilities of academic labs will allow Bio::Neos to reach the full market for bioinformatics software.

Although a large number of software LIMS exist, Bio::WebLab provides something unique: the PAR algorithm. Bio::Neos, Inc. will make use of this advantage by operating within a focused area of expertise, efficient mutation identification. Working with prominent mutation identification researchers such as Dr. Thomas Casavant from the CBCB will allow Bio::Neos, Inc. to enter into the bioinformatics and LIMS software markets. The affiliation with the University of Iowa and the CBCB will also serve to distinguish Bio::Neos, Inc. from other bioinformatics software companies. New algorithms and advanced research techniques produced from this collaboration will allow Bio::Neos to maintain its position in this target market.

Nearly the entire pharmaceutical industry uses genomic data to assist in target identification. Yet this new data by itself has not significantly decreased the time to develop new pharmaceuticals. It has become clear that mere access to data is not the panacea to biomedical questions. Without strong analytical tools and sufficient computational resources, genomic research will be severely limited. Therefore, there is an increasing need for bioinformatics software companies. With an energetic work ethic and committed university-business relationship, Bio::Neos is poised to become an important supplier of bioinformatics and LIMS software.