Biomax Informatics AG

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BIOMAX INFORMATICS AG and BRUNAK RESEARCH announce collaboration

MARTINSRIED, Germany and COPENHAGEN, Denmark — 5 August 2003 — Biomax Informatics and Brunak Research today announced a collaboration enabling Biomax to incorporate several functional prediction algorithms developed at the Center for Biological Sequence Analysis (CBS, Lyngby, Denmark) with their bioinformatics solutions on a non-exclusive basis. In exchange, Biomax will promote the algorithms to new and existing Biomax customers.

Under the agreement, Biomax will wrap and promote SignalP, ChloroP, TargetP, NetPhos, NetOGlyc, NetNGlyc and TMHMM as premiere prediction algorithms in Biomax bioinformatics products. These tools accurately predict protein cellular localization and post-translational modifications by phosphorylation or glycosylation independent of sequence similarity to other proteins.

Dr. Jan Brunak at Brunak Research, endorsed the collaboration by noting, “With its proven record as a leader in delivering tailored bioinformatics solutions to customers worldwide, Biomax is an excellent partner to help increase awareness to the developments at CBS and expand the presence of Brunak Research in the marketplace. While academic use of the prediction servers at CBS (http://www.cbs.dtu.dk/services/) is free (they receive several 100,000 hits per month) high throughput commercial usage requires an in-house installation. Integration by Biomax provides an environment for such high-throughput usage.”

Dr. Dieter Maier, Project Manager at Biomax, echoed this enthusiasm, “Several of our customers are already taking advantage of the value of the CBS prediction methods. We have been recommending these methods to customers for some time because they are the best available prediction algorithms. This agreement is designed to add structure and strengthen our relationship with Brunak Research by adding clear co-development, marketing and sales objectives, and making these objectives more transparent for both sides. The goal at Biomax has always been to provide state-of-the-art bioinformatics capabilities to life science organizations. We consider this agreement with Brunak Research as a way to further add momentum to this goal.”

Biomax will integrate the CBS algorithms as value-added features of their Pedant-Pro™ Sequence Analysis Suite and ReqALLer™ Bioinformatics Tool Box. In addition, the comprehensive Biomax™ Human Genome Database will allow users to directly compare the CBS predictions with results from other prediction sources, such as PROSITE.

Licenses for the CBS algorithms will be available through Brunak Research.

About Biomax

Biomax Informatics AG (Martinsried, Germany), a leader in the development of customized bioinformatics solutions, was founded in 1997 as a spin-off of the GSF-MIPS academic research group, now the German Research Center for Environment and Health-Institute for Bioinformatics (GSF-IBI). Founded by Prof. Dr. D. Frishman, Dr. K. Heumann and Prof. Dr. H. W. Mewes, Biomax developed the well-known Pedant-Pro™ Sequence Analysis Suite, the HarvESTer™ EST Clustering and Assembly System, and other bioinformatics tools used in metabolic pathway analysis, proteomics, and gene expression analysis. Additional information about Biomax can be found at the company's site on the World Wide Web at www.biomax.com.

About the Center for Biological Sequence Analysis

Since 1993, the Center for Biological Sequence Analysis has worked on the elucidation of the functional aspects of complex biological mechanisms, focusing primarily on gene finding and expression, protein post-translational modification and protein function, immunological bioinformatics, molecular evolution, comparative microbial genomics and integrative systems biology. Headed by Prof. Dr. Søren Brunak, the center, with its staff of approximately 35, represents one of the large bioinformatics groups in European academia (www.cbs.dtu.dk).

About Brunak Research

Brunak Research, a scientific software provider, sells bioinformatics prediction tools, typically developed in academia, for commercial use in the pharma and biotech industries. The firm offers licenses at different levels (company-wide, individual site, single machine) for a wide range of platforms (including Linux®, SGI™/ IRIX®, SGI/Linux, SUN™/SunOS™, HP™, IBM®/AIX®). The company is owned by Jan Brunak, with offices in Copenhagen, Denmark (www.brunak.dk).

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