

Obituary

In Memory of Dan S. Prestridge

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DAN PRESTRIDGE — LATE JUSTIFICATION OF A VISIONARY SCIENTIST

Dan Prestridge passed away of cancer in 1999, more than half a year before the human genome draft was ready (see also the announcement of the University of Minnesota). As the dust of the first excitement settles it is becoming clear that the ideas he pursued almost 10 years ago were pointing into the right direction. He pioneered both the computerized search for regulatory elements (transcription factor binding sites) by publishing SignalScan in 1991 as well as the field of eukaryotic promoter recognition by publishing his program PromoterScan in 1995 [5,6]. Both programs were milestones in the development of bioinformatics of regulatory sequences and have influenced many other developments that later on improved the concepts.

Dan Prestridge deserves the credit for being one of the first scientists in bioinformatics who correctly foresaw the requirements for meaningful analysis of genomic regulatory sequences — and went on to implement his ideas into applicable programs.

It is a tragedy that it became clear no earlier than almost a year after his untimely death that gene regulation actually occupies a much larger part of the genome than sequences coding for proteins. Nevertheless, although his name will not appear on the numerous publications concerning functional annotation of the human genome, it should not be forgotten, that visionary scientists like Dan Prestridge helped to pave the way to a meaningful interpretation of the vast amount of non-protein-coding sequences in the human genome.

CURRENT PERSPECTIVE

In the meantime bioinformatics of regulatory sequences advanced significantly. The basis of experimental results in the TRANSFAC database [10] (already used by Prestridge for SignalScan) increased severalfold, a variety of new algorithms for the detection of transcription factor binding sites was developed (MatInspector [7], Matrix Scan [1], TESS, TFSEARCH to name a few). The field of promoter finding also saw constant development (e.g. PromFD [2], FunSiteP [3], Promoter 2.0 [4], TSSG, TSSW

Electronic publication can be found in *In Silico Biol.* **1**, 000122 <<http://www.bioinfo.de/isb/2000/01/0022/>>.

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[9]. The most recent development was the first successful large-scale promoter finding program [8] with which the bioinformatics of regulatory regions finally reached true genomic dimensions. The future will certainly see the development of further algorithms for functional analysis of the ever growing amount of sequence data as well as the design and population of new database concepts in order to keep the avalanche of published data manageable.

Also just recently, we put SignalScan on the Gene Regulation portal site since it is still a widely used and useful tool, and we feel it is justified to honor Dan's contribution to this field of bioinformatics.

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