

UNIVERSITY OF CALIFORNIA, SANTA CRUZ

**COMMITTEE ON FACULTY RESEARCH LECTURE
2000-01**

To the Academic Senate, Santa Cruz Division:

It is our pleasure to recommend Professor David Haussler, the University of California Presidential Chair of Computer Science as Faculty Research Lecturer for 2001-2002. Recently, the DNA sequence of the human genome has been solved. Originally proposed by UCSC Chancellor Robert Sinsheimer in 1985, this enormous international collaborative science project recently culminated in the assembly of the raw sequence data into the DNA sequences of the human chromosomes by powerful computer programs running on parallel arrays of microprocessors. This final but most difficult step was achieved at UCSC, by David Haussler's research group. These findings have brought international recognition not only to Professor

Haussler and his colleagues, but also to our campus.

Professor Haussler has for many years been recognized as a world leader in the field of computational learning theory, computational biology and bioinformatics. At UCSC, one of his most important accomplishments has been to forge deep and fruitful scientific interactions between computer scientists and molecular biologists, a prominent example of the often-invoked but all-too-rarely successful phrase "interdisciplinary research". His most stellar contributions (together with his students and collaborators in the Departments of Computer Sciences and MCD Biology) have been in the areas of:

- Discovery and implementation of the most powerful methods for alignment and analysis of the sequence of biological macromolecules (DNA, RNA and proteins)
- Pioneering the use of Hidden Markov Models (HMMs) for analysis of sequences of biological macromolecules
- Application of HMMs in powerful new algorithms for predicting the three-dimensional folding of proteins (called "the biggest unsolved problem in molecular biology")
- Prediction of positions of "introns" in the DNA sequences of genomes (regarded as one of the most difficult problems in identifying the genes in the human genome)
- Assembling the DNA sequence of the human genome (published recently in Nature, and the subject of the cover of the N.Y. Times and a recent announcement at the White House)

Professor Haussler was recently appointed Director of the UCSC Center for Biomolecular Science and Engineering, now an official Focused Research Activity (FRA) of the University of California. Realization of the Center was largely the result of Professor Haussler's own efforts. He was also recently appointed Associate Director of the systemwide Institute for Bioengineering, Biotechnology and Quantitative Biomedical Research (QB3), one of three California Institutes for Science and Innovation (CISI). Haussler is also Program Head of the Bioinformatics Program, one of three programs that make up the Institute.

In the year 2000, Professor Haussler was appointed the first Full Investigator of the prestigious Howard Hughes Medical Institute at UCSC. He also holds appointments as Adjunct Professor in the Department of Biopharmaceutical Sciences at UCSF and as Consulting Professor in the Department of Medicine at Stanford University.

Professor Haussler's research accomplishments have established him as a world leader in the field of Bioinformatics and represent a powerful testament to the quality of our intellectual environment here at UC, Santa Cruz.

Respectfully submitted,

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