

# Eric Eugene Snyder

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## 1. Research Interests

- Development and application of computational methods for understanding the human genome and its molecular biology, in particular, pre-mRNA processing and alternative splicing
- Design of *ab initio* gene prediction methods and the prediction of regulated alternative splicing
- Creating on-line object-oriented databases for specific domains of knowledge based on experts' understanding of the relationships between data within that domain
- Understanding the role of chaos and nonlinear system behavior in biological processes such as gene expression, signaling and cognition

## 2. Education

1990 – 1994 Ph.D. University of Colorado, Boulder, CO, 80302  
Department of Molecular, Cellular and Developmental Biology  
1988 – 1990 B.A. University of Colorado, Boulder, CO, 80302  
Chemistry/Biochemistry and Molecular Cellular and Developmental Biology  
(Double Major)  
1984 – 1986 Johns Hopkins University, Baltimore, MD, 21218

## 3. Professional Experience

2000 - Associate Professor, Pennington Biomedical Research Center, Louisiana State University, Baton Rouge, LA 70808-4124  
1997 - 1999 Director of Computational Biology, Genomica Corporation, Boulder, CO 80303-7817  
1994 - 1997 Director of Genome Analysis, Sequana Therapeutics, La Jolla, CA 92137  
1992 - 1994 Graduate Research Assistant, University of Colorado, Boulder, CO 80306  
1991 - 1992 Teaching Assistant, University of Colorado, Boulder, CO 80306  
1989 - 1990 Research Assistant, Department of Biochemistry, University of Colorado, Boulder, CO 80306  
1987 - 1988 Laboratory Assistant III, Department of Immunology/Virology, Damon Reference Laboratory, Newbury Park, CA 91380  
1984 - 1986 Research Assistant, Department of Psychology, Johns Hopkins University, Baltimore, MD 21218

## 4. Professional Society Memberships

1995 - 1998 Human Genome Organization (HUGO)  
2000 - present International Society for Computational Biology (ISCB)  
1994 - present American Association for Advancement of Science  
1988 - 1998 American Chemical Society

## 5. Grants and Contracts

1990-91, '93-'94 NIH Training Grants  
2003 NIH R01 Alternative Splicing Prediction by Hidden Markov Model (submitted 2/03, not funded)

## 6. Honors and Awards

### Invited Speaker at Major Conferences, Symposia and Institutions

1. **Snyder, E.E.**, Stormo, G.D. (1993) Identification of coding regions in genomic DNA. Presented at the Third International Workshop on the Identification of Transcribed Sequences, New Orleans, LA.
2. **Snyder, E.E.** (1996) Dynamic programming methods for gene structure prediction. Presented at Glaxo-Wellcome, Research Triangle Park, NC, at the invitation of Rainer Fuchs.
3. **Snyder, E.E.**, St-Amand, J. (2000) SAGEparser: A program to analyze SAGE results and control for artifacts. Presented at the SAGE 2000: Frontiers in Gene Expression Analysis. Baltimore, MD, USA.

### Fellowships

1. Merrell Dow Fellowship (1986), National Institute on Drug Abuse (NIDA), Francis Scott Key Medical Center, Baltimore, MD.

## 7. Publications

### Original Manuscripts

1. **Snyder, E. E.**, Buoscio, B. W., Falke, J. J. (1990) Calcium(II) site specificity: Effect of size and charge on metal ion binding to an EF-hand-like site. *Biochemistry* **29**(16): 3937-3943.
2. **Snyder, E. E.**, Fall, R. R. (1990) Western blotting with a concanavalin A-horseradish peroxidase conjugate. *Biochem. Ed.* **18**(3): 147-148.
3. Falke, J. J., **Snyder, E. E.**, Thatcher, K. C., Voertler, C. S. (1991) Quantitating and engineering the ion specificity of an EF-hand-like Ca<sup>+2</sup> binding site. *Biochemistry* **30**(35): 8690-8697.
4. **Snyder, E. E.**, Stormo, G. D. (1993) Identification of coding regions in genomic DNA: an application of dynamic programming and neural networks. *Nucl. Acids Res.* **21**(3): 607-613.
5. Rinquist, S., Jones, T., **Snyder, E. E.**, Boni, I., Gold, L. (1995) High affinity RNA ligands to *E. coli* ribosomes and ribosomal protein S1: comparison of natural and unnatural binding sites, *Biochemistry*. **34**(11): 3640-3648.
6. **Snyder, E. E.**, Stormo, G. D. (1995) Identification of protein coding regions in Genomic DNA. *J. Mol. Biol.* **248**: 1-18.
7. Nichols, K.E., Harkin, D.P., Levitz, S., Krainer, M., Kolquist, K.A., Genovese, C., Bernard, A., Ferguson, M., Zuo, L., **Snyder, E.**, Buckler, A.J., Wise, C., Ashley, J., Lovett, M., Valentine, M.B., Look, A.T., Gerald, W., Housman, D.E., Haber, D.A. (1998) Inactivating mutations in an SH2 domain-encoding gene in X-linked lymphoproliferative syndrome. *PNAS* **95**: 13765-13770.
8. Pérusse, L., Chagnon, Y.C., Weisnagel, S.J., Rankinen, T., **Snyder, E.**, Sands, J., Bouchard, C. (2001) The Human Obesity Gene Map: The 2000 Update. *Obesity Res.* **9**(2): 135-169.
9. Ukkola, O., Ravussin, E., Jacobson, P., **Snyder, E. E.**, Chagnon, M., Sjostrom, L., Bouchard, C. (2001) Mutations in the preproghrelin/ghrelin gene associated with obesity in humans. *J. Clin. Endocrinol. Metab.* **86**(8): 3996-3999.
10. Rankinen, T., Pérusse, L., Weisnagel, S.J., **Snyder, E. E.**, Chagnon, Y.C., Bouchard, C. (2002) The human obesity gene map: the 2001 update. *Obesity Res.* **10**(3): 196-243.
11. Jacobson, P., Ukkola, O., Rankinen, T., **Snyder, E.E.**, Leon, A.S., Rao, D.C., Skinner, J.S., Wilmore, J.H., Lonn, L., Cowan, G.S., Jr, Sjostrom, L., Bouchard, C. (2002) Melanocortin 4 receptor sequence variations are seldom a cause of human obesity: the Swedish Obese Subjects, the HERITAGE Family Study, and a Memphis cohort. *J. Clin. Endocrinol. Metab.* **87**(10): 4442-4446.
12. Yoshioka, M., Tanaka, H., Shono, N., **Snyder, E.E.**, Shindo, M., St-Amand, J. (2003) Serial analysis of gene expression in the skeletal muscle of endurance athletes compared to sedentary men. *FASEB J.* **17**: 1812-1819.
13. Chagnon, Y.C., Pérusse, L., Weisnagel, S.J., **Snyder, E. E.**, Chagnon, Y.C., Rankinen, T., Bouchard, C. (2003) The human obesity gene map: the 2002 update. *Obesity Res.* **11**(3): 313-67.
14. Jacobson, P., Rankinen, T., **Snyder, E.E.**, Tremblay, A., Pérusse, L., Chagnon, Y.C. and Bouchard, C. (2003) Resting metabolic rate and respiratory quotient: results from a genome-wide scan in the Quebec Family Study. *Physiol. Genomics* (in press).
15. **Snyder, E. E.**, Chagnon, Y.C., Pérusse, L., Weisnagel, S.J., Chagnon, Y.C., Rankinen, T., Bouchard, C. (2004) The human obesity gene map: the 2003 update. *Obesity Res.* (in press).

## Chapters and Reviews

1. **Snyder, E. E., Stormo, G. D.** (1995) "Identifying Genes in Genomic DNA Sequences", In: Nucleic Acid and Protein Sequence Analysis: A Practical Approach. 2nd Edition, Eds. M. J. Bishop, C. J. Rawlings, IRL Press.
2. **Snyder, E. E., Stormo, G. D.** (1995) "Neural network applications in biology: Identifying coding regions in DNA sequences". Handbook of Neural Computation, IOP Publishing, Oxford University Press.

## 8. Inventions and Patents

1. **GeneParser v1.0** identifies protein-coding regions in genomic DNA sequences using a hybrid neural network-dynamic programming system. Version 1.0 assembles internal exons using a two-layered linear network. Graphics are displayed using SGI GL. Details of the algorithm and performance assessment are published in *Nucl. Acids Res.* **21**(3): 607-613. Patent not applied for. (1993)
2. **GeneParser v2.0** is an elaborated version of v1.0. New features include terminal exon prediction, fast sub-optimal solutions using bi-directional dynamic programming and a faster single-layer neural network. The program has a graphical and command-line user interface. The program has also been optimized to be highly tolerant of sequencing errors. At the time of publication (*J. Mol. Biol.* **248**: 1-18), GeneParser 2.0 was the best performing gene identification software available. Patent not applied for. (1994)
3. **UnderDog** is a genomic DNA sequence analysis pipeline developed at Sequana Therapeutics to annotate sequence data produced during the positional cloning of disease genes. The pipeline was written in Perl to execute various annotation tools such as the gene prediction programs GeneParser, GRAIL, MZEF and GenScan, sequence alignment programs [t]BLAST[nxp], [t]FASTA/P and Smith-Waterman, repetitive sequence filters RepeatMasker, XNU, SEG, as well as various other in-house and third-party algorithms. The sequences and output of all programs are parsed into ACeDB objects and read into a purpose-build ACeDB database. ACeDB provides a front end for browsing and querying the resulting annotation as well as monitoring annotation quality control. The Underdog package was in active development and use at Sequana Therapeutics from 1995 to 1998.
4. **SAGEparser** is a software package for interpreting sequence data from Serial Analysis of Gene Expression (SAGE) experiments. The program extracts tag sequences representing individual cDNA species from sequenced concatemers, counts them and identifies their corresponding mRNA sequence (if known). The program performs a rapid comparison of SAGE tag frequencies from different experiments, allowing the user to identify differentially expressed genes. (2000-2001)
5. **Obesity Gene Map Database** (<http://obesitygene.pbrc.edu>) Bouchard *et al.* have been publishing an annual review of the obesity genetics literature since 1996. In an effort to automate and computerize what had been essentially a manual operation, I began the Obesity Gene Map Database (OGMDB) in 2001. Using ACeDB as the database engine and the AceBrowser CGI framework, the manuscript was developed into a full-featured web site, with access to additional data provided through web links from the original data. ACeDB's chromosomal map functionality is now used to automate the preparation of the gene map figures for the printed version. Work on this project continues to date.

## 9. Languages Computer Skills

Languages: C/C++, Perl, sed, awk, 15+ years working in the UNIX environment, Irix, Solaris, Linux  
Databases: ACeDB, MySQL (some Sybase and Oracle)  
Libraries: BioPerl for working with biological sequences, AcePerl for biological databases  
Administration: UNIX (specifically: Irix, Linux, Solaris), Windows

## 10. Service

### Conference Organization

Chairman, Graduate Student Symposium on the Human Genome Project, University of Colorado, Boulder, April 15 – 17, 1994.

## **Ad Hoc Manuscript Reviewer**

*Nucleic Acids Research*  
*Computer Applications in Biological Sciences*  
*Journal of Molecular Biology*

## **Consultant Positions**

Apocom, Inc.: Reviewed and evaluated novel gene identification methods. Critiqued feature set of their GRAIL software (Oct.-Nov., 1994)

## **Lectures and Discussion Groups**

**Bioinformatics Group** Organized bioinformatics resources and seminar series in Basic Sciences division. Planned meetings, organized schedule of speakers, set up bioinformatics web site for internal use by Pennington employees (2000 -).

**Saturday Science Series** Gave presentations for lecture series aimed at students from high schools in the Baton Rouge area with an interest in careers in the natural sciences (2003).

## **11. Teaching and Mentoring**

### **Courses Taught**

Introductory Biology. Fall, 1991, University of Colorado, Boulder, CO  
Molecular Cell Biology. Spring, 1992, University of Colorado, Boulder, CO

### **Employees Supervised**

Martin Ferguson, Ph.D., Sequana Therapeutics; 1995 – 1997.  
Mike Engle, B.A., Sequana Therapeutics; 1995 – 1997.  
Jason Martin, M.S., Sequana Therapeutics; 1995 – 1997.  
Brandon Walts, M.A., Genomica Corporation; 1997 – 1999.  
Joe Horton, B.Sc., Genomica Corporation; 1997 – 1999.  
John Bearden, B.A., Pennington Biomedical Research Center; 2001 – 2002.  
Brandon Walts, M.A., Pennington Biomedical Research Center; 2002 – current.  
Marc Boudreaux, B.A., Pennington Biomedical Research Center; 2000 – current.

### **Graduate Students Supervised**

Karthik Chepudira, B.Sc., Pennington Biomedical Research Center; 2003 – current.

### **Postdoctoral Fellows Supervised**

Agron Collaku, Ph.D., Pennington Biomedical Research Center, Louisiana State University, Baton Rouge, LA; 2001.  
Dawn Graunke, Ph.D., Pennington Biomedical Research Center, Louisiana State University, Baton Rouge, LA; 2000 – 2001.  
Julie Marchand, Ph.D., Pennington Biomedical Research Center, Louisiana State University, Baton Rouge, LA; 2003 – current.

## **12. References:**

### **Gary D. Stormo**

(Thesis advisor)

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