Anita,

Jay Snoddy asked me to send this abstract to you so it can be sent through the ORNL review/approval process. He said you did those for him.

Thanks,
Lois

Date: Mon, 19 May 2003 08:36:24 -0400
To: snoddyj
From: Lois Thurston <thurstonle@ornl.gov>
Subject: Fwd: Re: Fwd: abstract.

Date: Mon, 19 May 2003 08:35:25 -0400
From: Lois Thurston <thurstonle@ornl.gov>
Subject: Re: Fwd: abstract.
To: Lois Thurston <thurstonle@ornl.gov>

Looks good to me, Jay. Since you are there with the other co-authors, perhaps you should get their feedback and then send it since I won't be there till later on.
Lois

At 08:08 AM 5/19/2003, you wrote:

Date: Fri, 16 May 2003 21:30:33 -0400
From: Jay Russell Snoddy <snoddyj@ornl.gov>
Subject: abstract.
To: 241-4228 Lois Thurston
<thurstonle@ornl.gov>
Cc: "Jay Snoddy (Copy)" <snoddyj@ornl.gov>,
Stefan Kirov <kirovsa@ornl.gov>,
Bing Zhang <zhangb@ornl.gov>, "Jay Snoddy
(Copy)" <snoddyj@ornl.gov>
Reply-to: snoddyj@ornl.gov
Keywords: SENT

My membership number is in a previous email.

The p a s s w o r d is bliastuf.

The SAVED abstract there is also copied below at the web site, you will need the membership number.

If you or my co-authors do not see any fixes, please submit for me ASAP on monday. (you have my card info...or let me do it.

The COMPARATIVE AND COLLABORATIVE BIOINFORMATICS FOR THE ANALYSIS OF GENE AND CELLULAR REGULATORY NETWORKS.

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Key words: TRANSCRIPTION, GENE REGULATION, GENE PROMOTER, SEQUENCE ANALYSIS

Abstract: New bioinformatics approaches are needed to help elucidate the complex gene and cellular regulatory networks that function in the development of the brain and the creation of phenotype from genomes and the cellular environment.

Advances in Collaborative Bioinformatics are needed to enable large collaborations of researchers to work together. Supporting bioinformatics systems will be presented that were developed by these and other researchers to promote the work of the Tennessee Mouse Genome

Consortium (www.tnmouse.org), an Integrative Neuroscience Initiative on Alcoholism (www.intiastress.org) and the Program for the Comparative and Collaborative Analysis for Mammalian Phenotypes (www.ccbioinfo.org).

Advances in Comparative Bioinformatics are needed to do large-scale comparisons in intersecting data sets about regulatory networks. The comparisons can be done with data from genetically-variant individuals in the same species and with data from different species. In particular, GeneKeyDB and other related bioinformatics systems will be presented that can provide a gene-centered method of data mining and comparisions in intersecting data sets. Several applications of this GeneKeyDB will be presented. A specific application is finding sets of conserved genome sequence motifs that are found upstream of some genes thought to be coregulated in the chordate brain. These genome sequence motifs are likely to be cis-regulatory elements that are critical to gene transcription networks that function in the chordate brain.

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<http://sfn.abstractcentral.com/main.html>

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