

# CURRICULUM VITAE

## **Liudmila Sergeevna Mainzer, PhD**

Technical Program Manager, National Center for Supercomputing Applications

Research Assistant Professor, Institute for Genomic Biology

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## **Research interests**

High performance computing for biology; genomics; sequence bioinformatics; high-volume, high throughput biological data analysis; big data distributed platforms; mathematical modeling and computer simulation of complex biological systems.

## **Education**

- 2009                      Neuromorphic Engineering workshop, Telluride, Colorado, USA
- 2006                      PhD in Biophysics and Computational Biology, University of Illinois at Urbana-Champaign, USA. Thesis: Neural substrates of decision in foraging by a predatory marine mollusk, *Pleurobranchaea californica*.
- 1999                      BS in physics, specialty biophysics at Belarus State University, Minsk, Belarus. Thesis: Optimization of the training procedure for multilayer perceptrons using vector quantization.
- 1995-1997               Undergraduate student at the Department of Law, Belarus State University, Minsk, Belarus

## **Work Experience, University of Illinois**

### 2017-present: Technical Program Manager, NCSA Genomics

- Leading the NCSA Genomics group to excel in engaging with biomedical partners.
- Areas of engagement include: developing production-grade genomic workflows for clinical use; innovating statistical and machine learning models for complex biomedical datasets; introducing performance optimizations into computer code to decrease run time of analyses; developing software for massively parallel analyses; performing big data analyses for various biomedical applications; providing software and hardware support services for private and academic partners.
- Acting as liaison among the Computational Genomics and BioHealth communities within the NCSA, elsewhere at UIUC, and outside the University, including industry.
- Pursuing collaborative research with faculty at UIUC, elsewhere in the US and internationally, as well as with Industry, to develop cutting edge computing technologies for computational biology, especially genomics.
- Actively pursuing new funding opportunities within UIUC, governmental funding agencies, private endowments and companies.

### 2014-present: Research Assistant Professor, Institute for Genomic Biology

- Providing domain expertise in bioinformatics and computational biology to UIUC faculty, staff and collaborators.
- Acting as a liaison between UIUC staff and software developers at NCSA.
- Acting as a liaison with off-campus collaborators, representing the University of Illinois to private companies, Mayo Clinic, Argonne National Lab, the Pan African Bioinformatics network, Ontario Institute for Cancer Research, and the University of Birmingham.
- Co-advising undergraduate and graduate students with faculty at IGB

### 2013-2017: Senior Research Scientist, National Center for Supercomputing Applications

- Leveraged NCSA computational resources to support biomedical research.
- Designed and implemented novel methods for high-throughput biological data analysis.
- Retooled bioinformatics workflows for sustained throughput on Blue Waters.
- Identified and removed bottlenecks in software performance.
- Helped private biomedical informatics companies evaluate their software.
- Tested performance of bioinformatics software on early-access computer architectures, to help companies with their market and investment estimations.
- Participated in the formulation of grant proposals to national funding agencies.
- Assessed the IT needs to support biomedical research at the University of Illinois; provided estimated hardware budgets for projects.

### **Doctoral research**

#### Neurophysiology and behavior of a marine mollusk *Pleurobranchaea californica*

Advisor: Dr. Rhanor Gillette

- a behavioral study of turning behavior;
- electrophysiology of chemosensation in the slug's oral veil;
- modeling of neural networks mediating swimming, turning and feeding behavior;
- a cost-benefit analysis model to investigate decision making during foraging;
- immunocytochemical analysis of serotonin content in multi-function neurons;
- a data-driven model of cAMP diffusion and phosphodiesterase kinetics within a neuron.

#### Additional projects

- non-invasive neuronal spike detection technique by means of optical coherence tomography;
- population model of learning in artificial agents with flat and inverted-U learning curves;
- response threshold model of division of labor in social insects.

### **Postdoctoral research**

#### Origins on the three domains of life

Advisor: Dr. Gustavo Caetano-Anolles

- developed a new theory for the evolution of 6 organismal kingdoms and 3 cellular superkingdoms from the last common universal ancestor;
- large-scale protein architecture analysis in metabolic enzymes, supporting Morowitz' hypothesis of prebiotic "shells";
- proposed the existence of three epochs in the evolution of protein architecture
- mapped the protein structure data onto the physiology of organisms to elucidate the effect of environmental niches on evolution of protein fold architecture usage in proteomes.

## Bioinformatics analyses of plant/fungus symbiosis

Advisor: Dr. Matthew Hudson

- computational identification and annotation of plant, fungus and bacterial sequences in the metagenomics project studying fungal endosymbiosis in plant roots;
- assembly of high-throughput Illumina sequencing data from *Brachypodium*;
- differential expression analysis on RNA-Seq data from *Brachypodium*;
- identification of the genes responsible for initiation and maintenance of Arbuscular mycorrhizal symbiosis
- design and maintenance of web-based bioinformatics tools for research and teaching;
- large-scale comparative computational analysis of protein architectures in Soybean;
- collaborated on an iPlant project to develop web tools for identifying genetic regions of similar functions in the fully sequenced plants;
- identified the genetic bases of plant mineral nutrition, via automatic search and comparison of the quantitative trait loci;
- statistical analysis of function enrichment within plant sequence datasets;
- preparation of databases containing functional and structural annotation of fully sequenced plant species for a web-based bioinformatics tool;

## **Teaching experience, University of Illinois**

Fall 2007 and 2008      instructor in Introduction to Neuromorphic Engineering  
Spring 2005            teaching assistant in Developmental biology  
Fall 2004                teaching assistant in Cell and Membrane Physiology lab  
Spring 2003            teaching assistant in Neurophysiology lab  
Fall 2001-Spring 2002    teaching assistant in Plant and Animal Physiology lab

## **Outreach**

### 2003-2007

- Designed and built a biomorphic robot for educational purposes at Iguana Robotics Inc.
- Developed lesson plans for middle and high school, and college, using the robot to teach the functioning of neurons, synapses and simple neural networks.
- Supervised a team of high school teachers and an undergraduate student to design a web portal for school teachers to introduce advanced concepts of molecular biology and evolution into school curriculum.

### 2012-2018

- Led educational exercises at the yearly Genome Day (Orpheum Children's Science Museum, Champaign, IL)

## **Selected software products**

[https://github.com/ncsa/DigiPath\\_MLTK](https://github.com/ncsa/DigiPath_MLTK)

[https://github.com/ncsa/Genomics\\_SSR](https://github.com/ncsa/Genomics_SSR)

<https://github.com/ncsa/GenomicsCortexVarNextflow>

<https://github.com/ncsa/MayomicsVC>

[https://github.com/ncsa/Genomics\\_EpiQuant](https://github.com/ncsa/Genomics_EpiQuant)

<https://github.com/ncsa/DataHarmonizationPipeline>

<https://github.com/ncsa/Swift-T-Variant-Calling>

[https://github.com/ncsa/Genomics\\_VirtualChunker](https://github.com/ncsa/Genomics_VirtualChunker)

[https://github.com/ncsa/EpiQuant\\_GWAS\\_Simulations](https://github.com/ncsa/EpiQuant_GWAS_Simulations)  
[https://github.com/ncsa/NCSA-Genomics\\_UsageAnalyzer](https://github.com/ncsa/NCSA-Genomics_UsageAnalyzer)

## Awards

- 2002 John G. and Evelyn Hartman Heiligenstein Outstanding teaching assistant in Biology 121 award
- 2002 Graduate teaching certificate from the University of Illinois at Urbana-Champaign
- 2001 Francis M. and Harlie M. Clark research support grant, School of Life Science at University of Illinois.
- 2000 Francis M. and Harlie M. Clark research support grant, School of Life Science at University of Illinois.
- 2000 Conference travel grant, School of Life Science at University of Illinois.
- 1994 Soros Stipend by International Soros Science Education Program.

## Publications:

1. Voges, J., Paridaens, T., Müntefering, F., **Mainzer, L.S.**, Bliss, B., Yang, M., Ochoa-Alvarez, I., Fostier, J., Ostermann, J., Hernaez, M. (2019). GABAC: an arithmetic coding solution for genomic data. Oxford Bioinformatics, btz922, <https://doi.org/10.1093/bioinformatics/btz922>.
2. Brian E. Bliss, Joshua M. Allen, Saurabh Baheti, Matthew A. Bockol, Shubham Chandak, Jaime Delgado, Jan Fostier, Josep L. Gelpi, Steven N. Hart, Mikel Hernaez Arrazola, Matthew E. Hudson, Michael T. Kalmbach, Eric W. Klee, **Liudmila S. Mainzer**, Fabian Müntefering, Daniel Naro, Idoia Ochoa-Alvarez, Jörn Ostermann, Tom Paridaens, Christian A. Ross, Jan Voges, Eric D. Wieben, Mingyu Yang, Tsachy Weissman, Mathieu Wiepert (2019) Genie: an MPEG-G conformant software to compress genomic data. Supercomputing: The International Conference for High Performance Computing, Networking, Storage, and Analysis
3. Jacob R Heldenbrand, Saurabh Baheti, Matthew A Bockol, Travis M Drucker, Steven N Hart, Matthew E Hudson, Ravishankar K Iyer, Michael T Kalmbach, Eric W Klee, Eric D Wieben, Mathieu Wiepert, Derek E Wildman, **Liudmila S Mainzer** (2019) Recommendations for performance optimizations when using GATK3.8 and GATK4. BMC Bioinformatics 20, 557 <https://doi.org/10.1186/s12859-019-3169-7>
4. Kendig K, Baheti S, Bockol MA, Drucker TM, Hart SN, Heldenbrand JR, Hernaez M, Hudson ME, Kalmbach MT, Klee EW, Mattson NR, Ross CA, Taschuk M, Wieben ED, Wiepert M, Wildman DE, **Mainzer LS.** (2019) Sentieon DNaseq Variant Calling Workflow Demonstrates Strong Computational Performance and Accuracy. Frontiers in Genetics 10, 736 <https://doi.org/10.3389/fgene.2019.00736>
5. Chen AH, Ge W, Metcalf W, Jakobsson E, **Mainzer LS**, Lipka AE. An assessment of true and false positive detection rates of stepwise epistatic model selection as a function of sample size and number of markers. Heredity. 2019 May;122(5):660. <https://www.nature.com/articles/s41437-018-0162-2>
6. Baichoo S, Souilmi Y, Panji S, Botha G, Meintjes A, Hazelhurst S, Bendou H, de Beste E, Mpangase PT, Souiai O, Alghali M, Yi L, O'Connor BD, Crusoe M, Armstrong D, Aron S, Joubert F, Ahmed AE, Mbiyavanga M, van Heusden P, Magosi LE, Zermeno J, **Mainzer LS**, Fadlilmola FM, Jongeneel CV, Mulder N Developing reproducible bioinformatics analysis workflows for heterogeneous computing environments to support African genomics. BMC bioinformatics. 2018 Dec;19(1):457. <https://rdcu.be/bb7Pc>
7. Ahmed A, Heldenbrand J, Asmann Y, Fadlilmola F, Katz D, Kendig K, Kendzior M, Li T, Ren Y, Rodriguez E, Weber M, Wozniak JM, Zermeno J, **Mainzer LS.** (2019) Managing genomic

- variant calling workflows with Swift/T. PLoS ONE. 14(7): e0211608.  
<https://doi.org/10.1371/journal.pone.0211608>
8. Azza E. Ahmed, Phelelani T. Mpangase, Sumir Panji, Shakuntala Baichoo, Gerrit Botha, Faisal M. Fadlelmola, Scott Hazelhurst, Peter Van Heusden, C. Victor Jongeneel, Fourie Joubert, **Liudmila Sergeevna Mainzer**, Ayton Meintjes, Don Armstrong, Michael R. Crusoe, Brian D. O'connor, Yassine Souilmi, Mustafa Alghali, Shaun Aron, Hocine Bendou, Eugene De Beste, Mamana Mbiyavanga, Oussema Souiai, Long Yi, Jennie Zermeno, Nicola Mulder. Organizing and running bioinformatics hackathons within Africa: The H3ABioNet cloud computing experience AAS Open Res 2018, 1:9 (doi: 10.12688/aasopenres.12847.1)
  9. Yingxue Ren, Joseph S. Reddy, Cyril Pottier, Vivekananda Sarangi, Shulan Tian, Jason P. Sinnwell, Shannon K. McDonnell, Joanna M. Biernacka, Minerva M. Carrasquillo, Owen A. Ross, Nilüfer Ertekin-Taner, Rosa Rademakers, Matthew Hudson, **Liudmila Sergeevna Mainzer** and Yan W. Identification of missing variants by combining multiple analytic pipelines. BMC 2018 19:139. <https://doi.org/10.1186/s12859-018-2151-0> . <https://rdcu.be/LJPL>
  10. Jongeneel CV, Achinike-Oduaran O, Adebisi E, Adebisi M, Adeyemi S, Akanle B, Aron S, Ashano S, Bendou H, Botha G, Chimusa E, Choudhury A, Donthu R, Drnevich J, Falola O, Fields CJ, Hazelhurst S, Hendry L, Isewon I, Khetani RS, Kumuthini J, Kimuda MP, Magosi L, **Mainzer LS**, Maslamoney S, Mbiyavanga M, Meintjes A, Mugutso D, Mpangase P, Munthali R, Nembaware V, Ndhlovu A, Odia T, Okafor A, Oladipo O, Panji S, Pillay V, Rendon G, Sengupta D, Mulder N. (2017) Assessing computational genomics skills: Our experience in the H3ABioNet African bioinformatics network. PLoS Comput Biol 13(6): e1005419. <https://doi.org/10.1371/journal.pcbi.1005419>
  11. Stephens, Z. D., Hudson, M. E., **Mainzer, L. S.**, Taschuk, M., Weber, M. R., & Iyer, R. K. (2016). Simulating Next-Generation Sequencing Datasets from Empirical Mutation and Sequencing Models. PloS one, 11(11), e0167047.fg
  12. Banerjee, S. S., Athreya, A. P., **Mainzer, L. S.**, Jongeneel, C. V., Hwu, W. M., Kalbarczyk, Z. T., Iyer, R. K. (2016, June). Efficient and Scalable Workflows for Genomic Analyses. In Proceedings of the ACM International Workshop on Data-Intensive Distributed Computing (pp. 27-36). ACM.
  13. Mulder, Nicola J., et al. "H3ABioNet, a sustainable pan-African bioinformatics network for human heredity and health in Africa." Genome research 26.2 (2016): 271-277. Co-authored as part of the H3Africa Consortium.
  14. **Liudmila Sergeevna Mainzer**, Brad A. Chapman, Oliver Hofmann, Gloria Rendon, Zachary D. Stephens, Victor Jongeneel (2015) Validation of Illumina's Isaac variant calling workflow. bioRxiv doi: <https://doi.org/10.1101/031021>
  15. **Yafremava, L. S.**, Di Giulio, M., & Caetano-Anollés, G. (2013). Comparative analysis of barophily-related amino acid content in protein domains of *Pyrococcus abyssi* and *Pyrococcus furiosus*. Archaea, 2013.
  16. **Yafremava, L. S.**, Wielgos, M., Thomas, S., Nasir, A., Wang, M., Mittenthal, J. E., & Caetano-Anollés, G. (2013). A general framework of persistence strategies for biological systems helps explain domains of life. Frontiers in genetics, 4, 16.
  17. **L.S.Yafremava**, R.Gillette (2011) Putative lateral inhibition in sensory processing for directional turns. Journal of Neurophysiology 105(6), 2885-2890
  18. G Caetano-Anollés, **Liudmila Yafremava** and Jay E. Mittenthal (2010) Modularity and Dissipation in Evolution of Macromolecular Structures, Functions, and Networks. Chapter 20 (pages 431–449) in Evolutionary Genomics and Systems Biology, Wiley-Blackwell.
  19. Caetano-Anolles G, Sun FJ, Wang M, **Yafremava LS**, Harish A, Kim HS, Knudsen V, Caetano-Anolles D, Mittenthal JE. (2008) Origins and evolution of modern biochemistry: insights from genomes and molecular structure. Front Biosci. 2008 May 1;13:5212-40.

20. Caetano-Anollés G, **LS Yafremava**, H Gee, D Caetano-Anollés, and JE Mittenhal (2008) The origin and evolution of modern metabolism. *International J Biochemistry & Cell Biology* 41: 285-297.
21. M. Wang, **L.S. Yafremava**, J.E. Mittenhal, G. Caetano-Anollés (2007) Reductive Evolution of Architectural Repertoires in Proteomes and the Birth of the Tripartite World. *Genome Research* 17: 1572-1585.
22. **L.S.Yafremava**, C.W.Anthony, L.Lane, J.K.Campbell, R.Gillette (2007) Orienting and avoidance turning are precisely computed by the predatory sea-slug *Pleurobranchaea californica* McFarland. *The Journal of Experimental Biology* 210, 561-569
23. **L.Yafremava**, J.Rogers, A.Lewis (2007) Robotics Tools in Neuroscience Education. Proceedings of AAAI Spring Symposium in Robots in robot venues: resources for AI education. <http://www.aaai.org/Papers/Symposia/Spring/2007/SS-07-09/SS07-09-043.pdf>

### News articles and reports

1. [http://www.ncsa.illinois.edu/news/story/ncsa\\_collaborates\\_with\\_illinois\\_aces\\_to\\_identify\\_genes\\_responsible\\_for\\_comp](http://www.ncsa.illinois.edu/news/story/ncsa_collaborates_with_illinois_aces_to_identify_genes_responsible_for_comp)
2. <https://www.hpcwire.com/off-the-wire/collaborative-efforts-produce-clinical-workflows-for-fast-genetic-analysis/>
3. [http://www.ncsa.illinois.edu/news/story/ncsa\\_student\\_spotlight\\_angelynn\\_huang\\_and\\_sophia\\_torrellas](http://www.ncsa.illinois.edu/news/story/ncsa_student_spotlight_angelynn_huang_and_sophia_torrellas)
4. Uncovering Alzheimer's complex genetic networks. NFS Discoveries: [https://www.nsf.gov/discoveries/disc\\_summ.jsp?cntn\\_id=134049](https://www.nsf.gov/discoveries/disc_summ.jsp?cntn_id=134049)
5. Blue Waters Supercomputer Supporting Development of Genotyping Chip for African Populations. GenomeWeb: <https://www.genomeweb.com/informatics/blue-waters-supercomputer-supporting-development-genotyping-chip-african-populations>
6. Benchmarking the Human Variation Calling Pipeline. Blue Waters Annual Report 2014. December 16, 2014. PI: Christopher J. Fields. Collaborators: Liudmila S. Yafremava; Gloria Rendon; C. Victor Jongeneel
7. Epistatic interactions for brain expression GWAS in Alzheimer's disease. Blue Waters Annual Report 2015. Nilufer Ertekin-Taner, Mariet Allen, Liudmila Mainzer, Curtis Younkin, Victor Jongeneel, Thierry Schüpbach, Gloria Rendon, Julia Crook, Julie Cunningham, Summit Middha, Chris Kolbert, Dennis Dickson, Steven Younkin.
8. Instrumenting human variant calling workflow. Blue Waters Annual Report 2015. L. S. Mainzer, Arjun Athreya, Subho Banerjee, Ravishankar K. Iyer, Victor C. Jongeneel, Volodymyr Kindratenko, Zachary Stephens.

### Notable and Invited talks

- (2020) Invited speaker at the NextGen Omics Congress, Boston, USA.
- (2019) On panel for inauguration of the Center for Digital Agriculture, UIUC.
- (2018) iHPCug, Chicago
- (2017) Illinois Health Data Analytics Summit, Champaign, Illinois
- (2016) Blue Waters Symposium, Oregon
- (2015) High performance computing practices for biological big data. Corn Breeder School, Champaign, Illinois
- (2015) Big data problems and solutions in sequence bioinformatics. Big Data Summit, Champaign, Illinois

- (2015) High performance computing practices for biological big data. IGB Fellows Symposium, Champaign, Illinois
- (2014) Biological Data Science, CSHL
- (2010) Why life is tripartite in nature. SE & T Colloquim Series, Saginaw Valley State University.

### Conference posters and talks

1. Cold Spring Harbor Laboratory Conference in Genome Informatics, November 2019: A novel engine to build multi-locus epistatic model in complex diseases.
2. BioIT World – April 2019 Advancements in Supercomputing for Biomedical Applications
3. Personal Genomes Conference – April 2019 Structural variant calling by assembly in whole human genomes: applications in hypoplastic left heart syndrome
4. New Mexico Bioinformatics, Science and Technology (NMBIST) Symposium in Santa Fe, NM. – March 2019 Benchmarking the Performance and Accuracy of Minimap2
5. Biological Data Science – November 2018 Cold Spring Harbor Laboratory Search Space Reduction in Stepwise Modeling for GWAS
6. Mayo Clinic Individualizing Medicine Conference – September 2018 Structural variant calling by assembly in human genomes
7. Mayo Clinic Individualizing Medicine Conference – September 2018 NCSA performance benchmarking of GATK3.8, GATK4 and Sentieon
8. International Society for Computational Biology – July 2018 A-403: Search Space Reduction for Stepwise Epistatic Model Selection of Complex Continuous Traits
9. International Society for Computational Biology – July 2018 A-116: Comparative Analysis of Genomic Sequencing Workflow Management Systems
10. A Raj, J Mittenthal, **L Mainzer** (2018) Architecture and Dynamics of Biomolecular Networks Facilitate Evolution of Persistence Strategies in Living Organisms. NCUR, Edmond, OK
11. J Heldenbrand, A Ahmed, Y Asmann, F Fadlelmola, D Katz, M Kendzior, T Li, Y Ren, E Rodriguez, M Weber, J Zermeno, **L Mainzer** (2017) Modular genomic variant calling workflow in Swift/T. Rocky mountains bioinformatics conference, Colorado.
12. Y Ren, J Reddy, V Sarangi, S Tian, J Sinnwell, N Ertekin-Taner, O Ross, R Rademakers, S McDonnell, J Biernacka, M Carrasquillo, **L Mainzer**, Y Asmann (2017) Rescue the missing variants-lessons learned from large sequencing projects. Translational Bioinformatics Conference
13. T Li, C Steffen, R Chui, R Haas, **LS Mainzer** (2017) Benchmarking Parallelized File Aggregation Tools for Large Scale Data Management. Supercomputing conference, Denver, CO
14. **LS Mainzer**, A Athreya, S Banerjee, R Iyer, V Jongeneel, V Kindratenko, G Rendon, Z Stephens (2016) Sustained high throughput variant calling: HPC challenges and software options. Genome Informatics, Hinxton, UK
15. **LS Mainzer** (2016) Instrumenting Human Variant Calling Workflow on BlueWaters, part 1. Blue Waters Annual Symposium, Oregon, USA
16. **LS Mainzer** (2015) Instrumenting Human Variant Calling Workflow on BlueWaters, part 1. Blue Waters Annual Symposium, Oregon, USA
17. **LS Mainzer**, V. Kindratenko, G. Rendon, ZD Stephens, SS Banerjee, AP Athreya, RK Iyer, V Jongeneel (2014) Profiling accuracy and performance of human variant calling workflows on Blue Waters. Biological Data Science, CSHL.
18. **L Yafremava**, G Battu, KK. Bhattarai, JJ. Hong, Y-S Park, M Harrison, ME. Hudson ,

- (2013) Comparative Study Of Brachypodium Transcriptome In Three Arbuscular Mycorrhizal Symbioses. Plant And Animal Genome XXI, California, USA
19. G Caetano-Anollés, M Wang, **LS Yafremava**, D Caetano-Anollés, J Mittenthal (2008) The origins of modern proteomes and the ancestral eukaryotic cell. Annual Meeting of the Society for Molecular Biology and Evolution (SMBE), Barcelona, Spain.
  20. **L Yafremava**, M Wang, J Mittenthal, G Caetano-Anollés (2008) Primordial strategy hypothesis for the evolution of tripartite world. Annual Meeting of the Society for Molecular Biology and Evolution (SMBE).
  21. R Gillette, **LS Yafremava** (2006) Evolution and function in serotonergic systems. Society for Integrative and Comparative Biology (SICB) Annual Meeting.
  22. **LS Yafremava**, R Gillette (2006) Multiplexed function in serotonergic neurons of gastropod molluscs. Society for Integrative and Comparative Biology (SICB) Annual Meeting.
  23. M Lewis, JJ Rogers, **LS Yafremava** (2005) A Biomorphic Robot That Teaches the Connection between Neurons and Behavior. Neural Information Processing Systems (NIPS) Annual Conference.
  24. **LS Yafremava**, R Gillette (2004) Neural network simulation of switching between multiple behaviors based on hunger state and learning. Society for Neuroscience (SFN) Annual Meeting.
  25. **LS Yafremava**, J Rogers, MA Lewis (2004) Biomorphic robots as a teaching tool in neuroscience. Society for Neuroscience (SFN) Annual Meeting.
  26. A Bowonder, C Vinegoni, **L Yafremava**, R Gillette, SA Boppart (2004) Optical coherence tomography of neural activity. Chicago Universities Bioengineering Industry Consortium (CUBIC).
  27. **LS Yafremava**, CW Anthony, L Lane, R Gillette (2003) Orienting and avoidance turning in the predatory sea-slug Pleurobranchaea. Society for Neuroscience (SFN) Annual Meeting.
  28. **LS Yafremava**, TJ Anastasio, R Gillette (2001) Utility Theory And Neural Network Modeling Of Cost-Benefit Decision-Making In A Predatory Foraging Marine Snail. Computational Neuroscience Conference (CNS).
  29. NG Hatcher, LL Moroz, K Potgieter, JV Sweedler, **LS Yafremava**, X Zhang, R Gillette (2001) A model of feeding regulation by neuronal 5-HT and NO in the sea-slug Pleurobranchaea. The Sixth International Congress of Neuroethology.
  30. **LS Yafremava**, R Gillette (2001) Mechanisms of decision-making: a neural network simulation. Society for Neuroscience (SFN) Annual Meeting.
  31. K Potgieter, F Angenstein, **L Yafremava**, X Zhang, N Hatcher, L Moroz, J Sweedler, R. Gillette (2001) Serotonin as an arousal factor determining appetite in the feeding network of Pleurobranchaea. Society for Neuroscience (SFN) Annual Meeting.
  32. JK Wenzel, **LS Yafremava**, R. Gillette (2001) Precise computation in orienting turning by the predatory snail Pleurobranchaea. Society for Neuroscience (SFN) Annual Meeting.
  33. NG Hatcher, **LS Yafremava** Modeling the dynamics of intracellular processes: diffusion, enzyme kinetics and neuromodulation. Special Applied Math Seminar, October 15, 2001.
  34. R Gillette, **LS Yafremava** (2000) Towards A Computational Neural Network Model Of Behavioral Choice In Pleurobranchaea. Society for Neuroscience (SFN) Annual Meeting.
  35. **LS Yafremava**, TJ Anastasio, R Gillette (2000) Probabilistic Utility-Theory Model Of Foraging Behavior In The Predatory Marine Slug Pleurobranchaea Californica. Society for Neuroscience (SFN) Annual Meeting.
  36. **LS Yafremava**, AT Vlassov. (1999) Optimization of the training procedure for multilayer perceptrons using vector quantization. Proceedings of 55th student conference at Belarus State University, BSU press, Minsk, Belarus.



37. **LS Yafremava**, AT Vlassov (1998) Using the Liapunov Function for the Investigation the Memory Processes and Pattern Recognition in Neural Networks. Proceedings of 54th student conference at Belarus State University, BSU press, Minsk, Belarus.