Lorena Pantano

Research Scientist
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Personal

October 29, 1982.

Spanish Citizen.

1 Education

B.S Biochemistry, University of Granada, 2005.

M.S. in Bioinformatics for health science, University of Pompeu Fabra, 2008.

Ph.D. in Biomedicine, Center for Genomic Regulation, 2011.

2 GitHub contribution

Community supported project I actively participate:

bcbio-nextgen

cloudbiolinux

bcbio.rnaseq

bioconda

multiqc

Open source projects I own:

seqcluster

seqclusterViz

isomiRs

DEGreport

mirTOP

3 Work experience

Research Associate at Harvard Chan School Bioinformatic Core, 2014–to date.

Development of tools for NGS data analysis

Analyst of high-throughput data

Leading Bioinformatic analysis in the fibrosis project collaboration between Harvard and Boehringer Ingelheim

Post-doct fellow at IBB, 2013–2014.

Analyzing de-novo transcripts due to inversion

Differential expression due to inversion in HapMap population

Involve in inversion database development

Founder and CTO at ASCIDEA (http://ascidea.com), 2011-2014

Leading a group of 3 bioinformaticians

Cloud computing architect

Development of computational pipelines

Post-doctoral fellow at Institut de Medicina Predictiva i Personalitzada del Cancer, 2011–2013.

small RNA characterization in human sperm samples

PhD student at Center for Genomic Regulation, 2006–2011.

small RNA characterization in human mental diseases

Development of tools for miRNA and small RNA analysis

Msc student at Granada University, 2004–2006.

Studing lipids solubility in micro-drops

4 Skills

LINUX SO

Cloud computing: Amazon EC2, S3, SQS, IAM

Control version system: svn and git

High Performance Computing systems: lsf, slurm, sge

Basic web Server Development: HTML, DHTML, javascript, ccs3, php and cgi

Advance database management: mysql, sqlite3 and google datastore

Programming knowledge:

Basic C,C++ environment

Intermediate Java environment

Advance Perl and Python environment

Expert in R and Bioconductor for statistics and visualisation

Analysis of large-scale data:

Analysis of microarrays with R/Rstudio
SNPs data mining: samtools, BayesSeq, GATK, freebayes, verdict, mutect.
RNA-Seq: tuxedo kit, STAR, salmon, sailfish, kallisto, sleuth, DESeq2 and edgeR/limma.
Chip-Seq for histone modifications and transcription factor: macs2, diffbind.
Small RNA-Seq: mirdeep2, seqbuster, seqcluster, targetscan custom

Biostatistics:

Machine learning applications for phenotype classification of case/control studies
Regression model application to data integration

5 Courses

Principles of fMRI 1 @ Coursera 2016

Practical Machine Learning @ Coursera 2016

Calculus One @ Coursera 2015

Regression Model @ Coursera 2014

HPC programming (not finished) @ Coursera 2013

Analysis of hight-throughput sequencing data @ EMBL-EBI 2012

Web applications @ Udacity (CS253) 2012

Machine learning @ Coursera 2012

Introduction to Artificial Intelligence (www.ai-class.org) 2011

Advance R (CRG) 2008

6 Talks

small RNAseq data in bcbio-nexgen December 03, 2015 *Talk at MIT, Cambridge, MA*

Characterization of the small RNA transcriptome using the bcbio-nextgen python framework July 09, 2016 *Talk at Walt Disney World Yacht, Orlando, Florida*

miRNA and isomiR annotation December 15, 2016 *Talk at MIT, Cambridge, MA*

7 Service and leadership

Founder of women in bioinformatics meet up at cambridge, 2014 – to date.

Co-founder of RSG Spain, the spanish student group of ISCB student council, 2010.

Former member of ISCB student council, 2010–2014.

Peer review, NAR journal, 2017

Programme committee, BOSC, 2014-to date

Organizer/Chair, Mind the Gap Barcelona, 2013

Master Thesis Supervisor, 2014, Universidad Autonoma de Barcelona

Programme committee, Student Council Symposium, 2010-2014

Travel Fellowship chair, ISCB Student Council Symposium Long Beach, 2012

Program committee chair, Spain, Portugal and North Africa Student Symposium Barcelona, 2012

Organizer/Chair, ISCB Student Council Symposium Vienna, 2012

Organizer/Chair, Spain, Portugal and North Africa Student Symposium Malaga, 2011

Volunteer, ISCB Student Council Symposium Boston, 2010

Professor activities

RNA-seq differential expression analysis (assistant), 2017, Harvard Chan School workshop, Boston

Small RNAseq analysis, 2016 (Summer), Harvard Chan School workshop, Boston

Small RNAseq analysis, 2016 (Spring), Harvard Chan School workshop, Boston

Data visualization, 2013, PRBB, Spain

Workshop of ChIP-Seq analysis, 2013, University of Vic, Spain

Workshop of Metagenomic, 2013, University of Vic, Spain

Workshop of small RNA analysis, 2010, CRG, Spain

Languages skills

Language	Speech	Writing	Reading
Spanish	Native	Native	Native
English	Proficient	Proficient	Proficient
Catalan	Conversant	Good	Conversant

Journal Articles

1. **bcbioRNASeq R package for bcbio RNA-seq analysis** . M Steinbaugh,**L Pantano**,R Kirchner,V Barrera,B Chapman,M Piper,M Mistry,R Khetani,K Rutherford,O Hofmann,J Hutchinson,S Ho. *F1000Research*. 2017.

2. **Viewing RNA-seq data on the entire human genome** B Busby,E Weitz,**L Pantano**,J Zhu,B Upton. *F1000Research*. 2017.

3. **Comparative analysis of LIN28-RNA binding sites identified at single nucleotide resolution** E Ransey,A Bjorkbom,V Lelyveld,P Biecek,**L Pantano**,J Szostak,P Sliz. *RNA Biology*. 2017.

4. **Empirical comparison of reduced representation bisulfite sequencing and Infinium BeadChip reproducibility and coverage of DNA methylation in humans.** J Carmona,W Accomando,A Binder,J Hutchinson,**L Pantano**,B Izzi,A Just,X Lin,J Schwartz,P Vokonas,S Amr,A Baccarelli,K Michels . *npj Genomic Medicine*. 2017. doi: 10.1038/s41525-017-0012-9.

5. **Molecular, phenotypic, and sample-associated data to describe pluripotent stem cell lines and derivatives.** Daily K, Ho Sui SJ, Schriml LM, Dexheimer PJ, Salomonis N, Schroll R, Bush S, Keddache M, Mayhew C, Lotia S, Perumal TM, Dang K, **Pantano L**, Pico AR, Grassman E, Nordling D, Hide W, Hatzopoulos AK, Malik P, Cancelas JA, Lutzko C, Aronow BJ, Omberg L. *Scientific Data*. 2017. doi: 10.1038/sdata.2017.30.

6. **Maintenance of macrophage transcriptional programs and intestinal homeostasis by epigenetic reader SP140**. S Mehta,D Cronkite,M Basavappa,T Saunders,F Adiliaghdam,H Amatullah,S Morrison,J Pagan,R Anthony,P Tonnerre,G Lauer,J Lee,S Digumarthi,**L Pantano**,S Ho,F Ji,R Sadreyev,C Zhou,A Mullen,V Kumar,Y Li,C Wijmenga,R Xavier,T Means,K Jeffrey . *Science Immunology*. 2017. URL

7. **Genomic analyses identify molecular subtypes of pancreatic cancer.** Bailey P, Chang DK, Nones K, Johns AL, et al. *Nature*. 2016. doi: 10.1038/nature16965.

8. **Specific Small-RNA Signatures in the Amygdala at Premotor and Motor Stages of Parkinson Diseases Revealed by Deep Sequencing Analysis. Pantano, L.**, Friedlander, M. R., Escaramis, G., Lizano, E., Pallares-Albanell, J., Ferrer, I., Estivill, X., Marti, E. *Bioinformatics*. 2015. http://doi.org/10.1093/bioinforma

9. **The small RNA content of human sperm reveals pseudogene-derived piRNAs complementary to protein-coding genes. Pantano, L.**, Jodar, M., Bak, M., Ballesca, J. L., Tommerup, N., Oliva, R., Vavouri, T. *RNA*. 2015. http://doi.org/10.1261/rna.046482.114

10. **InvFEST, a database integrating information of polymorphic inversions in the human genome.** Martinez-Fundichely A, Casillas S, Egea R, Ri mia M, Barbadilla A, **Pantano L**, Puig M, Caceres M.*Nucleic Acids Res*. 2013 Nov 18.

11. **Microarray and deep sequencing cross-platform analysis of the mirRNome and isomiR variation in response to epidermal growth factor.** Llorens F, Hummel M, **Pantano L** Pastor X, Vivancos A, Castillo E, Mattlin H, Ferrer A, Ingham M, Noguera M, Kofler R, Dohm JC, Pluvinet R, Bayes M, Himmelbauer H, Del Rio JA, Marti E, Sumoy L.*BMC Genomics*,1;14:371,2013.

12. **A highly expressed miR-101 isomiR is a functional silencing small RNA.** Llorens F, Banez-Coronel M, **Lorena Pantano**, Del Rio JA, Ferrer I, Estivill X, Marti E. *BMC Genomics.*, 14(1):104,2013.

13. **A pathogenic mechanism in Huntington's disease involves small CAG-repeated RNAs with neurotoxic activity.** Monica Banez-Coronel, Silvia Porta, Birgit Kagerbauer, Elisabet Mateu-Huertas, **Lorena Pantano**, Isidre Ferrer, Manuel Guzman, Xavier Estivill, Eulalia Marti, *In PLoS genetics*, volume 8, pp. e1002481, 2012.

14. **A non-biased framework for the annotation and classification of the non-miRNA small RNA transcriptome. Lorena Pantano**, Xavier Estivill, Eulalia Marti, *In Bioinformatics*, volume 27, pp. 3202-3203, 2011.

15. **A myriad of miRNA variants in control and Huntington's disease brain regions detected by massively parallel sequencing.** Eulalia Marti, **Lorena Pantano**, Monica Banez-Coronel, Franc Llorens, Elena Minones-Moyano, Silvia Porta, Lauro Sumoy, Isidre Ferrer, Xavier Estivill, *In Nucleic acids research*, volume 38, pp. 7219-7235, 2010.

16. **SeqBuster, a bioinformatic tool for the processing and analysis of small RNAs datasets, reveals ubiquitous miRNA modifications in human embryonic cells. Lorena Pantano**, Xavier Estivill, Eulalia Marti, *In Nucleic acids research*, volume 38, pp. e34-e34, 2010.

17. **Identification of copy number variants defining genomic differences among major human groups.** Lluis Armengol, Sergi Villatoro, Juan R Gonzalez, **Lorena Pantano**, Manel Garcia-Aragones, Raquel Rabionet, Mario Caceres, Xavier Estivill, *In PloS one*, volume 4, pp. e7230, 2009.

18. **Fibroblast-derived induced pluripotent stem cells show no common retroviral vector insertions.** Florencio Varas, Matthias Stadtfeld, Luisa de Andres-Aguayo, Nimet Maherali, Alessandro di Tullio, Lorena Pantano, Cedric Notredame, Konrad Hochedlinger, Thomas Graf, *In Stem cells (Dayton, Ohio)*, volume 27, pp. 300-306, 2009.

19. **ProSeeK: a web server for MLPA probe design. Lorena Pantano**, Lluis Armengol, Sergi Villatoro, Xavier Estivill, *In BMC genomics*, volume 9, pp. 573, 2008.

20. **Genome assembly comparison identifies structural variants in the human genome.** Razi Khaja, Junjun Zhang, Jeffrey R MacDonald, Yongshu He, Ann M Joseph-George, John Wei, Muhammad A Rafiq, Cheng Qian, Mary Shago, **Lorena Pantano**, Hiroyuki Aburatani, Keith Jones, Richard Redon, Matthew Hurles, Lluis Armengol, Xavier Estivill, Richard J Mural, Charles Lee, Stephen W Scherer, Lars Feuk, *In Nature genetics*, volume 38, pp. 1413-1418, 2006.

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