

CURRICULUM VITÆ

PERSONAL DATA

Rodrigo Santamaría Vicente

Date of birth: September 27, 1980

Place of birth: Salamanca, Spain

<http://carpex.usal.es/~visusal/rodrigo>

CURRENT WORK

Category: Assistant PhD professor

Start: September 2010

Organism: University of Salamanca

Center: Faculty of Sciences

Department: Computer Sciences and Automation

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CURRENT RESEARCH LINES

Gene expression analysis

Systems biology

Biclustering algorithms

Information visualization

Visual analytics

ACADEMIC BACKGROUND

PhD in Computer Science

University of Salamanca

2009

Engineer in Computer Science

University of Salamanca

2004

FORMER ACTIVITIES

Category: Postdoctoral student (orden EDU/2934/2009)

Time frame: may – september 2010

Organism: Ministerio de Educación

Center: European Bioinformatics Institute (EBI)

Category: PhD student (orden EDU/1453/2005)

Time frame: 2006–2010

Organism: Junta de Castilla y León

Center: Universidad de Salamanca

Category: Art. 83 LOU contract

Time frame: 2004–2006

Organism: Universidad de Salamanca

Center: Laboratorio de Radiaciones Ionizantes

LANGUAGES

Spanish (native speaker)

English (fluent)

French (basic)

Italian (basic)

PUBLICATIONS

R. Santamaría, R. Theron and L. Quintales. Bi-cOverlapper 2.0: visual analysis for gene expression, *Bioinformatics*, **2014**, 30(9), 1785–1786, doi: 10.1093/bioinformatics/btu120.

R. Santamaría. Biological knowledge visualization, *Biological Knowledge Discovery Handbook: Preprocessing, Mining and Post-processing of Biological Data*, M. Elloumi, A. Y. Zomaya (Eds.), John Wiley and Sons, Inc., **2014**, New Jersey.

R. Santamaría and P. Pierre. Voronto: mapper of expression data to ontologies, *Bioinformatics*, **2012**, doi: 10.1093/bioinformatics/bts428.

J. Paredes, L. Carreto, J. Simes, A. R. Bezerra, A. C. Gomes, R. Santamaria, M. Kapushesky, G. Moura, and M. Santos. Low level genome mis-translations deregulate the transcriptome and translome and generate proteotoxic stress in yeast. *BMC Biology* **2012**, 10:55
www.biomedcentral.com/1741-7007/10/55/abstract.

R. Santamaría, L. Rizzetto, M. Bromley, T. Zelante, W. Lee, D. Cavalieri, L. Romani, B. Miller,

I. Gut, M. Santos, P. Pierre, P. Bowyer, M. Kapushesky. Systems biology of infectious diseases: a focus on fungal infections, *Immunobiology*, **2011**, 216:11, 1212–1227.

R. Santamaría, and R. Theron. Visualization of intersecting groups based on hypergraphs. *IEICE Transactions on Information and Systems*, **2010**, E93-D: 7, 1957–1964

Y. Chen, R. Santamaría, A. Butz, and R. Theron. TagClusters: Enhancing Semantic Understanding of Collaborative Tags. *International Journal of Creative Interfaces and Computer Graphics*, **2010**, 1:2, 15-28

R. Santamaría, and R. Therón. Treevolution: visual analysis of phylogenetic trees. *Bioinformatics*, **2009**, 25, 1970–1971

R. Santamaría, R. Therón and L. Quintales. BiClusterOverlapper: A tool for bicluster visualization. *Bioinformatics*, **2008**, 24, 1212–1213

R. Santamaría, R. Therón and L. Quintales. A visual analytics approach for understanding biclustering results from microarray data. *BMC Bioinformatics*, **2008**, 9, www.biomedcentral.com/1471-2105/9/247

COMMUNICATIONS (LAST 5 YEARS)

R. Santamaría. Systems biology approaches to infectious diseases: a data perspective. *Invited talk. Integrating omic approaches to host-pathogen interactions*, EMBO, Liverpool **2013**.

R. Santamaría. Visualization of biological ontologies via Voronoi tessellations: introducing Voronto. *Invited talk. Oxford e-Research Center*, Univ. of Oxford, **2012**

R. Santamaría. Voronto: mapping expression into voronoi ontology tessellations. *Invited talk. Biomarkers for infectious fungal disease.*, CIML Marseille. **2012**

R. Santamaría. Statistical meta-analysis of transcriptomics data: immune response biomarkers of infectious diseases. *Invited talk. International Conference on Systems Biology*, Edinburgh. **2010**

Y. Chen, R. Santamaría, A. Butz and R. Therón.
TagClusters: Semantic Aggregation of Collaborative Tags beyond TagClouds in *Lecture Notes in Computer Science. Smart Graphics 2009*, 56–57, Salamanca. **2009**

OTHER MERITS

Graduate award by the University of Salamanca for the work *Galea: analizador experto de líneas gamma*

First award in the *14th Annual Graph Drawing Contest, Social Network Category*, of the 2007 Graph Symposium (Sydney, Australia).

Contribution to the package *biclust* for the Cran-R project.

<http://cran.r-project.org/web/packages/biclust>

Development of the tool BicOverlapper 2.0 for microarray analysis.

<http://carpex.usal.es/~visusal/bicoverlapper2>

Development of the tool Treevolution for the analysis of phylogenetic trees.

<http://carpex.usal.es/~visusal/treevolution>

Development of the tool Voronto for the analysis of gene ontologies.

<http://carpex.usal.es/~visusal/voronto>

Member of the MiDa and VisUsal research groups of the University of Salamanca.

Member of the International Society of Computational Biology (ISCB).

Reviewer for *Eurovis2008*, *Infovis2009* and *VAST2009*.

Reviewer for the journals *Bioinformatics*, *BMC Bioinformatics*, *Nucleic Acids Research* and *Pattern Recognition*.

September 16, 2014