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EDUCATION, QUALIFICATIONS AND TRAINING

05/2005-2009	**Researcher at the Artificial Intelligence and Soft Computing Department**, Informatics Faculty of Granada University. **Collaborator of the Molecular Biophysics Dpt.** at the German Cancer Research Center (DKFZ), Germany. **Collaborator of the Dpt. of Molecular Microbiology**, HMMI Washington University School of Medicine. St Louis, USA.
2002-05/2005	**Postdoctoral Fellow at the** DKFZ (German Cancer Research Centre), **Division of Molecular Genome Analyses** Prof. Annemarie Poustka and the **Dpt. of Molecular Biophysics**, HUSAR Bioinformatics Group. Im Neuenheimer Feld, Technologie Park 580, 69120 Heidelberg (Germany). Head of the Dpt.: Prof. Sandor Suhai
2000-2002	**Guest Scientist at the** DKFZ (German Cancer Research Center), **Dpt. of Molecular Biophysics**, HUSAR Bioinformatics Group. Im Neuenheimer Feld, Technologie Park 580, 69120 Heidelberg (Germany).Head of the Dpt.: Prof. Sandor Suhai
1999-2000	**Postdoctoral** fellow at the CSIC (Spanish Research Council), Dept. of Microbiology and Symbiotic Systems, Estación Experimental del Zaidin, Granada (Spain). Advisors: Prof. Concepción Azcon and J. Miguel Barea
1994-1999	**Ph.DThesis** at the CSIC (Spanish Research Council), Dept. of Microbiology and Symbiotic Systems, Estación Experimental del Zaidin, Granada (Spain). Advisors: Prof. Concepcion Azcon and J.Miguel Barea **Projects:** “Arbuscular Mycorrhizal Fungal Diversity in Heavy Metal Contaminated Soils” “Biotechnology and Ecological Interactions of Microbial Inoculants (IMPACT II)”. Qualification: ***“Sobresaliente cum laudem” equivalent to “Suma cum laudem”.***
1996	**COST:** Grant awarded for the exchange of scientists between countries.
1995	**XXXII International Edafology and Plant Biology UNESCO Master** (1039 hours), qualification A (outstanding). Granada University
1989-1994	**Degree:** Biological Science at the Faculty of Science, University of Granada. Specialisation: Biochemistry, Microbiology and Genetics (Spanish grade: expedient 3, 15 of 4, American equivalent: A)

PUBLICATIONS:

1. **del Val C**, Kuryshev VY, Glatting KH, Ernst P, Hotz-Wagenblatt A, Poustka A, Suhai S, Wiemann S: **CAFTAN: a tool for fast mapping, and quality assessment of cDNAs**. *Bmc Bioinformatics* 2006, 7.

2. Vinayagam A, **del Val C**, Schubert F, Eils R, Glatting KH, Suhai S, Konig R: **GOPET: A tool for automated predictions of Gene Ontology terms**. *Bmc Bioinformatics* 2006, 7.

3. Mehrle A, Rosenfelder H, Schupp I, **del Val C**, Arlt D, Hahne F, Bechtel S, Simpson J, Hofmann O, Hide W et al: **The LIFEdb database in 2006**. *Nucleic Acids Research 2006*, 34:D415-D418.

4. Giordano FA, Fehse B, Hotz-Wagenblatt A, Jonnakuty S, **del Val C**, Appelt JU, Nagy KZ, Kuehlcke K, Naundorf S, Zander AR et al: **Retroviral vector insertions in T-lymphocytes used for suicide gene therapy occur in gene groups with specific molecular functions.** *Bone Marrow Transplantation* 2006, 38(3):229-235.

5. Laufs S, Guenechea G, Gonzalez-Murillo A, Nagy KZ, Lozano ML, **del Val C**, Jonnakuty S, Hotz-Wagenblatt A, Zeller WJ, Bueren JA et al: **Lentiviral vector integration sites in human NOD/SCID repopulating cells.** ***Journal of Gene Medicin****e* 2006, 8(10):1197-1207.

6. Hose D, Rossi JF, Ittrich C, De Vos J, Reme T, Benner A, Mahtouk KN, **del Val C**, Moreaux J, Hotz-Wagenblatt A et al: **Molecular classification of multiple myeloma (MM) based on gene expression profiling (GEP) and fluorescence in situ hybridisation (FISH) is an independent predictor for event free survival (EFS)**. *Blood* 2005, 106(11):151A-152A.

7. **del Val C**, Mehrle A, Falkenhahn M, Seiler M, Glatting KH, Poustka A, Suhai S, Wiemann S: **High-throughput protein analysis integrating bioinformatics and experimental assays**. *Nucleic Acids Research* 2004, 32(2):742-748.

8. Cremer FW, De Vos J, Hose D, Rossi JF, Ittrich C, Reme T, Benner A, Jourdan E, Raab MS, Bila J, del **Val C** et al: **Multiple myeloma: Global expression profiling (GEP) indicates upregulation of the ribosomal machinery in hyperdiploid clones**. *Blood* 2004, 104(11):398A-398A.

9. **del Val C**, Glatting KH, Suhai S: cDNA2Genome**: A tool for mapping and annotating cDNAs**. *Bmc Bioinformatics* 2003, 4.

10. **del Val C**, Ernst P, Brauning R, Glatting KH, Suhai S: **PATH: a task for the inference of phylogenies**. *Bioinformatics* 2002, 18(4):646-647.

11. Leyval C, Joner EJ, **del Val C**, Haselwandter K: **Potential of arbuscular mycorrhizal fungi for bioremediation. In: Mycorrhizal Technology in Agriculture: from Genes to Bioproducts**. 2002: 175-186.

12. **del Val C**, Barea JM, Azcon-Aguilar C: **Assessing the tolerance to heavy metals of arbuscular mycorrhizal fungi isolated from sewage sludge-contaminated soils**. *Applied Soil Ecology* 1999, 11(2-3):261-269.

13. **Del Val C**, Barea JM, Azon-Aguilar C: **Diversity of arbuscular mycorrhizal fungus populations in heavy-metal-contaminated soils.** *Applied and Environmental Microbiology* 1999, 65(2):718-723.

14. J.M. Barea, E. Pérez Solis, **C. del Val** y C. Azcón-Aguilar. **“Importancia de las micorrizas en el establecimiento y protección de las plantas en suelos degradados”.** *Phytoma.* 1999 *Vol.* 111 (18-30).

PROCEEDINGS

1. Hose D, De Vos J, Ittrich C, Rossi JF, Reme T, Benner A, Mahtouk K, del Val C, Hotz-Wagenblatt A, Moreaux J et al: **A molecular classification of multiple myeloma (MM) based on gene expression profiling and fluorescence in situ hybridisation as independent prognostic factor for event free survival** (EFS). Ejc Supplements 2006, 4(6):34-35.

2. Romero-Zaliz R, Rubio-Escudero C, Cordon O, Harari O, **del Val C**, Zwir I: **Mining structural databases: An evolutionary multi-objetive conceptual clustering methodology.** In: Applications of Evolutionary Computing, Proceedings. vol. 3907. Berlin: Springer-Verlag Berlin; 2006: 159-171.

3. Rubio-Escudero C, Romero-Zaliz R, Cordon O, Harari O, **del Val C**, Zwir I: **Optimal selection of microarray analysis methods using a conceptual clustering algorithm.** In: Applications of Evolutionary Computing, Proceedings. vol. 3907. Berlin: Springer-Verlag Berlin; 2006: 172-183.

4. Rubio-Eseudero C, **del Val C**, Cordon O, Zwir I: **Decision making association rules for recognition of differential gene expression profiles.** In: Intelligent Data Engineering and Automated Learning - Ideal 2006, Proceedings. vol. 4224. Berlin: Springer-Verlag Berlin; 2006: 1137-1149.

PUBLICATIONS IN PREPARATION

1. **C. del Val,** P. Ernst, M. Falkenhahn, C.Fladerer,’ KH Glatting’ , S. Suhai’ and A. Hotz-Wagenblatt· **ProtSweep, 2Dsweep, and DomainSweep: protein analysis suite at DKFZ**. *Nucleic Acid Research Web Server Issue*, 2007. (Submitted)

2. **C. del Val**, E. Rivas, N. Toro and J. I. Jiménez-Zurdo. ***In silico*** **identification of small non-coding RNAs in the intergenic regions of the nitrogen-fixing symbiont *Sinorhizobium meliloti* by comparative genomics.** *Nucleic Acid Research. (in preparation)*

BIOINFORMATICS

Fields of expertise:

- **Development and implementation of fully automated tasks for high-throughput analysis identification, and annotation of genomes and proteins**. Software developed: **PATH** a task for the inference of phylogenies. **ProtSweep** (verion2): task for the identification of protein homologs and orthologs. **2Dsweep** a task for protein secondary structure prediction. **DomainSweep** task for protein domain architecture analysis, cDNA2genome task for the localization, identification and annotation of full-length cDNAs
- **Gene Expression Profile Analysis** for multiple myeloma and gene therapy
- **Gene prediction, Promoter analysis and DNA motifs analysis** (Gribskov Profiles, Hidden Markov Models, etc.)
- Algorithm design for cDNA mapping annotation and its automatic quality assessment using sequence information by rule based approaches
- SVM for the automatic annotation of unknown sequences using the GO Ontology
- Information quality assessment

RESEARCH PROYECTS

- *Project**:*** **Identificacion de informacion compleja en biologia: de colecciones de datos a conocimiento basado en redes organizadas** Ministerio de Ciencia y Tenologia **2004-2007.** *Main Researcher:* Igor Zwir

- *Project:* **Hibridacion de algoritmos evolutivos basada en colonias de hormigas. Aplicación al aprendizaje de bases de reglas difusas y aproblemas de Bioinformati** Ministerio de Ciencia y Tenologia **2003-2006.** *Main Researcher:* Oscar Cordon
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- *Project:* **German Human Genome Project (DHGP)** German Government **2001-2003.** *Main Researcher:* Sandor Suhai

- *Project:* **NGFN-1 German National Genome Research Network for the finding of genes involved in the onset of widespread diseases** German Government **2001-2003.** *Main Researcher:* Sandor Suhai

- *Project:* **German cDNA sequencing Consortium. German Human Genome Project**. German Government (DHGP/NGNF). **2001-2004.** *Main Researcher:* Stephen Wiemman

- *Project:* **REDMED. Restoration of degraded ecosystems in mediterranean regions (ref: ENV4CT97-0682)**. *EU* **1999 – 2000.** *Main Researcher:* José Miguel Barea Navarro

- *Project:* **Interaction between Microbial Inoculants and resident populations in the Rizosphere (IMPACT II) (ref. BIO 4-CT96-0027)** *EU.* **1996 – 1999.** *Main Researcher:* José Miguel Barea Navarro

- *Project:* **Microbial Diversity and Function in Metal Contaminated Soils (ref. EV5V-0415)** *EU.* **1994 – 1997.** *Main Researcher:* Concepción Azcón González de Aguilar

WORKSHOPS:

- **Course in Practical DNA Microarray Analysis**. 2006. DKFZ. Germany
- **BCB-Workshop on Gene Annotation Analysis and Alternative Splicing**. 12-14 December 2004. Max Plank Institute for Molecular Genetics, Berlin
- **R language**: November 2004. German Cancer Research Center. Heidelberg, Germany
- **Statistical analysis methods for mycroarray data:** 2-4 Februar 2004. German Cancer Research Center. Heidelberg, Germany.
- **EMBOSS programing course for developers** del 13-15 Januar 2004. European Bioinformatic Institute (EBI). Cambridge.
- **Bioinformatics for the management, analysis and interpretation of microarray data**. 26-28 November. Bolonia, Italia. NETTAB2003
- **Experimental designs and multivariant analisys.** 40 hours**.** CSIC, Granada. 2000
- **International Course on Bioinformatics.** EMBnet node, CNB, Madrid. 1999
- **Evolutionary Biology of the Glomales.** Copenhagen, 1995.
- **Biotechnology and Ecological Interactions of Microbial inoculants**. April 1997. Granada.
- **Molecular and Cellular approaches to gametic Embryogenesis**. July 1997. Granada.

TEACHING

2007	**Bioinformatic Module in the master "Soft Computing and Intelligent Systems".** Universidad de Granada, Departamento de Ciencias de la Computacion e inteligencia Artificial.
2005 -present	Computational Biology at the Informatics Faculty of Granada University
2005 -present	PhD courses of the Genetics Department of the Granada Univerity: Bioconductor and R And use of resources in the web for genome annotation
2000 - present	HUSAR Advance Bioinformatic Courses at the german Cancer Research Center
2002-2004	Lecturer assistant of the course "Databases searches, algorithms and sequence analysis" of the Biotechnology degree, Ruprecht-Karls-Universität **Heidelberg**.
2002-present	Lecturer assistant of the course "Bioinformatics"of the Informatics Medicine degree, Ruprecht-Karls-Universität **Heidelberg**.

2000 Organization and lecturer of the course **"Initiation Course on Bioinformatics for researchers**". Sponsored by CSIC (Spanish Research Council).

CONFERENCES

- **EVO-BIO 2006** Optimal Selection of Microarray Analysis Methods Using a Conceptual Clustering Algorithm. Applications of Evolutionary Computing, Rubio-Escudero, C., Romero-Zaliz, R., Cordón, O., Harari, O., del Val, C., Zwir, I. LNCS 3907, 2006.

- **EVO-BIO 2006** An Evolutionary Multi-Objective Conceptual Clustering Methodology. Applications of Evolutionary Computing Romero-Zaliz, R., Rubio-Escudero, C., Cordón, O., Harari, O., del Val, C., Zwir, I. Mining Structural Databases :, LNCS 3907, 2006.

- **Asociación Americana de Hematologia 2005**: Molecular classification of multiple myeloma by gene expression profiling and fluorescence in situ hybridisation delineates four groups predictive for event free survival. D.Hose, J. Rossi, C. Ittrich, J. De Vos, T. Rème, A. Benner, K. Mahtouk, C. del Val, J. Moreaux, A. Hotz-Wagenblatt, J. Moreaux, M. Raab, P. Kaukel, M. Moos, V. Grau, A. Jauch, E. Jourdan, H. Goldschmidt, B. Klein, F. W Cremer

- **MCCMB-2005** Caftan a strategy for cDNA quality assessment and quick frequent annotation update. C. del Val, V. Kurysev , K-H Glatting, A. Poustka , S. Suhai and S. Wiemann, Moscow, 2005

- **ECCB-2004.** ExpressMiner: Algorithm tool for Gene Expression data analysis. S. Jonnakuty, C.del Val, K-H Glatting and S. Suhai. Glasgow, 2004

- **HUGO 2004**. High-troughput protein análisis integrating bioinformatics and experimental assays. C. del Val, A. Mehrle, M. Falkenhahn, M. Séller, KH Glatting , A. Poustka , S. Suhai and S. Wiemann. Poster. Berlín (4-7 de Abril) Alemania, 2004.

- **VI Jornadas de Bioinformática y Biología Computacional**. The use of the W3H-Task-System for the design of custom-made automated analysis pipelines. C. del Val, P. Ernst, K-H Glatting , A. Hotz-Wagenblatt, M. Falkenhan, B. Pardon and S. Suhai. La Coruña, España 2003

- **ECCB-2003.** Annotation Tools in the W3H-Task-System: cDNA2Genome. C. del Val, P. Ernst, K-H Glatting and S. Suhai. Poster Paris, 2003

- **ECCB-2002.** Development of Annotation Tools in the W3H-Task-System. Poster C. del Val, P. Ernst, K-H Glatting and S. Suhai. Saarbücken, Germany,2002

- **DHGP (German Human Genome Project)**. Biocomputing support fot the DHGP (German Human Genome Project). C. del Val, P. Ernst, K-H Glatting , A. Hotz-Wagenplotz, M. Falkenhan, B. Pardon and S. Suhai. *Poste.* Leipzig, Germany: 2003

- **GCB German Conference on Bioinformatics**. The German EMBnet Node: GENIUSnet. C. del Val**,** R. Bräuning, P. Ernst, K-H Glatting and S. Suhai. Póster

- **Bioinformatics 2001**. PATH, Phylogenetic Analysis Task in HUSAR C. del Val, P. Ernst, R. Bräuning, K-H Glatting and S. Suhai .Póster. Skoevde, Suecia 2001

- **Second International Conference on Mycorrhiza.** Arbuscular mycorrhizal fungi diversity and tolerance in heavy metal contaminated soils. C. del Val, J.M. Barea y C. Azcón-Aguilar. Póster. Uppsala , Suecia 1998.

- **Sampling and Identification of Parasitic and Pathogenic Microorganisms in Agrobiology.** Strategy for the study of Arbuscular Mycorrhizal fungi diversity in metal contaminated soils. C. del Val, J.M. Barea y C. Azcón-Aguilar. Póster. Lisboa, Portugal 1997

- **Novel Biotechnological Approaches to Plant Production: from Sterile Root to Mycorrhizosphere.** C. del Val Pisa, Italia, 1996.

VISITING SCIENTIST IN OTHER RESEARCH CENTERS:

- **HMMI Washington University School of Medicine. St Louis, USA.** Dpt. of Molecular Microbiology, 2006. ; Permanent Collaborator
- **German Cancer Research Center (DKFZ)**, Dpt. of Molecular Biophysics, HUSAR Bioinformatics Group. October 2000- Mai 2005; Permanent Collaborator
- **European Bioinformatic Institute (EBI),** Hinxton Campus, EMBOSS Group. 12-16th Januar 2004. Course for EMBOSS developers.
- **CNRS, Centre de Pedologie Biologique Henri-Poincaré University**, Nancy, France, 1997. Two weeks stay, in order to identify with molecular biology techniques mycorrizhal fungi. European proyect EV5V-CT 94-0415.
- **Biology department at York University,** UK, 1996. Learning and development of new molecular techniques for the identification and characterization of MA fungi. Glomales Taxonomy.
- **INRA Station de genetique et D'amelioration des plantes**. Dijon, France 1995. One week, training in PCR techniques.

ADDITIONAL SCIENTIFIC ACTIVITIES:

- Reviewer for the following journals:
  Applied Bioinformatics, BMC Bioinformatics, Nucleic Acid Research and Computational Statistics.