

Marcel Brun - Curriculum Vitae



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Member of

- IEEE (USA) – Institute of Electrical and Electronics Engineers
- ISBC (USA) - The International Society for Computational Biology
- SABI (Argentina) – Sociedad Argentina de Bioingeniería
- SARP (Argentina) – Sociedad Argentina de Reconocimiento de Patrones
- A2B2C (Argentina) – Asociación Argentina de Bioinformática y Biología Computacional
- AMByG (Argentina) – Agrupación Marplatense de Bioinformática y Genómica

Current activities

- **Professor**
Department of Mathematics
School of Engineering
Universidad Nacional de Mar del Plata
Mar del Plata, Bs As, Argentina
- **Researcher**
Digital Image Processing Group
School of Engineering
Universidad Nacional de Mar del Plata
Mar del Plata, Bs As, Argentina
- **ViceDirector**
Departament of Mathematics
School of Engineering
Universidad Nacional de Mar del Plata
Mar del Plata, Bs As, Argentina

Research Interest

As a researcher I work on applications of pattern recognition principles to the area of biomedical imaging and genomic signal processing (GSP), which includes microarray data analysis, regulatory network modeling and biomarkers detection.

From 2000 I started working on the issues of clustering analysis for microarray data, while pursuing my Ph.D in computer sciences in the University of Sao Paulo, Brazil, and later while visiting Texas A&M University, Texas, in 2000 and 2002. In this work I developed the algorithms to show how data replications affects clustering results in microarray analysis, and collaborated in the design of an algorithm to select the best clustering algorithm for a specific dataset (Chen et al. 2000; Dougherty et al. 2002). This work resulted also in collaboration with the NHGRI, where I helped to implement the clustering algorithms for their online microarray analysis web page.

In 2003 I joined the Department of Biochemistry and Molecular Biology at the University of Louisville, Kentucky, as term professor, in charge of the microarray analysis and the development of a Matlab toolbox for automatism of the analysis pipeline, which were helpful in some of the research work ongoing in the lab (Stolf et al. 2003; Johnson et al 2004; Brun, Johnson and Ramos, 2005; Ramos et al 2007; Partridge et al. 2008).

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In 2004 I joined the Computational Biology group at the Translational Genomics Research Institute (TGen) in Arizona, as research associate and head of the algorithm development division. This stage allowed me to participate in many research projects, including microarray and SNP data analysis, the development of some algorithms to improve the analysis pipeline (Hua et al. 2007; Pearson et al. 2007), theoretical properties of regulatory network models (Brun, Dougherty and Shmulevich, 2005; Brun, Kim et al. 2007; Dougherty, Brun et al. 2009), and mainly on simulation studies to analyze the characteristics of classifier, feature selection and error estimation algorithms (Hsing et al. 2005; Choudhary et al. 2006; Dougherty and Brun 2006; Stafford and Brun 2007; Brun, Xu and Dougherty, 2008).

In the area of clustering analysis I was involved the evaluation of standard techniques and the application of clustering algorithm to data generated in the institute. I also collaborated in the development of clustering software for TGen's online microarray analysis web page, based on the previous experience with the NHGRI site. We used a probabilistic model for clustering developed earlier (Dougherty and Brun, 2004) to evaluate several clustering validation indices proposed in the literature for microarray data, revealing the weakness and strength of the most popular ones (Brun, Chao et al. 2007; Dalton et al. 2008)

I was able to participate in the "ADCC (Alzheimer's Disease Core Center)" project in 2006, where we developed a new algorithm for detection calls for the Affymetrix 500K SNP chip (Hua, Craig et al. 2007) and worked on new algorithms for association studies based on nonlinear relationships (Pearson et al 2007), and developed software tools for the management of the huge amount of data involved (1000 arrays with 500K SNP each). In this project we also started studying the issues involved with data balancing in classifiers design.

Actually I am sub-director of the Digital Image Processing group at the Signal Measurement and Processing Laboratory, University of Mar del Plata, co-directing a research project in biomedical image analysis, since 2007. Continuing the research direction from previous labs, I obtained a Young Researcher grant from the Agencia (PICT-06) to study error estimation techniques for classification of genomic data (Brun, Ballarin and Pagnuco 2010), and worked a project to determine SNP related to the quality of meat in collaboration with the Dr. Pablo Corva at the INTA (Gonzalez et al. 2010). During last years I dictated two graduate courses on GSP and clustering applied to microarray data, as part of the career of Ph.D. in Electronics, dictated a comprehensive seminar in GSP for professors for the School of Bioinformatics at the University of Entre Rios, and gave many talks in the topics in workshops and conferences (Brun 2008, Brun 2007, Brun 2006).

Software Development

In the are of software development, I was head of algorithm development at the Translational Genomics Research Institute in Phoenix, Arizona, developing and implementing several algorithms for genomics data analysis, having over 15 years of experience developing algorithms to solve some of the most complex issues facing biologists/companies today: gene network modeling, microarray analysis, pattern recognition techniques, signal processing and applying these to high throughput data, and the development of code for handling and analysis of large data sets can revolutionize your discoveries. The following list describes some of the commercial software developed during these years:

Programmer

Programming of software for commercial management in language Fox under D.O.S., XENIX and Windows.
Programming of information management software in language VBA, Argentina
From July 1991 to July 1996.

Researcher

Programming of algorithms for data processing, clustering, classification and visualization, applied to genomic data, in language C/C++ and Matlab, for University of Sao Paulo, University of Texas A&M, NIH and TGen, Brazil and USA.
1998-2007

Programmer

Programming of *Web on Disc* software for distribution of genomic data analysis results on HTML/Java/Javascript support, programmed in language Matlab, for Assuragen Inc., USA
2007

Programmer

Programming of software for data normalization and analysis in VBA language for Luminex Corp., USA

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2007-2008

Head of development

Programming of software for data normalization and analysis in VB.NET language for Luminex Corp. and Affymetrix Inc., USA

2008-2009

Head of development

Programming of software for newspaper ads detection and segmentation, for IBOPE, Brazil

2011-2012

Education

Sao Paulo University, Sao Paulo, Brazil

PhD in Computer Sciences, July 2002.

National University of Mar del Plata, Mar del Plata, Argentina

Bachelor in Mathematical Sciences, December 1997

ENET Nr. 1, Mar del Plata, Argentina

Electronic Technician, December 1989

Research experience

National University of Mar del Plata

Department of Mathematics, Engineering, Mar del Plata National University

Assistant Professor

Research on genomics signal processing and image processing.

Translational Genomics Research Institute.

Computational Biology Division

Associate Investigator and Senior Computational Scientist, since September 2004

Research on genomics signal processing and microarray data analysis

Dr. Kenneth Ramos. **Functional Genomics Lab**

Department of Biochemistry and Molecular Biology, University of Louisville, Louisville, KY

Research Associate, from October 2003 to August 2004

Research on genomics signal processing, microarray data analysis and clustering

Dr. Edward Dougherty. **Genomic Signal Processing Lab**

Department of Electrical Engineering, Texas A&M University, College Station, TX

Visiting Assistant Professor, from September 2002 to August 2003

Research on genomics signal processing and clustering.

Dr. Edward Dougherty. **CAMDI Lab**

Department of Electrical Engineering, Texas A&M University, College Station, TX

Visiting Scholar, from October 2000 to September 2001

Research on statistical design of morphological operators and small sample issues applied in genetic network inference.

Dr. Junior Barrera. **Bioinfo Lab**

Department of Mathematics and Statistics, University of Sao Paulo, Sao Paulo, SP, Brazil

PhD student, from January 1998 to July 2002

Research on statistical design of morphological operators, clustering and microarray data analysis.

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Teaching experience

Professor

National University of Mar del Plata
 Department of Mathematics, Engineering, Mar del Plata National University
 Since September 2013
 Courses: Numerical methods for engineers

Assistant professor

National University of Mar del Plata
 Department of Mathematics, Engineering, Mar del Plata National University
 Since February 2007 to September 2013
 Courses: Numerical methods for engineers

Visiting Assistant Professor

Electrical Engineering department
 Texas A&M University
 From September 2002 to May 2003
 Courses: Digital Signal Processing, Linear Circuit Analysis.

Teaching Assistant

Mathematics department - School of Exact and Natural Sciences
 National University of Mar del Plata. Argentina
 From July 1994 to December 1997
 With duties in: Geometry I, Logic and Introduction to Geometry, Mathematical Analysis II, Probability and Statistics, Topology, Real Functions and Mathematics I (for biology)

Teaching Assistant

Electronics Department - Engineering
 National University of Mar del Plata. Argentina
 From July 1996 to December 1996
 With duties in: Digital Image Processing

Scholarship and Grants

Period: 2012 a 2014
 Grant: Research
 Proyecto: Mathematical Morphology and Texture Models for Image Feature Extraction
 Place: Laboratorio de Procesamiento y Medición de Señales, Facultad de Ingeniería
 Universidad Nacional de Mar del Plata, Argentina
 Position: Researcher
 Agency: Universidad Nacional de Mar del Plata. Con evaluación externa.
 Project Nr.: 15G328
 Funding:
 Director: Virginia Ballarn
 Co-Director: Juan Ignacio Pastore

Period: January 2011 to December 2013
 Grant: Research
 Name: Pattern Recognition Techniques Applied to Genomic Signal Processing
 Place: Laboratorio de Procesamiento y Medición de Señales, Facultad de Ingeniería
 Universidad Nacional de Mar del Plata, Argentina
 Position: Director
 Agency: por: Universidad Nacional de Mar del Plata. Con evaluación externa.
 Project Nr.: 15/G299
 Funding: A\$ 1600

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Period: 2010 a 2012

Grant: Research

Name: Analysis and Classification of Biomedical Signals and Images

Place: Laboratorio de Procesamiento y Medición de Señales, Facultad de Ingeniería, Universidad Nacional de Mar del Plata, Argentina

Position: Co-Director

Agency: Universidad Nacional de Mar del Plata.

Project Nr.: 15G268

Funding: \$ 26.000

Period: 2008 a 2009

Grant: Research

Name: Classification and Analysis of Biomedical Signals and Images

Place: Laboratorio de Procesamiento y Medición de Señales, Facultad de Ingeniería Universidad Nacional de Mar del Plata, Argentina

Position: Co-Director

Agency: Universidad Nacional de Mar del Plata. Con evaluación externa.

Proyecto Nr.: 15G209

Funding: AR\$ 23.000

Period: February 2008 to March 2010

Grant: Scientific and Technologic Research 2006 – Young researchers

Name: Classifier error estimation applied to the analysis of high throughput genomic data

Place: Laboratorio de Procesamiento y Medición de Señales, Facultad de Ingeniería Universidad Nacional de Mar del Plata, Argentina

Agency: Agencia Nacional de Promoción Científica y Tecnológica – FONCyT - Argentina

Project Nr.: PICT-2006-02313

Period: May 1999 to July 2003

Scholarship: Graduate Student Scholarship

Name: Morphological operators design by statistical optimization.

Place: Laboratorio de Procesamiento de Imágenes, Instituto de Matemáticas y Estadística Universidad de San Pablo, Brasil

Agency: Fundación de apoyo a la investigación de San Pablo (FAPESP)

Period: March 1998 to March 1999

Scholarship: Technical Scholarship Category III

Project: Machine learning and mathematical morphology applied to OCR for faxes.

Place: Laboratorio de Procesamiento de Imágenes, Instituto de Matemáticas y Estadística

Agency: Fundación de apoyo a la investigación de San Pablo (FAPESP)

Period: October 1996 to October 1997

Scholarship: Undergraduate Student – Scientific Initiation

Name: Quantitative representation of the digital image's structural shape using mathematical morphology techniques.

Place: Laboratorio de procesamiento y medición de señales, Facultad de Ingeniería

Agency: Universidad Nacional de Mar del Plata.

Publications

Referred Journals

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1. A. Bouchet, D. S. Comas, J. I. Pastore, **M. Brun** and V. L. Ballarin, "Fuzzy Mathematical Morphology Toolbox and Graphical Interface", IEEE Latin America Transactions, Vol. 11, No. 4, pp. 1090 – 1096, June 2013
2. Marco E. Benalcázar, **Marcel Brun**, Virginia L. Ballarin, "Artificial Neural Networks Applied to Statistical Design of Window Operators", Pattern Recognition Letters, Vol. 34, Issue 9, pp. 970–979, July 2013. ISSN: 0167-8655
(Indexed in Thompson Reuters Journals Citations Reports)
3. Eduardo Blotta, Agustina Bouchet, **Marcel Brun**, Virginia Ballarin, "Characterization of bio-dynamic speckles through classical and fuzzy mathematical morphology tools", Signal Processing, Disponible online Iro de Febrero 2013, ISSN 0165-1684, 10.1016/j.sigpro.2013.01.001.
(Indexed in Thompson Reuters Journals Citations Reports)
4. Gonzalez M.A., Montini Ballarin F., **Brun M.**, Abraham G.A, Ballarin V., "*Morphological Quantification of Polymer Nanofibers in Tissue Engineering Images*", Latin American Applied Research, 42:89-95 (2012)
(Indexed in Research Alert, Science Citation Index Expanded, Current Contents/Engineering Index, Computing & Technology Index, Engineering Citation Index. It is also indexed by: Chemical Engineering & Biotechnology Abstracts (CEABA-VtB), Chemical Abstracts, LATINDEX, Periodica, UNCOVER.)
5. Bouchet Agustina, Pastore Juan Ignacio, Espin Andrade Rafael, **Brun Marcel**, Ballarin Virginia, "*AMBCL: Aritmetic Mean based in Compensatory Logic*", International Journal of Computational Intelligence and Applications, IJCA, Volume: 10, Issue: 2 (2011) pp. 231-243
(Indexed in Compendex, CompuScience, DBLP Computer Science Bibliography, Scopus)
6. Blotta Eduardo, Ballarin Virginia, **Brun Marcel**, Rabal Hector, "*Evaluation Of Speckle-Interferometry Descriptors To Measuring Drying-Of-Coatings*", Signal Processing, Volume 91, Issue 10, October 2011, Pages 2395-2403, doi:10.1016/j.sigpro.2011.05.002
(Indexed in Thompson Reuters Journals Citations Reports)
7. Agustina Bouchet, **Marcel Brun**, Virginia Ballarin (2010), "Morfología Matemática Difusa aplicada a la segmentación de angiografías retinales". Revista Argentina de Bioingeniería. Vol. 16, No. 1, pp. 7-10. Junio 2010. ISSN 0329-5257.
8. Lori Dalton, Virginia Ballarin and **Marcel Brun**, "*Clustering Algorithms: On Learning, Validation, Performance, and Applications to Genomics*", Current Genomics, Volume 10, Number 6, September 2009 , pp. 430-445(16)
9. Edward R. Dougherty, **Marcel Brun**, Jeffrey M. Trent, Michael L. Bittner, "*Conditioning-Based Modeling of Contextual Genomic Regulation*," IEEE/ACM Transactions on Computational Biology and Bioinformatics, vol. 6, no. 2, pp. 310-320, Apr.-June 2009, doi:10.1109/TCBB.2007.70247
10. Partridge CR, He Q, **Brun M**, Ramos KS., "*Genetic networks of cooperative redox regulation of osteopontin*", Matrix Biol. 2008 Jun;27(5):462-74. Epub 2008 Apr 18
11. **Marcel Brun**, Qian Xu, Edward R. Dougherty, "*Which is better: hold-out or full-sample classifier design?*" EURASIP Journal on Bioinformatics and Systems Biology, Volume 2008 (2008), Article ID 297945, 8 pages
12. Phillip Stafford, **Marcel Brun**, "*Three methods for optimization of cross-laboratory and cross-platform microarray expression data*", Nucleic Acids Res. 2007 May; 35(10): e72.
13. **Marcel Brun**, Seungchan Kim, Woonjung Choi, and Edward R. Dougherty, "*Comparison of network models via steady-state trajectories*", EURASIP Journal on Bioinformatics and Systems Biology, Volume 2007 (2007), 11 pages

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14. Jianping Hua, David W. Craig, **Marcel Brun**, Jennifer Webster, Victoria Zismann, Waibhav Tembe, Keta Joshipura, Matthew J. Huentelman, Edward R. Dougherty, and Dietrich A. Stephan, "*SNiPer-HD: improved genotype calling accuracy by an expectation-maximization algorithm for high-density SNP arrays*", *Bioinformatics* 23(1): pp. 57-63, 2007
15. Kenneth S. Ramos, Qiang He, Ted Kalbfleisch, Diego E Montoya-Durango, Ivo Teneng, Vilius Stribinskis, and **Marcel Brun**, "*Computational and biological inference of gene regulatory networks of the LINE-1 retrotransposon*". *Genomics*. 2007 August; 90(2): 176–185.
16. **Brun Marcel**, Sima Chao, Hua Jianping, Lowey James, Carroll Brent, Suh Edward, Dougherty Edward R., "*Model-based evaluation of clustering validation measures*", *Pattern Recognition*, 40 (3), pp. 807-824, 2007
17. John V. Pearson, Matthew J. Huentelman, Rebecca F. Halperin, Waibhav D. Tembe, Stacey Melquist, Nils Homer, **Marcel Brun**, Szabolcs Szelinger, Keith D. Coon, Victoria L. Zismann, Jennifer A. Webster, Thomas Beach, Sigrid B. Sando, Jan O. Aasly, Reinhard Heun, Frank Jessen, Heike Kölsch, Magdalini Tsolaki, Makrina Daniilidou, Eric M. Reiman, Andreas Papassotiropoulos, Michael L. Hutton, Dietrich A. Stephan, and David W. Craig, "*Identification of the genetic basis for complex disorders using pooling-based genome-wide SNP association studies*", *Am J Hum Genet*. 2007 January; 80(1): 126–139.
18. Edward R. Dougherty, **Marcel Brun**, "*On the Number of Close-to-Optimal Feature Sets*", *Cancer Informatics* 2006:2 pp. 189-196, 2006
19. Choudhary Ashish, **Brun Marcel** , Hua Jianping, Lowey James, Suh Edward, Dougherty Edward R., "*Genetic test bed for feature selection*", *Bioinformatic*, Vol. 22, No. 7, pp. 837-842, 2006.
20. **Brun M.**, Dougherty E. R., Shmulevich I., "*Attractors in Probabilistic Boolean Networks: Steady-State Probabilities and Classification* ", *Signal Processing*, Vol. 85, No. 10, pp. 1993-2013, 2005.
21. Hsing T., Liu L., **Brun M.**, Dougherty E., "*The coefficient of intrinsic dependence (feature selection using el CID)*", *Pattern Recognition* , 38 , pp.623-636 , 2005.
22. Johnson Charles D., Balagurunathan Yoga, Tadesse M., Falahatpisheh M.H., **Brun Marcel**, Dougherty Edward R., Walker M.K., Ramos K.S., "*Unraveling gene-gene interactions regulated by ligands of the aryl hydrocarbon receptor*", *EHP-Toxicogenomics* , 112 (4) , pp.403-412 , 2004
23. Dougherty E, **Brun M.**, "*A Probabilistic Theory of Clustering*", *Pattern Recognition*, 37 , pp.917-925 , 2004
24. **Brun M.**, Hirata Jr. R., Barrera J., Dougherty E., "*Nonlinear Filter Design Using Envelopes*", *Journal of Mathematical Imaging and Vision*, Vol. 21 (1), pp. 81-97, Jul 2004
25. Stolf, B. S.; Carvalho, A. F.; Maetins, W. K.; Runza, F. B.; **Brun, M.**; Hirata JR, R.; Neves, E. J.; Soares, F. A.; Kowalsk, L. P.; Postigo, J. e Reis, L. F. "*Differential expression of IGFBP-5 and two human ESTs are differentially expressed in thyroid diseases*". *Cancer Letters* Vol 191 (2), pp. 193-202, 2003.
26. **Brun M.**, Sabbagh D. L. , Kim S., Dougherty E. R., "*Corrected small-sample estimation of the Bayes error*", *Bioinformatics*, 19 (8), pp. 944-951, 2003
27. Hashimoto R. F., Dougherty E. R., **Brun M.**, Zhou Z., Bittner M. L., Trent J. M., "*Efficient Selection of Feature Sets Possessing High Coefficients of Determination Based on Incremental Determinations*", *Signal Processing*, Vol. 83 (4), pp. 695-712, April 2003
28. **Brun M.**, Dougherty E. R., Hirata Jr. R., Barrera J., "*Design of optimal binary filters under joint multiresolution-envelope constraint*", *Pattern Recognition Letters*, Vol. 24, 7, 2003, pp. 937-945
29. Dougherty E., Barrera J., **Brun M.**, Kim S., Cesar R.M., Chen Y., Bittner M., Trent J.M., "*Inference from clustering with application to gene-expression microarray*", *Journal of Computational Biology*, 9 (1), 2002, pp. 105-126

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30. Hirata Jr., **Brun M.**, R., Barrera J., Dougherty E., "Multiresolution Design of Aperture Operators", Journal of Mathematical Imaging and Vision, 16, 3, 199-222, 2002
31. Dougherty E., Barrera J., Mozelle G., Kim S, **Brun M.**, "Multiresolution Analysis for Optimal Binary Filters", Journal of Mathematical Imaging and Vision 14, 1, 53-72, 2001
32. Ballarin V., **Brun M.**, Moler E., "Scale invariant texture classification with mathematical morphology", Latin American Applied Research, Vol. 31: 79-82, 2001
33. **Barrera J., Dougherty E., Brun M.**, "Hybrid human-machine binary morphological operator design. An independent constraint approach", Signal Processing, Vol. 80 (8), pp.1469-1487 August 2000

Book Chapters

1. Agustina Bouchet, Juan Ignacio Pastore, Rafael Espin, **Marcel Brun**, Virginia Ballarin. "Compensatory Logic applied to Digital Image Processing", in Towards a trans-disciplinary technology of Business and Organizational Intelligence: Gathering Knowledge Discovery, Knowledge Management and Decision. Eds. Rafael A, Espin Andrade, Jorge Marx Gómez, Ariel Racet Valdéz. Chapter II, Knowledge Discovery, pages 226-239. Editorial: Shaker Verlag, Aachen, University of Oldenburg. Alemania, 2011. ISBN 978-3-8322-9718-3. ISSN 1863-8627
2. Roberto Hirata Jr., **Marcel Brun**, Junior Barrera, and Edward R. Dougherty, "Aperture filters: theory, application, and multiresolution analysis," Advances In Nonlinear Signal And Image Processing, eds. Sephen Marshall and Giovanni L. Sicuranza, EURASIP Book Series on Signal Processing and Communication, Hindawi Publishing Corporation, 2006.
3. **Brun Marcel**, Johnson Charles D., and Ramos Kenneth S., "Clustering: revealing intrinsic dependencies in microarray data," Genomic Signal Processing and Statistics, eds. E. R. Dougherty, I. Shmulevich, J. Chen, and Z. J. Wang, EURASIP Book Series on Signal Processing and Communication, Hindawi Publishing Corporation, 2005.
4. Barrera Junior, **Brun Marcel**, Terada Routo and Dougherty Edward R., "Boosting OCR Classifier by Optimal Edge Noise Filtering", in Mathematical Morphology and its Applications to Image and Signal Processing, eds. John Goutsias, Luc Vincent and Dan S. Bloomberg, Book Series on Computational Imaging and Vision, Vol 18, Springer US, 2002

Conferences

1. Lori A. Dalton, Marco Enrique Benalcazar Palacios, **Marcel Brun**, Edward R. Dougherty, "Bayes Clustering Operators for Known Random Labeled Point Processes", Accepted at Asilomar Conference on Signals, Systems, and Computers, Pacific Grove, California, USA, November 3-6th, 2013
2. Marco E. Benalcázar, **Marcel Brun**, y Virginia L. Ballarin, "Segmentación de Vasos Sanguíneos en Angiografías Retinales usando Ensamblados de Filtros Aperture", 3rd IIITEC International Symposium on Innovation and Technology ISIT2012, 26 al 28 de Noviembre de 2012, Cusco, Perú. ISBN 978-612-45917-3-0. ISSN 2305-9958. Organizado por Instituto Internacional de Innovación y Tecnología (IIITEC)
3. J. I. Pastore, A. Bouchet, E. L. Blotta, **M. Brun**, V. L. Ballarín, "Segmentación de ventrículos en imágenes de RMN de cerebro utilizando Morfología Matemática", 3rd IIITEC International Symposium on Innovation and Technology ISIT2012, 26 al 28 de Noviembre de 2012, Cusco, Perú. ISBN 978-612-45917-3-0. ISSN 2305-9958. Organizado por Instituto Internacional de Innovación y Tecnología (IIITEC)
4. **Brun Marcel**, Pagnuco Inti Anabella, Ballarin Virginia, "Advantages of balanced classifier design on microarray data classification", 3er Congreso Argentino de Bioinformática y Biología Computacional, organizado por la Asociación Argentina de Bioinformática y Biología Computacional. Universidad Nacional de Entre Rios, Oro Verde, Entre Rios, Argentina, 26, 27 y 28 de Septiembre de 2012.

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5. Marco Benalcázar, **Marcel Brun**, Virginia Ballarin, Isabel Passoni, Gustavo Meschino, and Lucía Dai Pra, “Automatic Design of Binary W-Operators Using Artificial Feed-Forward Neural Networks Based on the Weighted Mean Square Error Cost Function”, 17th Iberoamerican Congress in Pattern Recognition CIARP 2012. Alvarez et al. (Eds.): CIARP 2012, LNCS 7441, pp. 495--502. Springer, Heidelberg (2012)
6. Agustina Bouchet, Juan Ignacio Pastore, Rafael Espin Andrade, **Marcel Brun**, Virginia Ballarin, *Morfología Matemática Compensatoria aplicada a la segmentación de imágenes médicas*. Tercer Taller Internacional de Descubrimiento de Conocimiento, Gestión del Conocimiento y Toma de Decisiones, organizado por la Red Iberoamericana de Descubrimiento de Conocimientos (Eureka Iberoamérica), la Universidad de Cantabria y la Universidad de Oldenburgo. Universidad de Cantabria, Santander, España. 26 al 28 de Octubre de 2011.
7. Agustina Bouchet, Juan Ignacio Pastore, Rafael Espin Andrade, **Marcel Brun**, Virginia Ballarin, *Lógica Difusa Compensatoria basada en la Media Aritmética*. Tercer Taller Internacional de Descubrimiento de Conocimiento, Gestión del Conocimiento y Toma de Decisiones, organizado por la Red Iberoamericana de Descubrimiento de Conocimientos (Eureka Iberoamérica), la Universidad de Cantabria y la Universidad de Oldenburgo. Universidad de Cantabria, Santander, España. 26 al 28 de Octubre de 2011.
8. Benalcázar Marco, Padín Jimena, **Brun Marcel**, Pastore Juan Ignacio, Ballarin Virginia, Peirone Laura, Pereyra Irujo Gustavo. *Measuring Leaf Area in Soy Plants by HSI Color Model Filtering and Mathematical Morphology*. XVIII Congreso Argentino de Bioingeniería (SABI 2011). Mar del Plata, Bs. As., Argentina. 28 al 30 de Septiembre de 2011.
9. Andréa Britto Matos, Igor dos Santos Montagner, Alexandre Crivellaro, Bruno Klava, **Marcel Brun**, “Computer vision research at IBOPE Media: automation tools to reduce human intervention”, en XXIV Sibgrapi – Conference on Graphics, Patterns and Images, 28 al 31 de Agosto de 2011, Maceió, Alagoas, Brasil.
10. Benalcázar Marco, Padín Jimena, Bouchet Agustina, **Brun Marcel**, Ballarin Virginia, “Diseño Automático de Operadores Morfológicos Aplicado a la Segmentación de Angiografías Retinales”, aceptado para CAIS 2011, 2do Congreso Argentino de Informática y Salud, 39 JAIIO, Córdoba, Argentina, 29 de Agosto al 2 de Septiembre del 2011.
11. Ballarin Virginia, Gonzalez Mariela Azul, Abraham Gustavo, Montini Ballarin Florencia, **Brun Marcel**, *Cuantificación de la morfología en imágenes de nanofibras poliméricas para Ingeniería de Tejidos*, V Congreso Latinoamericano de Ingeniería Biomédica (CLAIB2011), Habana, 16 al 21 de Mayo de 2011.
12. Gonzalez M. Azul, Montini Ballarin Florencia, Brun Marcel, Abraham Gustavo, Ballarin Virginia, “Caracterización de la morfología de imágenes de Soportes para Ingeniería de Tejidos”, accepted for CAIS 2010, 1er Congreso Argentino de Informática y Salud, 38 JAIIO, Buenos Aires, Argentina, August 30 to September 3, 2010.
13. Abras Guillermo, Pastore Juan Ignacio, Brun Marcel, Ballarin Virginia, “Detección de Conjuntos Significativos de Genes via Silhouette”, accepted for CAIS 2010, 1er Congreso Argentino de Informática y Salud, 38 JAIIO, Buenos Aires, Argentina, August 30 to September 3, 2010.
14. Marcel Brun, Virginia Ballarín, Inti Anabela Pagnuco, “Diseño Balanceado de Clasificadores para Estudios de Asociación poligenética”, accepted for CAIS 2010, 1er Congreso Argentino de Informática y Salud, 38 JAIIO, Buenos Aires, Argentina, August 30 to September 3, 2010.
15. Agustina Bouchet, Juan Ignacio Pastore, Rafael Espin, **Marcel Brun**, Virginia Ballarin. “A Arithmetic Mean Based Compensatory Logic”, ALIO-INFORMS Joint International Meeting. Buenos Aires, Argentina. 6 al 9 de Junio de 2010.
16. Agustina Bouchet, Juan Ignacio Pastore, Rafael Espin, **Marcel Brun**, Virginia Ballarin, “Compensatory Logic Applied to Digital Image Processing”, ALIO-INFORMS Joint International Meeting. Buenos Aires, Argentina. 6 al 9 de Junio de 2010.

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17. Brun Marcel, Ballarin Virginia, “Data Balancing for Phenotype Classification Based on SNPs.”, 1er Congreso Argentino de Bioinformática y Biología Computacional, organizado por la Asociación Argentina de Bioinformática y Biología Computacional. Universidad Nacional de Quilmes, Quilmes, Bs. As., Argentina, 12, 13 y 14 de Mayo de 2010.
18. Agustina Bouchet, Juan Ignacio Pastore, Rafael Espin, **Marcel Brun**, Virginia Ballarin. “*Lógica Compensatoria Aplicada al Procesamiento digital de imágenes*”. Segundo Taller de Descubrimiento de Conocimiento, Gestión del Conocimiento y Toma de Decisiones, organizado por la Red Iberoamericana de Descubrimiento de Conocimientos (Eureka Iberoamérica) y el Proyecto Evaluación y Potenciación de Infraestructura de Datos Espaciales en Iberoamérica y el Caribe. Ciudad de Panamá. Panamá. Noviembre de 2009.
19. Agustina Bouchet, **Marcel Brun** y Virginia Ballarin, “*Morfología Matemática Difusa aplicada a la segmentación de angiografías retinales*”. XVII Congreso Argentino de Bioingeniería (SABI 2009). Rosario, Santa Fe, Argentina. Octubre de 2009.
20. M. Gonzalez, M.; **Brun, Marcel**; Corva, Pablo y V. L. Ballarin, “*Clasificación de razas bovinas por un número reducido de SNPs*”, XVII Congreso Argentino de Bioingeniería- VI Jornadas de Ingeniería Clínica (SABI), ISBN: 978-950-605-505-9, Polo Tecnológico Rosario, 2009.
21. Agustina Bouchet, **Marcel Brun** y Virginia Ballarin, “*Análisis comparativo de robustez entre operadores morfológicos clásicos y difusos para detección de bordes*”, RPIC 2009, XIII Reunión de Trabajo en Procesamiento de la Información y Control, 16 al 18 de Setiembre de 2009, Rosario, Argentina
22. Benalcázar Palacios F., Bouchet A., **Brun M.** y Ballarin V “*Análisis comparativo de robustez entre filtros morfológicos clásicos y difusos aplicados al Procesamiento Digital de Imágenes*”. 38° Jornadas Argentinas de Informática (JAIIO 2009). Mar del Plata, Buenos Aires, Argentina. Agosto de 2009.
23. Mariela A. Gonzalez, **Marcel Brun**, Pablo M. Corva, Virginia Ballarin, “*Análisis de señales genómicas para la clasificación de razas bovinas*”, CAI 2009, 1er Congreso Argentino de Agroinformática, in the 38 JAIIO, Mar del Plata, Argentina, 24-28 de Agosto 2009.
24. Agustina Bouchet, **Marcel Brun**, Virginia Ballarin, “*Análisis comparativo de robustez entre operadores morfológicos clásicos y difusos aplicados al Procesamiento Digital de Imágenes*”, SSI 2008 - Simposio sobre la Sociedad de la Información, in the 37 JAIIO, Santa Fe, Argentina, 8-12 September 2008
25. **Marcel Brun**, Qian Xu, Edward R. Dougherty, *A Criterion for Choosing between Full-sample and Hold-out Classifier Design*, IEEE International Workshop on Genomic Signal Processing and Statistics, 2008. GENSIPS 2008. Phoenix, AZ, USA, 8-10-June 2008
26. Agustina Bouchet, Mariela Azul Gonzalez, Juan Ignacio Pastore, Virginia Ballarin, **Marcel Brun**, “*Algoritmo goloso de selección de características aplicado a datos de microarray*”, MACI 2007: Procesamiento de Señales, Facultad de Cs. Exactas, Físicas y Naturales - UNC, Ciudad de Córdoba, Córdoba, Argentina, 2007
27. Yufang Yin, Yufei Huang, Viji Shanmugam, **Marcel Brun**, Jianping Hua, Edward Dougherty, “*A Bayesian approach for uncovering gene network motifs*”, Fifth IEEE International Workshop on Genomic Signal Processing and Statistics, June 10-12, 2007, Tuusula, Finland (GENSIPS 2007)
28. Darin M. Taverna, **Marcel Brun**, Edward R. Dougherty, Yidong Chen, “*Quality-based distance measures and applications to clustering*”, 2nd IEEE/NLM International Workshop on Life Science Systems and Applications, Bethesda, Maryland, 2006 (LSSA 2006)
29. **Marcel Brun**, Edward R. Dougherty, “*Clustering algorithms do not learn, but they can be learned*”, Proc. SPIE Int. Soc. Opt. Eng. 5916, 59160T (2005)

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30. **Brun, Marcel**; Balagurunathan, Yoganand; Barrera, Junior; Dougherty, Edward R., "*Clustering granulometric features*", Proc. SPIE, Image Processing: Algorithms and Systems, Edward R. Dougherty; Jaakko T. Astola; Karen O. Egiazarian; Eds., Vol. 4667, p. 36-42, 2002
31. **Brun M.**, Barrera J., Hirata N., Trepode W., Dantas D., Terada R., "*Multi-resolution Classification Trees in OCR Design*", Proceedings of the SIBGRAPI 2001, pp. 59-66, October 2001, Florianópolis, Brazil.
32. **Brun M.**, Hirata R., Barrera J., Dougherty E.R., "*Hybrid Human-machine Non-linear Filter Design Using Envelopes*", Proceedings of the SIBGRAPI 2001, pp. 106-112, October 2001, Florianópolis, Brazil.
33. Dougherty E.R., Barrera J., **Brun M.**, Kim S., Marcondes R., Chen Y., Bittner M.L., Trent J.M., "*Time series inference from clustering*", Proc. SPIE Vol. 4266, p. 222-227, Microarrays: Optical Technologies and Informatics, Michael L. Bittner; Yidong Chen; Andreas N. Dorsel; Edward R. Dougherty; Eds., January 2001
34. Hirata Jr. R., **Brun M.**, Barrera J., Dougherty E.R., "*Image Restoration by Multiresolution Non-linear Filters*", Proc. SPIE Vol. 4304, p. 256-264, Nonlinear Image Processing and Pattern Analysis XII, Edward R. Dougherty; Jaakko T. Astola; Eds., January 2001
35. Chen Y., Jiang Y., Dougherty E., Kim S., Yakhini Z., Ben-Dor A., Sampas N., Radamacher M., Simon R., **Brun M.**, Gubitoso M.D., Barrera J., Gooden C., Glatfelter A., Meltzer P., Trent J., Bittner M.L., "*Estimating the reliability of inferences based on cDNA microarray ratio data*", en Beyond the Identification of Transcribed Sequences: Functional and Expression Analysis, Heidelberg, Germany, October 2000
36. Barrera J., **Brun M.**, Terada R., Dougherty E., "*Boosting OCR classifier by optimal edge noise filtering*", ISMM 2000, International Symposium on Mathematical Morphology and its Applications to Image and Signal Processing V, June 26-28, 2000, Palo Alto, California, USA
37. Dougherty E., Kim S., Mozelle G., Barrera J., **Brun M.**, "*Multiresolution Filter Design*", Proc. SPIE Vol. 3961, p. 12-21, Nonlinear Image Processing XI, Edward R. Dougherty; Jaakko T. Astola; Eds., January 2000
38. J. Barrera, E. R. Dougherty and **M. Brun**, "*Hybrid human-machine binary morphological operator design*", Proc. SPIE Vol. 3646, p. 162-173, Nonlinear Image Processing X, Edward R. Dougherty; Jaakko T. Astola; Eds., January 1999
39. Barrera J., **Brun M.**, "*Translation Invariant Transformation of Discrete Random Sets*", Proceedings of the SIBGRAPI 98, pp. 450-455, INPA, Rio de Janeiro, October 1998
40. **M. Brun**, E. Moler, V. Ballarin, "*Scale Invariant Texture Classification With Mathematical Morphology*", EUSPICO 98, Rhodes, Greece, September 1998
41. **M. Brun**, V. Ballarin, E. Moler, M. Gonzalez, F. Schleich, "*Una optimización en el cálculo de máscaras espaciales a partir de especificaciones del dominio frecuencial para realce de imágenes*", VII RPIC, San Juan, Argentina, September 1997

Workshops and posters

1. Pagnuco Inti Anabella, **Brun Marcel**, Ballarin Virginia, "*Comparison of Classifier Design Algorithms on a Small Sample Microarray Data*", 3er Congreso Argentino de Bioinformática y Biología Computacional, organizado por la Asociación Argentina de Bioinformática y Biología Computacional. Universidad Nacional de Entre Ríos, Oro Verde, Entre Ríos, Argentina, 26, 27 y 28 de Septiembre de 2012.
1. **Brun Marcel**, Ballarin Virginia, "*Bolstered Error Estimation for Discrete Classifier Applied to Genomic Signal Processing*", 1er Congreso Argentino de Bioinformática y Biología Computacional, organizado por la Asociación Argentina de Bioinformática y Biología Computacional. Universidad Nacional de Quilmes, Quilmes, Bs. As., Argentina, 12, 13 y 14 de Mayo de 2010.

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2. Juan Ignacio Pastore, Guillermo Abras, Diego Comas, **Marcel Brun**, Virginia Ballarin, “Gene Selection via Significant Subsets using Silhouette Index”, 1er Congreso Argentino de Bioinformática y Biología Computacional, organizado por la Asociación Argentina de Bioinformática y Biología Computacional. Universidad Nacional de Quilmes, Quilmes, Bs. As., Argentina, 12, 13 y 14 de Mayo de 2010.
3. **Marcel Brun**, Qian Xu and Edward R. Dougherty, “*A Criterion For Choosing Between Full-Sample And Hold-Out Classifier Design*”, GENSIPS 2008: IEEE International Workshop on Genomic Signal Processing and Statistics, Phoenix, Arizona, June 8-10, 2008
4. Jianping Hua, David Craig, **Marcel Brun**, Jennifer Webster, Matthew Huentelman, Edward Dougherty, Dietrich Stephan, “*SNiPer 500K: A Novel SNP Genotype Calling Algorithm*”, 2nd IEEE/NLM International Workshop on Life Science Systems and Applications, 2006 (LSSA 2006)

Invited Talks

1. **Marcel Brun**, “Clustering: Modelado probabilístico, Aprendizaje, Validación y aplicaciones en Bioinformática”, SSI 2008 - Simposio sobre la Sociedad de la Información, in the 37 JAIIO, Santa Fe, Argentina, 8-12 September 2008.
2. **Marcel Brun**, “*Comparison of gene regulatory networks via steady-state trajectories*”, X-meeting 2007 - 3rd International Conference of the Brazilian Association of Bioinformatics and Computational Biology – AB3C. November 1-3, 2007
3. **Marcel Brun**, “*Clustering: Probabilistic Modeling, Learning and Validation*”, Training Program in Bioinformatics, Texas A&M University, October 26 2006.
4. **Marcel Brun**, “*Bayes Clusterer*”, Workshop on Mathematical Methods in Imaging and Vision, Department of Mathematics, University of Florida, January 24 to 27, 2004

Current training of human resources

1. Juan Ignacio Pastore – “Segmentación de estructuras y texturas en Imágenes Biomédicas Color utilizando Morfología Matemática Color” – Co-Director – **PostDoc Student** – CONICET Scholarship
2. Agustina Bouchet – “Morfología Matemática Difusa Aplicada a la Segmentación de Imágenes Biomédicas” – Co-Director – **PostDoc Student** – CONICET Scholarship
3. Facundo Orts – “Redundancia y Diversificación Funcional de Sedolisinas y Subtilisinas de Hongos fitopatógenos” – Co-Director – **PhD Student** – CONICET Scholarship
4. Maria Victoria Revuelta – “Caracterización de Peptidasas Ácidas del Hongo Planta-Patógeno Botrytis cinerea” – Co-Director – **PhD Student** – CONICET Scholarship
6. Inti Pagnuco – “: Técnicas de clasificación supervisada aplicadas a datos genéticos de alta densidad” – Director – **PhD Student** – CONICET Scholarship
7. Marco Benalcazar Palacio – “Aprendizaje computacional y morfología matemática aplicados al procesamiento de imágenes biomédicas” – Director – **PhD Student** – CONICET Scholarship

Past training of human resources

1. Freddy Benalcazar Palacios. “Aplicación de Morfología Matemática Difusa al filtrado de imágenes de RMN”, Co-director - Master Thesis at the Instituto Balseiro. July 2008 to December 2008
2. Jimena Padin – “Diseño semi-automático de operadores morfológicos aplicado a imágenes biomédicas” – Director – Ph.D. student with CONICET.
3. Mariela Azul Gonzalez. “Segmentación de Imágenes Médicas Mediante la Transformada Watershed (2007-2008)” – Co-director – Postdoc with CONICET scholarship.
4. Agustina Bouchet. “Segmentación de Imágenes Médicas mediante Técnicas de Morfología Matemática Difusa”. Co-Director - Ph.D. student with CONICET scholarship.

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5. Inti Pagnuco – “Clasificación de fenotipos basado en SNP” – Director – Undergraduate Thesis at school of Bioinformatics of the University of Entre Rios.

Reviewer activity

Journals

1. IEEE Latin American
2. EURASIP Journal on Bioinformatics and Systems Biology (2006)
3. Bioinformatics
4. EURASIP
5. IEEE Signal Processing
6. BMC Bioinformatics
7. Journal of Biological Systems (JBS)
8. Pattern Recognition
9. International Scholarly Research Network (ISRN)

Conferences

1. CIARP 2012 - 17th Iberoamerican Congress on Pattern Recognition.
2. SABI 2011 – XVIII Congreso Argentino de Bioingeniería, Mar del Plata, Argentina
3. CIARP 2010 – 15th Iberoamerican Congress On Pattern Recognition. Sao Paulo, Brazil
4. CAIS 2010 - Congreso Argentino de Informática y Salud, dentro de la JAIIO 2010 (39th Jornadas de Argentinas de Informática, Buenos Aires, Argentina)
5. SABI 2009 – XVII Congreso Argentino de Bioingeniería, Rosario, Argentina
6. LSSA 2006 – 2nd IEEE/NLM International Workshop on Life Science Systems and Applications, Bethesda, Maryland, USA.
7. GENSIPS 2005 – Workshop on Genomic Signal Processing and Statistics. May 22-25. Newport, Rhode Island.
8. SIBGRAPI 2001 – 14th Brazilian Symposium on Computer Graphics and Image Processing, October 15-18 Florianopolis, Brazil. IEEE Computer Society.

Participation in Conferences As Comitee Member

1. SABI 2011 – XVIII Congreso Argentino de Bioingeniería, Mar del Plata, Argentina.
2. Primer Taller Marplatense de Bioinformática y Genómica, 11 Nov 2011, Mar del Plata, Argentina
3. Segundo Taller Marplatense de Bioinformática y Genómica, 3 Mar 2012, Mar del Plata, Argentina
4. Tercer Taller Marplatense de Bioinformática y Genómica, 1 Mar 2013, Mar del Plata, Argentina

Courses

Geostatistics

Dr. Javier Samper, Universidad de la Coruña, Spain
School of Exact and Natural Sciences. Mar del Plata National University, Argentina

B-Tree and their implementation

Valdemar Setzer, USP San Pablo, Brazil
Informatics sciences School 1993
School of Exact and Natural Sciences. Buenos Aires University, Argentina

Robotic Vision

Dr. Antonio Martinez, Univ. Politéc. de Cataluña, Spain
Informatics sciences School 1994
School of Exact and Natural Sciences. Buenos Aires University, Argentina

Morphological Methods in Image Processing

Dr. Jorge Lira, Instituto de geofisica, UNAM, Mexico
Informatics sciences School 1994

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School of Exact and Natural Sciences. Buenos Aires University, Argentina

Autosimilarity, Fractal Geometry and Image Processing

Ursula Mölter, U.B.A, Argentine

XLV Meeting of the Argentine Mathematical Union 1995

School of Exact and Natural Sciences. Rio Cuarto National University, Argentina