

Certainly my statement and motivation have not changed since last year candidacy, so here again is my experience in relation to ISB goals:



I've started in the biocuration field in 2005, and since then I've been an active biocurator in various projects (UniProt, Protein Ontology, and Literature mining). Though I would be considered a "junior" candidate, I believe I can bring new perspectives to the Society.

Aligned with the goals of the society, I have worked on outreach activities as part of the Protein Ontology project, organizing the annual protein ontology meetings and running the annotation tutorials (including one at the last Biocurator meeting). I also have vast experience in reaching out to students (to prepare and engage the next generation of biocurators). In this respect, at the Protein Information Resource (PIR) we have an annotation program for summer interns (both at the Master and high school levels) where students are given small projects and gain some experience in searching protein-related databases, in reading scientific literature, and in extracting information for annotation purposes.

Another important focus of the society is to foster connections with user communities to ensure that the databases and accompanying tools meet specific user needs. Related to this aspect, I have recently been involved in discussions with the text mining community with the goal of addressing the curator's need (biocurators being the user community in this case). I participated in the discussions leading to the organization of the text mining workshop at the 3rd Biocurator meeting, and as outcome of the workshop we conducted a survey for curators to find out what tools the curators are using, or would like to use. This survey inspired the organization of the interactive task in Biocreative III (<http://www.biocreative.org/tasks/biocreative-iii/iat/>) in which I am involved as an organizer. The aim of this task is to provide the component modules for text mining services for biocuration. In particular, to support real-life tasks by combining multiple text mining tasks to retrieve literature and extract relevant information, and provide results that can be integrated in the curation workflow. In this initiative, the involvement of biocurators is essential, and for this reason, I've been chairing a User Advisory Group composed of representatives from various major databases and pharma industry to come up with the proposed task and specification of the text mining systems as well as to test the developed systems. The results from these activities will likely guide the development of future text mining tools. I have also interacted with the research community to address their need through the help desk at PIR. I managed the help desk for 3 years, and have responded to the best extent to their needs.

In brief, I would like to actively participate in the ISB Executive Committee promoting biocuration activities and foster collaborations to address the community needs.

I hope I can bring my experience and enthusiasm to the ISB Executive Committee!

Thanks for reading about me!

Cecilia Arighi

My profile: http://bioinformatics.udel.edu/People/Cecilia_Arighi
<http://www.linkedin.com/in/ceciliaarighi>

Websites: <http://www.proteininformationresource.org>
<http://www.uniprot.org>
<http://www.biocreative.org>

Education

Institution	Degree	Date	Field
University of Buenos Aires, Argentina	B.S.	1996	Biological Sciences
University of Buenos Aires, Argentina	Ph.D.	2001	Biological Chemistry
National Institutes of Health, MD	Postdoc.	2004	Cell Biology

Positions and Employment

1992-1996	Research Assistant, Dept. Biological Chemistry, School of Pharmacy and Biochemistry, UBA, Argentina.
2001-2005	Postdoctoral Fellow. Laboratory of Dr. Juan S. Bonifacino, NICHHD, NIH
2005-2009	Research Assistant Professor, Dept. Biochemistry and Molecular Biology, Georgetown University Medical Center (GUMC)
2009-Present	Research Assistant Professor. Dept. Computer and Information Sciences, University of Delaware

Honors (in US)

2001-2003	PEW Trust Latin American Fellowship for the Biomedical Sciences
2003-2005	National Institutes of Health Visiting Fellowship
2008	Fellowship for Computational and Comparative Genomic Course at Cold Spring Harbor Laboratory

Service (in US)

2004-	Reviewer for BMC Bioinformatics, BMC genomics, and ISMB conference papers.
2007-Present	Organizer of the Protein Ontology Workshops and the Protein Ontology Annotation Jamboree.
2008	Thesis committee member for Linshan Yuan, M.S. in Biostatistics (GUMC)
2009-Present	Member of the International Society for Biocurators.
2010	Organizer of the BioCreative III workshop.
2010	Organizer of the PIR workshop at the Plant and Animal Genome meeting.

Teaching (in US)

2005-2009	Lecturer in graduate level bioinformatic-related courses at GUMC: TBIO-530 and BCHB521
2006-Present	Proteomics Workshop, FAES, NIH. Instructor.
2008-Present	Bioinformatics Workshop. FAES, NIH. Instructor.

Selected Publications**Book Chapters**

1. [Cecilia Arighi](#), Amy Siu, Catalina O Tudor, Jules Nchoutmboube, Cathy H Wu, and K Vijay-Shanker, *eFIP: A Tool for Mining Functional Impact of Phosphorylation from Literature*, Bioinformatics for Comparative Proteomics. A volume in *Series Methods in Molecular Biology*. Humana Press. (in press).
2. [Cecilia Arighi](#). *A Tutorial on Protein Ontology Resources for Proteomic Studies*. Bioinformatics for Comparative Proteomics. A volume in *Series Methods in Molecular Biology*. Humana Press. (in press).

Refereed Publications (* Co-first authorship)

3. [Arighi CN](#), Hartnell LM, Aguilar RC, Haft CR, Bonifacino JS. Role of the mammalian retromer in sorting of the cation-independent mannose 6-phosphate receptor. *J Cell Biol.* 165(1):123-133 (2004) [PMC2172094].
4. Anastasia N. Nikolskaya, [Arighi C.](#), Hongzhan Huang, Winona C. Barker and Cathy H. Wu PIRSF Family Classification System for Protein Functional and Evolutionary Analysis. *Evolutionary Bioinformatics Online* 2, 209-221 (2006) [PMC2674652].
5. Natale DA, [Arighi CN*](#), Barker W, Blake J, Chang T, Hu ZZ, Liu H, Smith B, Wu CH. Framework for a Protein Ontology. *BMC Bioinformatics* 8(Suppl 9):S1, 2007 [PMC2217659].
6. Huang H, Hu ZZ, [Arighi C](#), Wu CH. Integration of Bioinformatics Resources for Functional Analysis of Gene Expression and Proteomic Data. *Frontiers in Biosciences* 12, 5071-5088, 2007 [PMID:17569631]
7. Anna M. Masci, [Cecilia N. Arighi](#), Alexander D. Diehl, Anne E. Lieberman, Chris Mungall, Richard H. Scheuermann, Barry Smith, and Lindsay G. Cowell, "An improved ontological representation of dendritic cells as a paradigm for all cell types", 2009 *BMC Bioinformatics* 10:70 [PMC2662812].
8. [Cecilia Arighi](#), Hongfang Liu, Darren Natale, Winona Barker, Harold Drabkin, Zhangzhi Hu, Judith Blake, Barry Smith and Cathy Wu, "TGF-beta Signaling Proteins and the Protein Ontology", 2009 *BMC Bioinformatics* 10 Suppl 5:S3 [PMC2679403].
9. UniProt Consortium*. The Universal Protein Resource (UniProt). *Nucleic Acids Res.* 38(Database issue):D142-148 (2010) [PMC2808944].