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WORK EXPERIENCE & POSITIONS HELD

Oct 2011 – present **Computational Science Analyst I, Cold Spring Harbor Laboratory, Cold Spring Harbor, NY.**
Developing novel algorithms and computational systems to analyze DNA sequences, concentrating on the assembly and alignment of next generation sequencing reads. Applications include analysis of genetic variations in human genome to identify the genetic causes of various human diseases including autism, cancer, and other psychiatric conditions.

Jun 2011 – Sept 2011 **Assistant Research Scientist, Courant Institute of Mathematical Sciences, New York University.**
Designed, researched and implemented novel algorithms, databases, and software solutions for analyzing next-generation DNA sequencing data.

1. Designed and implemented in C++ a novel DNA sequence assembler based on combinatorial optimization techniques (Branch-and-Bound method) to achieve high accuracy.
2. Designed novel base-calling software that combines base calling and alignment into an improved and flexible re-sequencing framework.

Oct 2005 – Aug 2007 **Junior Research Scientist, NYU Bioinformatics Group, Courant Institute of Mathematical Sciences.**

1. Team-leader and primary collaborator for the Large-Scale Emergency Readiness (LaSER) project at the NYU Center for Catastrophe Preparedness & Response.
2. Designed, researched and implemented in Java a scalable hybrid-agent simulation tool for modeling, analyzing and planning against urban catastrophic scenarios.

EDUCATION

Sept 2007 - May 2011 **Courant Institute of Mathematical Sciences, New York University, New York, NY.**
Ph.D. in Computer Science (GPA 3.919/4.0).

May 2005 - May 2008 **Department of Mathematics & Computer Science, University of Catania, Italy.**
Ph.D. in Computer Science.

Sept 1999 - Jul 2004 **Department of Mathematics and Computer Science, University of Catania, Italy.**
"Laurea" Degree (Bachelor) in Computer Science, Final graduation marks: 110/110 cum Laude.

ACADEMIC EXPERIENCE

Jan 2009 – May 2009 **Teaching Assistant at Courant Institute of Mathematical Sciences, New York University.**
Held recitation sections and office hours for the course "Data Structures".

May 2009 –Aug 2009 **Teaching Assistant at Courant Institute of Mathematical Sciences, New York University.**
Held recitation sections and office hours for the course "Programming Languages".

SUMMER SCHOOLS

Aug 31 – Sept 4 2007 SECEVitA 2007, Summer Course on Evolutionary Computation and Artificial Life, Sampieri, Italy.

Sept 12-16 2005 Second International School on Biology, Computation and Information (BCI 2005), Dobbiaco (BZ), Italy.
Topics: Biological Systems as Reactive Systems, Optimization Methods for Computational Biology, Algorithmic and Combinatorial Analysis of Genomes.

Jul - Aug 2005 Full-time course of English language, EF International School of English, Cambridge, Great Britain.

RESEARCH INTERESTS

Bioinformatics: Next-Generation Sequencing, Variant Calling, Genome Assembly, Assembly Validation, High Performance Computing.
Proteomics: Protein Structure Prediction.
Artificial Intelligence: Multi-objective Optimization, Evolutionary Computation, Multi-Agent Systems.

AWARDS & FELLOWSHIPS

- IBM PhD Fellowship award for the 2010-2011 academic year.
- Best Paper Award at the Int. Conference on Biosciences – BIOINFO, 2010.
- "McCracken" award - Guaranteed Financial Support 2007-2011, Ph.D. Program, NYU.
- "ARCHIMEDE" award from Department of Mathematics and Computer Science, University of Catania, Italy, 2003-2004.
- ICARIS Bursary - Travel Grant, 4th International Conference on Artificial Immune Systems 2005.

PUBLICATIONS

BOOK CHAPTERS:

1. Watson M., Andrews S., Cock P., Blaxter M., Schatz M., Nielsen C., **Narzisi G**., Freeman T., Kumar S.: Book chapter in **Visualizing Biological Data: A Practical Guide to Data Visualization for Biologists**, edited by Dr Seán O'Donoghue and Dr. Jim Procter (to appear).
2. Cutello V., **Narzisi G**., Nicosia G.: *Computational Studies of Peptide and Protein Structure Prediction Problems via Multi-Objective Evolutionary Algorithms*. Book chapter in Joshua Knowles, David Corne and Kalyanmoy Deb (Eds), **Multi-Objective Problem Solving from Nature: From Concepts to Applications**, Springer 2007, pp 93-114 (DOI: 10.1007/978-3-540-72964-8_5).

JOURNALS:

3. **Narzisi G**., O'Rawe J.A., Iossifov I., Fang H., Lee Y., Wang Z., Wu Y., Lyon G.J., Wigler M., and Schatz M.C. *Accurate detection of de novo and transmitted INDELs within exome-capture data using micro-assembly.* **CSHL bioRxiv** 2013 (DOI: 10.1101/001370).
4. Ming R., VanBuren R., Liu Y., Yang M., Han Y., Li L., Zhang Q., Kim M, Schatz M., Campbell M., Li J., Bowers J., Tang H., Lyons E., Ferguson A., **Narzisi G.**, Nelson D., Blaby-Haas C., Gschwend A., Jiao Y., Der J., Zeng F., Han J., Min X.J., Hudson K., Singh R., Grennan A., Karpowicz S., Watling J., Ito K. et al.:
Genome of the long-living sacred lotus (Nelumbo nucifera Gaertn.). **Genome Biology**, 2013, 14:R41.
(DOI: 10.1186/gb-2013-14-5-r41).
5. Vezzi F., **Narzisi G**., Mishra B.: *Reevaluating Assembly Evaluations with Feature Response Curves: GAGE and Assemblathons*. **PLoS ONE**, 2012, 7 (12): e52210 (DOI:10.1371/journal.pone.0052210).
6. Iossifov I., Ronemus M., Levy D., Wang Z., Hakker I., Rosenbaum J., Yamrom B., Lee Y., **Narzisi G**., Leotta A., Kendall J., Grabowska E., Ma B., Marks S., Rodgers L., Stepansky A., Troge J., Andrews P., Bekritsky M., Pradhan K., Ghiban E., Kramer M., Parla J., Demeter R., Fulton L.L., Fulton R.S., Magrini V.J., Ye K., Darnell J.C., Darnell R.B., Mardis E.R., Wilson R.K., Schatz M.C., McCombie R.W., Wigler M. *De Novo Gene Disruptions in Children on the Autistic Spectrum*. **Neuron**, Vol. 74, Issue 2, pp. 285-299, 26 April 2012 (DOI: 10.1016/j.neuron.2012.04.009).
7. Vezzi F., **Narzisi G**., Mishra B.: *Feature-by-Feature – Evaluating De Novo Sequence Assembly*. **PLoS ONE** 7(2): e31002, 2012 (DOI: 10.1371/journal.pone.0031002).
8. Schatz M. C., Phillippy A. M., Sommer D., Delcher A. L., Puiu D., **Narzisi G**., Salzberg S. L., Pop M.: *Hawkeye and AMOS: visualizing and assessing the quality of genome assemblies*. **Briefings in Bioinformatics** 2011 (DOI: 10.1093/bib/bbr074).
9. Menges F., **Narzisi G**. and Mishra B. *TotalReCaller: Improved Accuracy and Performance via Integrated Alignment & Base-Calling* **Bioinformatics**, Oxford Journals, 2011 (DOI: 10.1093/bioinformatics/btr393).
10. **Narzisi G**. and Mishra B.: *Comparing De Novo Genome Assembly: The Long and Short of It.* **PLoS ONE**, 6(4):e19175. April 2011. (DOI: 10.1371/journal.pone.0019175).
11. **Narzisi G**. and Mishra B.: *Scoring-and-Unfolding Trimmed Tree Assembler: Concepts, Constructs and Comparisons.* **Bioinformatics**, Oxford Journals, 2010 (DOI: 10.1093/bioinformatics/btq646).
12. Pavone M., **Narzisi G**., Nicosia G.: *Clonal Selection - An Immunological Algorithm for Global Optimization over Continuous Spaces*. **Journal of Global Optimization**, Springer 2011 (DOI: 10.1007/s10898-011-9736-8).
13. Smith S.W., Portelli I., **Narzisi G**., Nelson L.S., Menges F., Rekow E.D., Mincer J.S., Mishra B., Goldfrank L.R.: *A Novel Approach to Multi-Hazard Modeling and Simulation*. **Disaster Medicine and Public Health Preparedness (DMPHP), The American Medical Association (AMA)**, 2009 (DOI: 10.1097/DMP.0b013e3181a88899).
14. Cutello V., **Narzisi G**., Nicosia G.: *A Multi-Objective Evolutionary Approach to the Protein Structure Prediction Problem*. **Journal of the Royal Society Interface**, Royal Society Publications London, vol. 3, issue 6, pp. 139-151, 22 February 2006 (DOI: 10.1098/rsif.2005.0083).
15. Anile A.M., Cutello V., **Narzisi G**., Nicosia G., Spinella S.: *Determination of protein structure and dynamics combining immune algorithms and pattern search methods*. **Natural Computing Int. Journal**, Springer 2006 (DOI: 10.1007/s11047-006-9027-3).
16. **Narzisi G**., Mysore V., Nelson L., Rekow D., Triola M., Halcomb L., Portelli I., and Mishra B.: *Complexities, Catastrophes and Cities: Unraveling Emergency Dynamics*. **InterJournal of Complex Systems** (ISSN: 1081-0625), Manuscript Number:[1745] 2006.

PH.D. THESIS:

17. **Narzisi G**.: *Scoring-and-Unfolding Trimmed Tree Assembler: Algorithms for Assembling Genome Sequences Accurately and Efficiently.* Ph.D. Thesis, Department of Computer Science, Courant Institute of Mathematical Sciences, New York University, New York, USA, May 2011.
18. **Narzisi G**.: *Optimization and Tradeoffs in Protein Structure Prediction*. **Ph.D. Thesis**, Department of Mathematics and Computer Science, University of Catania, Italy, October 2008.

CONFERENCE PROCEEDINGS:

19. **Narzisi G**., Mishra B., Schatz M.C. *On Algorithmic Complexity of Biomolecular Sequence Assembly Pr*oblem. **1st International Conference on Algorithms for Computational Biology** (AlCoB 2014), Springer LNBI series.
20. **Narzisi G**., Nicosia G. and Stracquadanio G. **(**Best Paper Award**):** *Robust Bio-Active Peptide Prediction using Multi-Objective Optimization.* **The First International Conference on Advances in Bioinformatics and Applications (**BIOINFO 2010**)**, March 7-13 2010, Cancun, Mexico, IEEE Press (DOI: 10.1109/BioSciencesWorld.2010.13).
21. Menges F., Mishra B. and **Narzisi G**.: *Modeling and Simulation of E-Mail Social Networks: A New Stochastic Agent-Based Approach.* **Winter Simulation Conference (WSC 2008)**, December 7-10, Miami, Florida, USA (DOI:

10.1109/WSC.2008.4736399).

22. Smith S.W., Nelson L.S., Rekow E.D., **Narzisi G**., Mincer J.S., Portelli I., Mishra B. and Goldfrank L.G.: *A New Approach to Multi-Hazard Modeling and Simulation*. **North American Congress of Clinical Toxicology (NACCT) 2007**, October 19-24, 2007, New Orleans, Louisiana, USA (DOI: 10.1080/15563650701610056).
23. **Narzisi G**., Mincer J.S., Smith S., Mishra B.: *Resilience in the Face of Disaster: Accounting for Varying Disaster Magnitudes, Resource Topologies, and (Sub)Population Distributions in the PLAN C Emergency Planning Tool*. **3rd International Conference on Industrial Applications of Holonic and Multi-Agent Systems (HoloMAS 2007)**, September 3 - 5, 2007, Regensburg, Germany, Proceedings by Springer, LNAI 4659, pp. 433-446 (DOI: 10.1007/978-3-540-74481-8_41).
24. **Narzisi G**., Mysore V. and Mishra B.: *Multi-Objective Evolutionary Optimization of Agent Based Models: an application to emergency response planning*. **The IASTED International Conference on Computational Intelligence (CI 2006)**, Proceedings by ACTA Press, November 20-22, 2006 San Francisco, California, USA.
25. **Narzisi G**., Mysore V., Byeon J. and Mishra B.: *Complexities, Catastrophes and Cities: Emergency Dynamics in Varying Scenarios and Urban Topologies*. **International Conference on Complex Systems (ICCS 2006),** Boston, MA, USA June 25-30, 2006 (accepted for the print proceedings of the conference).
26. Mysore V., **Narzisi G**., Nelson L., Rekow D., Triola M., Shapiro A., Coleman C., Gill O., Daruwala R. S. and Mishra B.: *Agent Modeling of a Sarin Attack in Manhattan.* **The First International Workshop on Agent Technology for Disaster Management (ATDM)**, held in conjunction with the **Fifth International Joint Conference on Autonomous Agents and Multi-Agent Systems (AAMAS)**, Future University, Hakodate, JAPAN, 8th May 2006.
27. Cutello V., **Narzisi G**., Nicosia G., Pavone M.: *Real coded clonal selection algorithm for unconstrained global optimization using a hybrid inversely proportional hypermutation operator.* **The 21st Annual ACM Symposium on Applied Computing**, SAC 2006, Dijon, France, April 23 -27, 2006, ACM Press, vol. 2 pp. 950-954 (DOI: 10.1145/1141277.1141501).
28. Cutello V., **Narzisi G**., Nicosia G., Pavone M.: *An Immunological Algorithm for Global Numerical Optimization.* **7th International Conference on Artificial Evolution**, EA'05, October 26-28 2005, University of Lille, France, Springer-Verlag, Lecture Notes in Computer Science, vol. 3871, pp. 284-295 (DOI: 10.1007/11740698_25).
29. Cutello V., **Narzisi G**., Nicosia G., Pavone M.: *Clonal Selection Algorithms: A Comparative Case Study using Effective Mutation Potentials.* **4th International Conference on Artificial Immune Systems**, ICARIS 2005, 14th-17th August, 2005 in Banff, Alberta, Canada, Proceedings by LNCS, vol. 3627, pp. 13-28 Springer (DOI: 10.1007/11536444_2).
30. Anile A.M., Cutello V., **Narzisi G**., Nicosia G., Spinella S.: *Lipschitzian pattern search, immunological algorithm and quasi-Newton method for the Protein Folding Problem: An innovative multistage approach*. **Proceedings of the International Workshop on Natural and Artificial Immune Systems**, NAIS 2005, 9-10 June 2005, Vietri sul Mare (SA), Italy. Springer-Verlag, Lecture Notes in Computer Science, vol. 3931, pp.307-323, 2006 (DOI: 10.1007/11731177_38).
31. Cutello V., **Narzisi G**., Nicosia G. (Best Paper Award Candidate): *A Class of Pareto Archived Evolution Strategy Algorithms Using Immune Inspired Operators for Ab-Initio Protein Structure Prediction.* **EvoWorkshops 2005 - EvoBio 2005**, Lausanne, Switzerland, 30 March - 1 April, 2005, Proceedings by LNCS, vol. 3449, pp. 54-63 Springer (DOI: 10.1007/b106856).
32. Cutello V., **Narzisi G**., Nicosia G., Pavone M., Sorace G.: *How to Escape Traps using Clonal Selection Algorithms*. **The First International Conference on Informatics in Control, Automation and Robotics** (ICINCO 2004), INSTICC Press 1:322-326.

ABSTRACTS AND POSTERS:

33. **Narzisi G**., Iossifov I., Gurtowski J., O'Rawe J., Lyon G.J., and Schatz M.C.: *Scalpel: detection of de novo mutations in exome-capture data using micro-assembly*. **Personal Genomes & Medical Genomics**, November 14-17, 2012, CSHL, USA.
34. **Narzisi G**., Iossifov I., Lee Y., Wang Z., Pradhan K., Wigler M., and Schatz M.C.: *Detection and validation of de novo mutations in exome-capture data using micro-assembly*. **The Biology of Genomes**, May 8-12, 2012, CSHL, USA.
35. **Narzisi G**., Menges F., Mishra B.: *Improved Assembly Accuracy by integrating Base-Calling, Error Correction and Assembly.* **Eighth Annual Meeting of the Bioinformatics Italian Society (BITS 2011)**, June 20-22, 2011 Pisa, Italy.
36. **Narzisi G**.: *SUTTA: Scoring-and-Unfolding Trimmed Tree Assembler.* **9th IEEE International Workshop on Genomic Signal Processing and Statistics (**GENSIPS**)**, Cold Spring Harbor Laboratory (CSHL), November 10 - 12, 2010.
37. **Narzisi G**. and Mishra B.: *A novel Technologically Agnostic De Novo Sequence Assembler.* **Systems Biology and New Sequencing Technologies (**SBNST**)**, Centre for Genomic Regulation (CRG), Barcelona, 16-17-18 June, 2010.
38. Cutello V., Nicosia G. and **Narzisi G**.: *Protein Structure Prediction with Multi-objective Evolutionary Algorithms and Supersecondary Structure Prediction Constraints.* **First International School on Advanced BioMedicine and BioInformatics,** Lipari School for Scientific Research, Lipari Island, May 29 - June 5, 2004.

PATENTS

1. **System, Method, and Computer-Accessible Medium for Providing a Multi-Objective Evolutionary Optimization of Agent-Based Models**. (Co-Inventors: B. Mishra and M.P. Venkatesh) Filed: September 2007.
2. **Methods, Computer-Accessible Medium, and Systems for Score-Driven Whole-Genome Shotgun Sequence Assembly.** (Co-Inventor: B. Mishra) Filed: February 2009.
3. **Methods, Computer-Accessible Medium, and Systems for Base-Calling and Alignment.** (Co-Inventor: B. Mishra) Filed: April 2009.

COMPUTER SKILLS

₪ Programming Languages: C / C++, Java, PHP, Perl.

- Systems: Unix and Macintosh
- Toolkits: SAMtools, BWA, AMOS, Repast, Gnuplot.

SERVICE

PROGRAM COMMITTEES:

- 11th International Conference on Artificial Immune Systems (ICARIS 2012), Taormina, Italy.
- 12th International Conference on Parallel Problem Solving From Nature (PPSN 2012) - Taormina, Italy (**Tutorial Chair**).
- 10th International Conference on Artificial Immune Systems (ICARIS 2011), Cambridge, UK.
- International Conference on Evolutionary Computation 2010 (ICEC 2010), Valencia, Spain.
- The Second International Conference on Advances in Biotechnologies (BIOTECHNO 2010), Cancun, Mexico (**Session Chair**).
- The First International Conference on Computational and Systems Biology and Microbiology (BIOSYSCOM 2010), Cancun, Mexico.
- Second IEEE Symposium of Computational Intelligence in Multi-Criteria Decision Making (MCDM'09), Nashville, TN.
- 2nd Italian Workshop on Artificial Life and Evolutionary Computation (WIVACE 2008), Venezia, Italy.
- 2nd International Workshop on Nature Inspired Cooperative Strategies for Optimization (NICSO 2007), Acireale, (Italy).
- 1st Italian Workshop on Artificial Life and Evolutionary Computation (WIVACE 2007), Sampieri (Ragusa), Italy.

REFEREE FOR:

- **Bioinformatics**, Oxford Journals; **Proceedings of the Royal Society B**: Biological Sciences, International Journal; **BMC Bioinformatics** International Journal**; PLOS ONE** International Journal; **Nucleic Acids Research** (Oxford Journals); **Robust Intelligence** (RI) Division of Information and Intelligent Systems (IIS) at the National Science Foundation (NSF); **IEEE Transactions on Evolutionary Computation** (IEEE CIS); **Natural Computing** (Springer); **Journal of Mathematical Modelling and Algorithms** (Springer); **Information Sciences** (Elsevier); **Knowledge-Based Systems** (Elsevier); **Memetic Computing** (Springer);

HOBBIES

- Rock Climbing, Hiking, Biking, Electric Guitar.