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## Home

Cancer is a complex disease involving several intertwined phenomena and events, which collude to unleash the tumor cells' inherent programs to proliferate, live, and move. Thus it is the malfunction of the biomolecular machinery responsible for the "checks and balances," normally governed by various complex feedback loops among a population of various cell types. Breakdown of this machinery leads to uncontrolled growth of a cell population being selected by evolutionary pressures that ultimately costs the very survival of the host.

Understanding the many intricacies of all these interactions at the subcellular, cellular and tissue levels has greatly benefitted from the ever-improving applications of algorithmic, statistical and mathematical modeling tools. Moreover, during the past 15 years, new measurement technology for gene expression and, more recently, "deep" genome sequence data, have produced vast amount of data – waiting to be analyzed to deliver new interpretations. The design of novel "wet" experiments and appropriately matched algorithmic, statistical and mathematical modeling tools are expected to become the key to successful oncological science and practice.

The Workshop and School on Cancer Evolution and Complexity seeks to convene researchers from various related disciplines to explore multiple facets of the challenges posed by cancer – a "disease of the systems." The workshop will provide opportunities for the researchers to exchange new ideas and viewpoints, forge new collaborations and train the next generation of young scientists.

The program will provide an introduction to both cancer biology and mathematical and statistical methods used in analyzing the datasets currently being produced by several laboratories around the world. Next the program will provide an opportunity to interact with world renowned cancer and bioinformatics researchers and the chance for attendees to present their current work. Finally, all the attendees will receive a certificate of completion of the School.

### Organization:

- BIMIB, Dipartimento di Informatica, Sistemistica e Comunicazione, Università degli Studi di Milano Bicocca, Milan, ITALY
- NYUBIG, Courant Institute of Mathematical Sciences, New York University, New York, USA

### Directors:

- Marco Antonietti, DISCo Università Milano Bicocca, Italy
- Bud Mishra, NYUBIG, Courant Institute of Mathematical Sciences, New York University, New York, USA

### Sponsors:





## Workshop and School on Cancer, Evolution and Complexity





**Villa del Grumello**  
Como

**27 September - 1 October 2015**

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### Keynote speakers

**Mickey Atwal**  
Cold Spring Harbor Lab  
USA

**Gary Bader**  
The Donnelly Center  
University of Toronto  
Canada

**Charles Cantor**  
Agens Biosciences, Sequenom,  
Reitropo and Boston University  
USA

**Bud Mishra**  
Courant Institute of  
Mathematical Sciences, NYU  
USA

**Victor Moreno**  
Canadian Institute of  
Oncology  
Spain

**Rocco Piazza**  
Dept. of Health Sciences,  
University of Milan-Bicocca  
Italy

**Alberto Policristi**  
Applied Genomics Institute  
and University of Udine  
Italy

**Lloyd Trotman**  
Cold Spring Harbor Lab  
USA

**Henk van Ooijen**  
Philips Research  
the Netherlands



### School Directors

**Marco Antonietti**  
University of Milan-Bicocca, Italy

**Bud Mishra**  
NYU, USA

### Local organization

Fondazione Alessandro Volta  
Alessandro Casaniga

University of Milan-Bicocca  
Alex Gaudenzi, Giulio Caravagna,  
Daniela Ramazzotti, Giancarlo Maturi

### Registration

Early registration (until July 15th, 2015): 320€

Regular registration (on and after July 15th, 2015): 400€

Daily, on site registration: 90€

### Contacts

<http://ceac.lakecomoschool.org>

[ceacinfo@disco.unimib.it](mailto:ceacinfo@disco.unimib.it)



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## Speakers

### Gurinder Singh “Mickey” Atwal, Cold Spring Harbor Lab, USA.



#### Short bio

Fueled by massive amounts of data generated from DNA sequencing technologies, the Atwal Lab is currently focused on population genetics, cancer biology and high-performance computing. We often tackle scientific questions computationally by invoking theoretical concepts from statistical physics and machine learning.

A common thread in our research is the quest to understand collective biological phenomena from the perspective of the physical sciences. To this end, we develop and deploy mathematical and computational tools to address quantitative principles governing the behavior of many-body biological systems, ranging from molecular interactions in a single eukaryotic cell to the evolution of the species *Homo sapiens*. Our fantastic team of lab members and collaborators consists of physicists, biologists, mathematicians and computer scientists and we work closely with experimentalists and clinicians both here at Cold Spring Harbor Laboratory and around the world. For more details feel free to browse through our website.

### Gary Bader, The Donnelly Centre, University of Toronto, Canada.



#### Short bio

Gary D. Bader works on biological network analysis and pathway information resources as an Associate Professor at The Donnelly Centre at the University of Toronto. He completed post-doctoral work in the group of Chris Sander in the Computational Biology Center (cBio) at Memorial Sloan-Kettering Cancer Center in New York. Gary developed the Biomolecular Interaction Network Database (BIND) during his Ph.D. in the lab of Christopher Hogue in the Department of Biochemistry at the University of Toronto and the Samuel Lunenfeld Research Institute at Mount Sinai Hospital in Toronto. He completed a B.Sc. in Biochemistry at McGill University in Montreal. See <http://baderlab.org>

### Charles Cantor, Agena Biosciences, Sequenom, Retrotope and Boston University.



#### Short bio

Charles Cantor is currently affiliated with Agena BioSciences Inc., Sequenom Inc. and Retrotope Inc. He is Professor Emeritus, Biomedical Engineering Professor of Pharmacology, School of Medicine at Boston University, and former director of the DoE Human Genome Project. Charles Cantor's research is focused on identifying biological problems that are resistant to conventional analytical approaches and then developing new methodologies or techniques for solving these problems. His laboratory has developed methods for separating large DNA molecules, for studying structural relationships in complex assemblies of proteins and nucleic acids, and for sensitive detection of proteins and nucleic acids in a variety of settings. His current interests include the development of new methods for faster DNA sequencing, the development of new variations and analogs of the polymerase chain reaction, the development of bacterial strains suitable for environmental detoxification, and the discovery of human genes associated with sense and taste. He is also interested in exploring the possible use of biological molecules for applications in nanoengineering and microrobotics, and in making detectors capable of recognizing specific single molecules.

### Bud Mishra, Courant Institute of Mathematical Sciences, New York University, New York, USA.



#### Short bio

Professor of Computer Science & Mathematics, Courant Institute, New York University, Principal Investigator, NYU/Courant Bioinformatics Group; Principal Investigator, SEI/CMU/NYU Center for Malicious Behavior and Model Checking; Professor of Cell Biology, NYU School of Medicine, New York University; QB Visiting Scholar Simons Center for Quantitative Biology, Cold Spring Harbor Laboratory; Adjunct Professor Department of Human Genetics, Mt. Sinai School of Medicine; Adjunct Professor Tata Institute of Fundamental Research

### Victor Moreno, Iconcologia, Barcelona, Spain.



#### Short bio

Dr. Moreno is Professor of Preventive Medicine and Director of the Cancer Prevention and Control Program at the Catalan Institute of Oncology-IDIBELL in Barcelona, Spain. He has been long experience in genetic and molecular epidemiology studies on CRC. He has designed and conducted several case-control studies on CRC and contributed to the identification of genetic susceptibility loci, and molecular mechanisms involved in CRC etiology and progression. He leads the Unit of Biomarkers and Susceptibility at ICO, with strong expertise in biostatistics and bioinformatics. His team has experience both in the design of epidemiological and clinical studies and in the analysis of omics data. In his most recent project, COLONOMICs, ([www.colonomics.org](http://www.colonomics.org)) tumors and adjacent normal mucosa from a sample of 100 CRC patients have been extensively characterized at molecular level (gene expression, micro-RNA expression, methylation, genetic variation, CNVs and somatic mutations in exome). Also samples of normal mucosa from 50 healthy donors have been analyzed. This resource is the bases for diagnostic and prognostic biomarker discovery and to elucidate the mechanisms involved using systems biology approaches.

Websites:

<http://www.icoprevencio.cat/en/programa-biomarcadors>

<http://www.colonomics.org>

### Rocco Piazza, Dipartimento di Scienze della Salute, Università degli Studi di Milano Bicocca, Italy.



#### Short bio

### Alberto Policriti, Istituto di Genomica Applicata and Università degli Studi di Udine, Italy



#### Short bio

Prof. Policriti received his laurea degree in Mathematics from the University of Turin in 1984 "cum laude". Subsequently he was granted fellowships from the CNR and ENIDATA that have been spent in various periods at the Courant Institute of Mathematical Sciences from 1986 to 1992. Always at the Courant Institute he received his master degree in 1988 and his Ph.D. in 1990, in Computer Science under the direction of prof. M. Davis. From 1989 to 1992 he has been researcher, from 1992 to 2000 associate professor, and currently he is full professor at the Department of Mathematics and Informatics of the University of Udine. Prof. Policriti has been responsible or has been working in many projects financed by the CNR (Researches National Council of Italy), MURST (Italian Ministry of the University and Scientific and Technological Research), and the European Community. His main research interests are related with Computational Logic and in particular:

- algorithms and models for bioinformatics;
- set-theoretic and combinatorial algorithms and decision problems;
- computational logic.

Prof. Policriti has more than 120 scientific publications and has directed or is now following Ph.D. students at the universities of NYU, Amsterdam, Pisa, Stanford and Udine. He has been in the program committee of many international conferences and he is in the editorial board of a number of scientific journals.

He is member of the scientific board of the Gruppo Nazionale di Calcolo Scientifico of the Istituto Nazionale di Alta Matematica and of the European Association for Theoretical Computer Science. He has been chairman and committee member of the Beth prize and member of the committee of the Premio Tesi di Dottorato su argomenti di Informatica Teorica of the Italian Chapter of the European Association of Theoretical Computer Science.

He has been Coordinator of the Biotechnology program and he is now director of the PhD program in Informatics of the University of Udine.

He is european coordinator of the IEEE CS Technical Committee on Bioinformatics.

Prof. Policriti is one of the four founders of the Istituto di Genomica Applicata—the first genome sequencing center in Italy—, in which he is the director of the Bioinformatics division.

### Lloyd Trotman, Cold Spring Harbor Lab, USA.



#### Short bio

Lloyd Trotman's recent research path begins at his discovery some years ago that the loss of a single copy of a master tumor suppressing gene called PTEN is sufficient to permit tumors to develop in animal models of prostate cancer. His team later found that complete loss of PTEN paradoxically triggers senescence, an arrested state that delays or blocks cancer development in affected cells. These findings explained why many patients only display partial loss of this tumor suppressor when diagnosed with prostate cancer. Now the team is researching ways to restore the PTEN protein levels in these patients. This therapeutic approach could slow disease progression and thus greatly reduce the need for surgical removal of the prostate or similar disease interventions that carry the risks of incontinence and impotence. Their second approach to combat prostate cancer is to model the lethal metastatic disease in genetically engineered mice. They are developing a novel approach that allows for quick generation and visualization of metastatic disease. The efficacy of existing and novel late-stage therapies, such as antihormonal therapy, can then be tested and optimized in these animals. At the same time, the Trotman lab is exploring the genome alterations associated with metastatic disease and with resistance to therapy. To this end, they use single- and multicell genome sequencing techniques developed at CSHL by Drs. Wigler and Hicks.

### Henk van Ooijen, Philips Research, the Netherlands.



#### Short bio

Henk van Ooijen is a research scientist in the department of Precision & Decentralized Diagnostics at Philips Research. He studied biomedical engineering at the Eindhoven University of Technology (TU/e). After graduating with a specialization in biomodeling and bioinformatics he started modeling biological systems at Philips Research after a short stay at the National Institute for Public Health where he modeled human toxicology. His main research interests are modeling the hemostatic balance of critically ill patients as well as diagnosing tumor-driving signaling pathways. Up to March 2015 he has contributed to 14 patent families protecting inventions in the area of hemostasis and cancer diagnosis.





Schedule

Overview of the program

Detailed program below.

	Sun Sept 27	Mon Sept 28	Tue Sept 29	Wed Sept 30	Thu Oct 1
		Rocco Piazza (Biomed Tutorial)	Lloyd Trotman	Charles Cantor	Mickey Atwal
09:00		Bud Mishra (Math/Stat Tutorial)	Daniele Ramazzotti	Charles Cantor	Mickey Atwal
10:00		Break	Break	Break	Break
11:00		Bud Mishra (Math/Stat Tutorial)	Giulio Caravagna	Henk van Ooijen	Alberto Policriti
11:30		Gary Bader (Bioinformatics Tutorial)	Giulio Caravagna Rebeca Sanz-Pamplona	Henk van Ooijen	Bud Mishra
12:30		lunch	lunch	lunch	lunch
13:30		Registration	Gary Bader	Bud Mishra	Stefano De Pretis
14:30		Registration	Gary Bader	Raoul Bonnal	Christos Dimitrakopoulos
15:30		Registration	Victor Moreno	Giovanni Tonon	Nicola Toti
16:30	Welcome address and reception	Break	Break	Break	
17:30	Welcome address and reception				
18:30					
19:30					
20:30			Social dinner		

Detailed program

Sunday, September 27<sup>th</sup> 2015

14:30 Registration opens

17:30 Welcome Address and Reception

Monday, September 28<sup>th</sup> 2015

9:00 Rocco Piazza, School of Medicine, Università degli Studi di Milano Bicocca  
NGS FOR CANCER VARIANTS DISCOVERY

10:00 Bud Mishra, Courant Institute of Mathematical Sciences, New York University  
PROBABILITY, TIME AND CAUSALITY

11:00 Break

11:30 Bud Mishra ... continuing

12:30 Gary Bader, Donnelly Centre, University of Toronto  
PATHWAY AND NETWORK ANALYSIS OF GENOMICS DATA

13:30 Lunch

14:30 Gary Bader ... continuing  
COMPUTATIONAL APPROACHES TO IDENTIFY FUNCTIONAL GENETIC VARIATIONS IN CANCER

16:00 Victor Moreno, Iconcologia-IDIBELL  
TRANSCRIPTIONAL REGULATORY PROGRAMS OF NORMAL AND TUMOR COLON CELLS

17:30 Break

Tuesday, September 29<sup>th</sup> 2015

9:00 Lloyd Trotman, Cold Spring Harbor Lab  
ENGINEERING PROSTATE METASTASIS AND ITS ANALYSIS BY SINGLE CELL SEQUENCING

11:00 Break

11:30 Giulio Caravagna, BIMIB, Università degli Studi di Milano Bicocca  
ALGORITHMIC METHODS TO INFER THE EVOLUTIONARY TRAJECTORIES IN CANCER PROGRESSION

13:00 Rebeca Sanz-Pamplona, Iconcologia-IDIBELL  
SOMATIC MUTATIONAL LANDSCAPE OF STABLE STAGE II COLORECTAL CANCER

13:30 Lunch

14:30 Bud Mishra, Courant Institute of Mathematical Sciences, New York University  
PROBABILITY, TIME AND CAUSALITY

15:30 Raoul Bonnal, INGM  
THE STUDY OF lincRNAs IN THE HUMAN IMMUNE SYSTEM: OPPORTUNITIES FOR INNOVATIVE BIOINFORMATICS SOLUTIONS

16:30 Giovanni Tonon, Functional Genomics of Cancer Unit, San Raffaele Scientific Institute  
SYNTHETIC LETHAL APPROACHES EXPLOITING DNA DAMAGE

17:30 Break

20:30 Social Dinner, Restaurant "L'Angolo del Silenzio", Viale Lecco, 25, 22100 Como; tel. +39 031 337 2157

Wednesday September 30<sup>th</sup> 2015

9:00 Charles Cantor, Agena  
THE FUTURE OF NUCLEIC ACID DIAGNOSTIC

10:00 Charles Cantor, Agena  
THE OXYGEN PARADOX

11:00 Break

11:30 Henk van Ooijen, Philips  
NEXT GENERATION CANCER DIAGNOSTICS

13:30 Lunch

14:00 Address of the Rector of the Università degli Studi di Milano Bicocca  
Prof. Cristina Messa

14:30 Stefano De Pretis, IIT  
INSPECT: A COMPUTATIONAL TOOL TO INFER mRNA SYNTHESIS, PROCESSING AND DEGRADATION DYNAMICS FROM RNA- AND 4SU-SEQ TIME COURSE EXPERIMENTS

15:30 Christos Dimitrakopoulos  
NETWORK MODELS IN CANCER

16:30

17:30 Break

Thursday October 1<sup>st</sup> 2015

9:00 Mickey Atwal, Cold Spring Harbor Lab  
SINGLE-CELL GENOMICS OF TUMORS

11:00 Break

11:30 Alberto Policriti, Università degli Studi di Udine  
COMBINATORIAL AND COMPUTATIONAL PROBLEMS ARISING FROM CANCER-CELLS SUB-POPULATION DATA CLUSTERING

13:00 Bud Mishra  
Closing remarks

13:30 Lunch





# Cancer, Evolution and Complexity

Lake Como School of Advanced Studies, 27 September – 1 October 2015 (Como)



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## Participants



**1** Alberto Policriti **2** Bud Mishra **3** Marco Antoniotti **4** Daniele Ramazzotti **5** Giulia Caravagna **6** Lloyd Trotman **7** Nicola Prezza **8** Khalid Kunji **9** Giulio Spinozzi **10** Gary Bader **11** Stefano De Pretis **12** Niccolò Totis **13** Christos Dimitrakopoulos **14** Rebeca San-Pamplona **15** Victor Moreno **16** Martina Francesca Rizza **17** Alex Graudenzi **18** Gurinder Atwal **19** Charles Cantor **20** Henk van Ooijen **21** Sara Redaelli **22** Mathias Cardner **23** Giulio Casati (Fondazione Volta) **24** Federico Canobbio (Fondazione Volta)







## Registration

Registration fees include participation to the school, social events, coffe breaks and school material.

**Early registration (until July 15th, 2015): 320,00 EUR (VAT 22% included)**

**Regular registration (on and after July 16th, 2015): 400,00 EUR (VAT 22% included)**  
**Daily, on site registration: 90,00 EUR (VAT 22% included)**

**TO REGISTER, PLEASE FILL IN THE FORM BELOW:**

### Personal information (required)

Name

Surname

Institution

Street

Postal code

Town

State/Province

Country

Phone

Email

Registration fees (VAT 22% included)

☐ € 320,00 early registration (until June 15th 2015) ☐ € 400,00 regular registration (on and after June 16th 2015) ☐ € 90,00 daily, on site registration

### Payment information (required)

Payment option

☐ by credit card online ☐ by bank transfer

\*For credit card payment click the "pay now" button at the bottom of this page.

\*For bank transfer: make it out by bank transfer to Fondazione Alessandro Volta, ref. "Cancer and Evolution + name of the person registered", drawn on Banca di Credito Cooperativo Alta Brianza – Alzate Brianza, Como, Via Rubini 3, 22100 Como – IBAN: IT13L 08329 10900 00000 0300088 – BIC: ICRAITRR950

Type of document

☐ receipt ☐ invoice

Invoice to be sent to:

VAT id/Fiscal code

Indicate both if different: they are mandatory to issue invoices.

Accomodation at the Guesthouse of Villa del Grumello:

☐ yes ☐ no

Please note: accommodation has to be paid onsite. Please check the accommodation page for details.

☐ By submitting this registration form you authorise Fondazione Alessandro Volta to include your personal data on its mailing list for the distribution of information material. In accordance with the Law 196/2003, you may have access to these details at any time and request their modification and cancellation.

**PLEASE NOTE! PLEASE FIRST CLICK ON THE "SEND" BUTTON, THEN GO AHEAD WITH PAYMENT BY PAYPAL. IF YOU DO NOT CLICK ON THE "SEND" BUTTON, THE FORM WILL NOT BE SENT.**

CEAC Registration fee

Early registration (until June 15th 2015) - VAT 22% included ▼

Additional remarks :

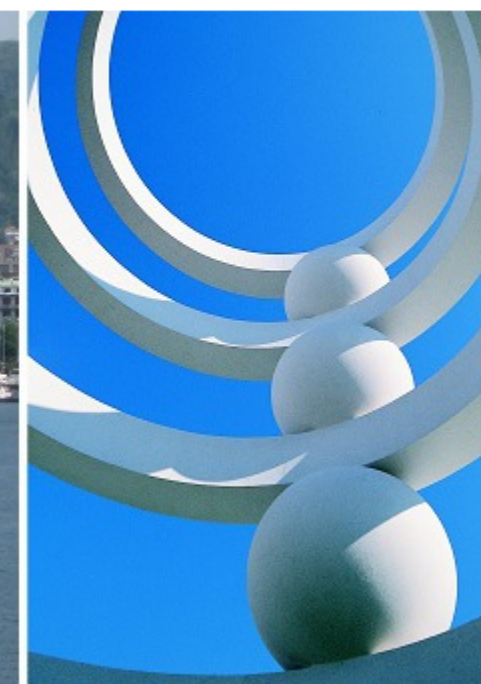






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## Accommodation

The first registrants may ask to be hosted directly at the Guesthouse of Villa Del Grumello (in a shared accommodation) for an additional cost of 37.00 EUR V.A.T. included, per night up to capacity (10 places).

The accommodation can be paid on site at the check out – accommodation is available from September 29th to October 2nd (departure date), 2015.

A list of local hotels will be provided soon. For any help or additional information: please contact the Organizing Secretariat (email: [alessandra.cazzaniga \[-a-\] centrovolta.it](mailto:alessandra.cazzaniga [-a-] centrovolta.it) )

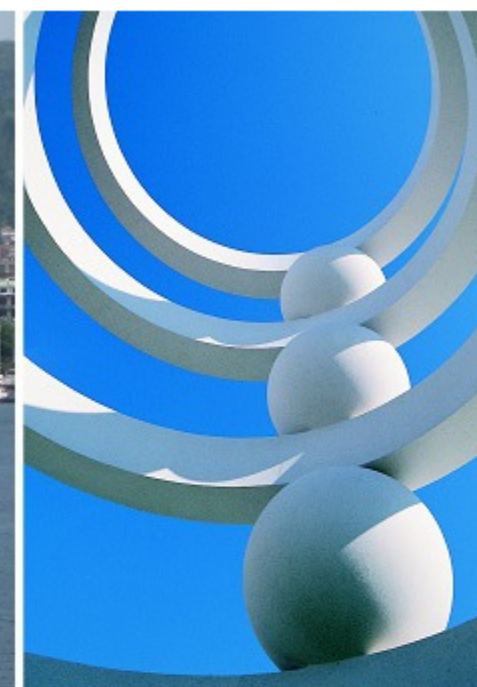






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## Contact us



Fondazione  
Alessandro Volta

### Fondazione Alessandro Volta

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