Stefano Monti, Ph.D.

Associate Professor

Education:

Postdoc, Robotics Institute, Carnegie Mellon
Ph.D., Intelligent Systems Program, University of Pittsburgh
M.S., Intelligent Systems Program, University of Pittsburgh
B.S., Computer Science, University of Udine, Italy

General field of research:

Computational Biology & Genomics

Affiliations other than medicine:

Affiliate Faculty, Bioinformatics Program
Affiliate Member, Broad Institute of MIT & Harvard
Affiliate Member, Hariri Institute for Computing and Computational Science & Engineering

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Keywords:

Cancer, Translational Medicine, Bioinformatics, Machine Learning, Statistics

Summary of academic interest:

Monti's research centers on the development and application of computational approaches for the dissection and characterization of the molecular machinery of human malignancies and their response to environmental insults. This multidisciplinary effort relies on the generation, analysis, and integration of high-throughput genomic data, and it is aimed at the identification of novel therapeutic targets and the development of diagnostic and prognostic biomarkers.

Monti's lab is involved in several projects, with collaborators in the School of Medicine, the School of Public Health, Harvard Medical School, and the Broad Institute. These projects include:

- • Development of gene expression-basedclinicalclassifiers for prognosis and clinical trial patientstratification.
- • Molecularcharacterization of lymphomamalignancies: genome, transcriptome, epi-genome, and their cross-talk.
- • Molecularcharacterization of the transcriptionalprogram in lungcancerbased on high-throughput RNA-sequencing.
- • Computationalgenomicmodels of environmental and chemicalcarcinogenesis.
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Recentpublications:

- Chiarle R, Zhang Y, Frock RL, Lewis SM, Molinie B, Ho Y, Myers DR, Choi VW, Compagno M, Malkin DJ, Neuberg D, Monti S, Giallourakis CC, Gostissa M, and Alt FW.Genome-Wide

TranslocationSequencingRevealsMechanisms of Chromosome Breaks and Rearrangements in B Cells. Cell, 147(1):107-119, 2011. PMCID: PMC3186939.

- Green M, Monti S, et al., Signaturesof murine B-celldevelopment implicate Yy1 as a regulator of the germinal center-specificprogram. PNAS, 108(7), 2873-78, 2011. PMCID: PMC3041080.
- Green M, Monti S, et al. Integrative analysisrevealsselective 9p24.1 amplification, increased PD-1 ligandexpression, and furtherinduction via JAK2 in nodularSclerosingHodgkinlymphoma and primarymediastinal large B-celllymphoma. Blood, 116(17): 3268-3277, 2010.
- The CancerGenome Atlas (TCGA) Research Network. Comprehensive genomiccharacterizationdefines human glioblastoma genes and core pathways. Nature, 455(7216):1061-8, 2008.
- Takeyama K, Monti S (co-first author), et al., Integrative Analysis Reveals 53BP1 Copy Loss and DecreasedExpressionin a Subset of Human Diffuse Large B-cellLymphomas. Oncogene, 27(3): 318-322, 2008. PMID: 17637749.
- Polo JM, Juszczynski P, Monti S, et al. A transcriptionalsignature with differentialexpression of BCL6 target genesaccuratelyidentifies BCL6-dependent diffuse large B-celllymphomas. PNAS, 104(9): 3207-3212, 2007. PMCID: PMC1805543.
- Monti, S., Savage, K.J., et al., Molecularprofiling of diffuse large B-celllymphomaidentifiesrobustsubtypesincludingonecharacterized by hostinflammatoryresponse. Blood, 2005. 105(5): p. 1851-1861. PMID: 15550490.
- Monti, S., et al., Consensus Clustering: A Resampling-Based Method for Class Discovery and Visualization of Gene ExpressionMicroarray Data. Machine Learning, 2003. 52(1-2): p. 91-118.
- Hartley SW, Monti S, Liu CT, Steinberg MH, and Sebastiani P (2012), Bayesianmethodsfor multivariate modeling of pleiotropic SNP associations and geneticriskprediction, Frontiers in Genetics, 3:176.
- Monti S, Chapuy B, Takeyama K, Rodig SJ, Yeda KT, Inguilizian H, Mermel C, Curie T, Dogan A, Kutok J, Beroukim R, Neuberg D, Habermann T, Getz G, Kung AL, Golub TR, and Shipp MA (2012) Integrative Analysis Reveals an Outcome-associated and Targetable Pattern of p53 and Cell CycleDeregulation in Diffuse Large B-cellLymphoma. Cancer Cell, 22(3):359-372.
- Caro P, Kishan AU, Norberg E, Stanley I, Chapuy B, Ficarro SB, Polak K, Tondera D, Gounarides J, Hong Y, Zhou F, Green MR, Chen L, Monti S, Marto JA, Shipp MA, and Danial NN (2012), MetabolicSignaturesUncoverDistinct Targets in MolecularSubsets of Diffuse Large B-Cell Lymphoma. Cancer Cell, In Press.
- Chiarle R, Zhang Y, Frock RL, Lewis SM, Molinie B, Ho Y, Myers DR, Choi VW, Compagno M, Malkin DJ, Neuberg D, Monti S, Giallourakis CC, Gostissa M, and Alt FW (2011), Genome-Wide TranslocationSequencingRevealsMechanisms of Chromosome Breaks and Rearrangements in B Cells. Cell, 147(1):107-119.
- Green MR, Monti S, Dalla-Favera R, Pasqualucci L, Walsh NC, Schmidt-Supprian M, Kutok JL, et al. (2011). Signaturesof murine B-celldevelopment implicate Yy1 as a regulator of the germinal center-specificprogram. PNAS, 108(7), 2873–2878.
- Green MR, Monti S, Rodig SJ, Juszczynski P, Currie T, O'Donnell E, Chapuy B, et al. (2010). Integrative analysisrevealsselective 9p24.1 amplification, increased PD-1 ligandexpression, and furtherinduction via JAK2 in nodularsclerosingHodgkinlymphoma and primarymediastinal large B-celllymphoma. Blood, 116(17), 3268–3277.
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- Monti S, Tamayo P, Mesirov J, &Golub T (2003). Consensus Clustering: A Resampling-Based Method for Class Discovery and Visualization of Gene ExpressionMicroarray Data. Machine Learning, 52(1 – 2), 91–118.