

Workshop TFDA Comp-Bio

Report of Contributions

Contribution ID : 5

Type : **not specified**

Prof. Mario Nicodemi (Coordinatore TFDA Biologia Computazionale e Quantitativa)

martedì 22 ottobre 2024 09:35 (8)

Prof. Mario Nicodemi (Coordinatore TFDA Biologia Computazionale e Quantitativa)

Department

Contribution ID : **10**

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Conclusioni

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Department

Workshop TFDA... / Report of Contributions

TBA

Contribution ID : 56

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TBA

Department

Contribution ID : 64

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Welcome

martedì 22 ottobre 2024 09:30 (5)

Department

Contribution ID : 65

Type : **not specified**

Force-biased nuclear import sets nuclear-cytoplasmic volumetric coupling by osmosis.

We have developed an innovative approach to simultaneously measure the volume of the cell and the volume of the nucleus in live cultured cells. Through this method, we have made a surprising discovery that challenges the conventional understanding of cellular growth. While the cytoplasm grows exponentially, in line with previous findings, we have found that the nucleus grows linearly. This contradicts the widely accepted notion that the scaling of nuclear and cellular volumes follows a universal law driven by osmotic balance across the nuclear envelope. Our groundbreaking research provides the first direct simultaneous observation of nuclear and cellular volume in single live mammalian cells. These observations defy a simple explanation based on osmotic balance, which predicts a constant ratio between the volumes of the nucleus and the cytoplasm as the cell grows. Through a combination of experiments and physical modeling, we have demonstrated that our findings can be explained by two well-established elements. Firstly, the ratio of the nucleus and cytoplasm volumes depends on an osmotic balance influenced by the ratio of protein contents in these compartments, which is determined by the import/export balance. Secondly, the forces exerted on the nucleus modulate the import/export balance. Consequently, changes in these forces lead to variations in import/export processes, altering the ratio of protein contents between the nucleus and the cytoplasm, thus influencing the ratio of their volumes. This general mechanism, ultimately impacting the concentration of nuclear proteins, including transcription factors, could have significant implications for nuclear organization, control of gene expression, and overall cell homeostasis [Pennacchio et al., Nat Commun 2024 - <https://doi.org/10.1038/s41467-024-45168-4>].

Department

Dipartimento di Medicina Molecolare e Biotecnologie Mediche

Primary author(s) : Dr. PENNACCHIO, Fabrizio A.; Dr. POLI, Alessandro; Dr. PRAMOTTON, Francesca Michela; Dr. LAVORE, Stefania; Dr. RANCATI, Ilaria; Dr. CINQUANTA, Mario; Dr. VORSELEN, Daan; Dr. PRINA, Elisabetta; Dr. ROMANO, Orso Maria; Dr. FERRARI, Aldo; Dr. PIEL, Matthieu; Prof. COSENTINO LAGOMARSINO, Marco; Prof. MAIURI, Paolo (Department of Molecular Medicine and Medical Biotechnology, Università degli Studi di Napoli "Federico II")

Presenter(s) : Prof. MAIURI, Paolo (Department of Molecular Medicine and Medical Biotechnology, Università degli Studi di Napoli "Federico II")

Contribution ID : 66

Type : **not specified**

A biomolecular circuit for high-performance in vivo biosensing: monitoring of copper levels in Wilson Disease

Copper is an essential trace element tightly regulated within organisms, particularly in hepatocytes, where the ATPase Copper Transporting Beta protein (ATP7B) maintains homeostasis. Mutations in ATP7B result in Wilson disease (WD), causing harmful copper accumulation and organ dysfunction. Despite its importance, accurately measuring copper concentrations remains challenging due to low levels, with no techniques available for in vivo intracellular measurement. Thus, developing a biomolecular copper biosensor could revolutionize drug screening and gene therapy monitoring in animal models. Here, we applied theoretical results from Control Engineering to design a biomolecular circuit that yielded a high-performance copper biosensor in terms of minimal leakiness, and significant fold change. Building on our previous work [<https://doi.org/10.1101/2023.09.20.558637>], we engineered an adenoviral vector carrying a synthetic gene circuit. This circuit included an artificial transcription factor (rtTA) controlled by a Metal Responsive Elements promoter. The rtTA drives the expression of Secreted Alkaline Phosphatase (SEAP), modified at its 3'UTR with a Direct Repeat sequence recognized by the CRISPR-Cas endonuclease CasRx that is under the control of a CMV/TO promoter. We transduced Hek293T cells with the adenoviral vector and confirmed that the SEAP concentration in the growth medium is proportional to the copper concentration, exhibiting extremely low leakiness in the absence of copper and about two orders of magnitude fold induction. We subsequently transduced the livers of both 6-week-old Atp7b knockout and wild-type mice through systemic injections and are currently collecting blood samples over time up to 24 weeks to measure SEAP levels and assess the biosensor's ability to accurately measure copper accumulation in hepatocytes. Our work provides a unique solution for monitoring copper levels in animal models, thus aiding the preclinical studies of gene therapy approaches to WD. This could also be applied to animal models of different diseases by changing the copper-sensitive promoter to another metal-responsive one.

Department

Università degli studi di Napoli Federico II, DIETI

Primary author(s) : Ms. FUSCO, Virginia (Università degli studi di Napoli Federico II); Dr. DE CARLUCCIO, Giuliano (MIT); Dr. PICCOLO, Pasquale (TIGEM); Prof. DI BERNARDO, Diego (Università degli studi di Napoli Federico II)

Presenter(s) : Ms. FUSCO, Virginia (Università degli studi di Napoli Federico II)

Contribution ID : 67

Type : **not specified**

Understanding Epigenetics of Sex Bias in Immune reactions by X chromosome inactivation

Immune functions have a general sex bias, with women showing stronger immune responses to pathogens and being more susceptible than men to autoimmune diseases. The presence of two X chromosomes has been widely associated with autoimmunity, independently of sex hormones. This might be explained by a failure of the mammalian sex-dosage compensation mechanism by which one of the two female X chromosomes is transcriptionally silenced. X chromosome inactivation (XCI) is controlled by the long non coding RNA XIST, which coats the inactive X chromosome (Xi) and recruits further chromatin repressive complexes. I have previously shown that delocalization of XIST from the underlying Xi chromosome territory is associated with increased gene escape from Xi silencing and/or reactivation^{1,2}. Here, we show that XIST RNA is delocalized in human T lymphocytes and comes back onto the Xi upon activation. Interestingly, XIST re-localization is incomplete and delayed in Multiple Sclerosis (MS) patients, an autoimmune disease that affects women more than men (3:1 ratio). This suggests that lymphocytes might have a more dynamic control of XCI leading to a wider number of genes escaping silencing and further hampered in autoimmune conditions. To test this hypothesis, we performed single-cell RNA sequencing on human T lymphocytes from MS patients and healthy controls and identified sex-differences in cell subtypes and gene expression. Notably, we have validated Xi escape of sex-differentially expressed genes and are currently investigating both the mechanistic role of XIST delocalization and the functional impact of candidate gene overexpression in specific lymphocyte subpopulations. The latest results will be presented.

References

1. Cantone I et al. Ordered chromatin changes and human X chromosome reactivation by cell fusion-mediated pluripotent reprogramming. *Nature Comm* (2016) PMID: 27507283
2. Cantone* I et al Allele-specific analysis of cell fusion-mediated pluripotent reprogramming reveals distinct and predictive susceptibilities of human X-linked genes to reactivation. *Genome Biol* (2017) PMID: 28118853

Department

Department of Molecular Medicine and Medical Biotechnology, University of Naples Federico II, Naples, Italy

Primary author(s) : Dr. SPAZIANO, Alessandra (Department of Molecular Medicine and Medical Biotechnology, University of Naples Federico II, Naples, Italy); Ms. PAGLIUSO, Anna (Department of Molecular Medicine and Medical Biotechnology, University of Naples Federico II, Naples, Italy); AD-DEO MARTINA (Department of Molecular Medicine and Medical Biotechnology, University of Naples Federico II, Naples, Italy); Ms. ZOPPOLI, Pietro (Sequencing facility, Department of Molecular Medicine and Medical Biotechnology, University of Naples Federico II, Naples, Italy); TOMEIO, Rita (ASL Caserta, San Giuseppe Moscati Hospital); MISSO, Saverio (ASL Caserta, San Giuseppe Moscati Hospital); MAN-ISCALCO, Giorgia Teresa (Multiple Sclerosis Regional Centre, Hospital Cardarelli, Naples, Italy); BRES-CIA MORRA, Vincenzo (Multiple Sclerosis Clinic, University Hospital and University of Naples Federico II, Naples, Italy); Dr. CANTONE, Irene (Department of Molecular Medicine and Medical Biotechnology, University of Naples Federico II, Naples, Italy)

Presenter(s): Dr. CANTONE, Irene (Department of Molecular Medicine and Medical Biotechnology, University of Naples Federico II, Naples, Italy)

Contribution ID : 68

Type : **not specified**

AI-based Design Workflow of De-Novo Antigens by Epitope Scaffolding

De-novo protein design allows a wider exploration of protein folding space than directed evolution and has been profitably employed in several fields of biochemistry and medicine, as metalloprotein design¹ and in-vitro diagnostics (IVD)¹. Among other design tasks, de novo protein binders can now be obtained with high success-rate that are highly specific towards a series of biological targets, thanks to the recent advances in the AI field [3,4,5]. Despite that, IVD industry still heavily relies on antibodies, as they are cheaper, and their production is well standardized. Therefore, a de-novo antigen may virtually speed-up and support the production of better antibodies. In this work, we present a workflow to scaffold small proteins (~50AA) around a known antigen epitope to elicit higher immune response in host organisms. The workflow is divided in two cyclic phases: generation and validation, each one using task-specific AI-models. The generation phase starts by creating several backbones of small scaffolds via diffusion models¹ around a chosen epitope, whose position and residues are held constant during the process. Subsequently, protein language models¹ are used on such backbones to assign the sequences. The structure of the generated sequences is then predicted through in-silico folding models¹ and the most promising sequences are screened in-silico for immunogenicity with MaSIF¹, a model evaluating protein-protein interaction sites based on geometric neural network. The methodology has been performed on one epitope of HPV-16, obtaining 6 different small proteins which are currently being screened in-vitro. The proposed workflow is fully generalizable to any epitope, and we envision that it can pose a novel methodology in the design of the de-novo antigens.

¹ Chino, M., Di Costanzo, L.F., Leone, L. et al. "Designed Rubredoxin miniature in a fully artificial electron chain triggered by visible light". *Nat Commun* 14, 2368 (2023). DOI: 1.

² Chu, A.E., Lu, T. & Huang, P.S. "Sparks of function by de novo protein design". *Nat Biotechnol* 42, 203–215 (2024). DOI: 2.

³ Watson, J.L., Juergens, D., Bennett, N.R. et al. "De novo design of protein structure and function with RFdiffusion". *Nature* 620, 1089–1100 (2023). DOI: 3.

⁴ Dauparas J. et al. "Robust deep learning-based protein sequence design using ProteinMPNN". *Science* 378,49-56(2022). DOI: 4.

⁵ Wu, R. et al. "High-resolution de novo structure prediction from primary sequence". *BioRxiv* (2022). DOI: 5.

⁶ Gainza, P., Sverrisson, F., Monti, F. et al. "Deciphering interaction fingerprints from protein molecular surfaces using geometric deep learning". *Nat Methods* 17, 184–192 (2020). DOI: 6.

Department

Dipartimento di Scienze Chimiche

Primary author(s) : CHINO, MARCO (Department of Chemical Sciences, University of Naples "Federico II"); ALTIERO, FRANCESCO (Università degli Studi di Napoli Federico II, Italy)

Presenter(s) : ALTIERO, FRANCESCO (Università degli Studi di Napoli Federico II, Italy)

Contribution ID : 69

Type : **not specified**

Multicellular PID Control of Gene Expression in Microbial Consortia

Synthetic Biology aims at the design and implementation of novel, and more reliable, genetic circuits by employing engineering principles, with applications ranging from health treatments to bioremediation and production of drugs or biofuels. The use of biomolecular PID controllers is particularly appealing in this field as it allows achieving perfect robust adaptation via the integral action as well as to exploit the proportional and derivative actions to modulate the steady-state and transient dynamics of the controlled process. However, embedding all the required circuits to implement a PID controller in a single cell could cause excessive metabolic burden and be cumbersome to implement *in vivo*; also requiring a complete redesign if the target process to be regulated changes or the parameters of the control action need to be varied. To overcome these problems we present a multicellular implementation of the classical PID feedback controller to regulate gene expression in a microbial consortium. Specifically, we propose to distribute the proportional, derivative and integral control actions between different cellular populations in a microbial consortium comprising a target population whose output needs to be regulated. By engineering communication among the different cellular populations via appropriate orthogonal quorum sensing molecules, we are able to close the feedback loop across the consortium. We derive analytical conditions on the biological parameters and the control gains that can be used to tune the static and dynamical properties of the closed-loop system, guaranteeing the regulation of the output of the target population. Finally, we evaluate the performance and robustness of the proposed multicellular control strategy via extensive *in silico* experiments in BSim, a realistic agent-based simulator of bacterial populations.

Department

Electrical Engineering and Information Technology

Primary author(s): MARTINELLI, Vittoria (University of Naples Federico II); FIORE, Davide; SALZANO, Davide; DI BERNARDO, Mario

Presenter(s): MARTINELLI, Vittoria (University of Naples Federico II)

Contribution ID : 70

Type : **not specified**

Serum multi-omics approach may help redefine management guidelines for patients with Glycogen storage disease type Ia

Glycogen storage diseases are inherited disorders of carbohydrate metabolism resulting from the deficiency of individual enzymes involved in the synthesis, transport and breakdown of glycogen 1. In particular, glycogen storage disease type Ia (GSDIa) is caused by deficient activity of glucose-6-phosphatase, which plays a key role in glucose homeostasis by hydrolysing glucose-6-phosphate (G6P) to glucose and phosphate in the final step of gluconeogenesis and glycogenolysis. As a result, patients with GSDIa accumulate G6P, leading to excessive storage of glycogen and fat in the tissues. Specifically, the clinical picture of GSDIa includes a broad spectrum of biochemical alterations (e.g. hypoglycaemia, lactic acidemia, hyperlipidaemia, hyperuricaemia) and clinical manifestations (e.g. hepatomegaly, growth retardation, renal disease) that, if not properly managed, may lead to secondary metabolic disorders and/or disease complications (e.g. hepatic adenomas and carcinoma, chronic kidney disease). For patients with GSDIa, adherence to a highly individualised dietary regimen is the mainstay of treatment and has improved prognosis and long-term outcomes in recent decades. Nevertheless, the (re-)definition of guidelines for the management of patients with GSDIa remains a critical and essential priority 1. To this end, an integrative multi-omics approach including mass spectrometry-based proteomics and metabolomics was carried out on serum samples from n. 12 patients with GSDIa (8 males and 4 females, median age 16.5 ± 9 years, age range 5-34 years) and n. 12 age- and sex-matched healthy controls (HC) to better dissect the metabolic perturbations occurring in GSDIa. Univariate and multivariate statistical methods were used for downstream data analysis. In addition, correlation analyses based on Pearson's coefficient were performed to define a GSDIa-specific multi-omics serum profile by examining the strength and direction of relationships between omics features. Overall, the analyses revealed a specific multi-omics serum profile and protein-metabolite network signature in patients with GSDIa in comparison to HC, shedding new light on the pivotal role of the liver in the pathogenesis of GSDIa and providing new insights into the metabolic alterations in GSDIa. Collectively, and combined with our previous lipidomics findings on GSDIa 1, our results may help to redefine recommendations for the management of GSDIa and develop strategies to counteract disease complications.

1 Koeberl DD et al, J Inherit Metab Dis 2024, DOI: 10.1002/jimd.12654. 1 Derks TGJ et al, Nutrients 2021, DOI: 10.3390/nu13113828. 1 Rossi et al, J Lipid Res 2024, DOI: 10.1016/j.jlr.2024.100651

Department

Department of Molecular Medicine and Medical Biotechnology, University of Naples Federico II, NAPOLI, Italy

Primary author(s) : Mrs. PIROZZI, Francesca (Department of Molecular Medicine and Medical Biotechnology, University of Naples Federico II, NAPOLI, Italy; CEINGE Biotecnologie Avanzate Franco Salvatore s.c.a r.l., NAPOLI, Italy.)

Co-author(s) : Mr. AMIRI, Ramin (Department of Civil, Chemical, Environmental and Materials Engineering (DICAM), University of Bologna ALMA MATER STUDIORUM, Bologna, Italy); Prof. LUNI, Camilla (Department of Civil, Chemical, Environmental and Materials Engineering (DICAM), University of Bologna ALMA MATER STUDIORUM, Bologna, Italy); Dr. ROSSI, Alessandro (Department of Translational Medical Science, Section of Pediatrics, University of Naples Federico II, NAPOLI, Italy); Prof.

MELIS, Daniela (Department of Medicine, Surgery and Dentistry "Scuola Medica Salernitana", University of Salerno, Baronissi (SA), Italy); Mrs. FEDELE, Roberta (CEINGE Biotecnologie Avanzate Franco Salvatore s.c.a r.l., NAPOLI, Italy.); Mrs. ROSANO, Carmen (Department of Translational Medical Science, Section of Pediatrics, University of Naples Federico II, NAPOLI, Italy); Prof. STRISCIUGLIO, Pietro (Department of Translational Medical Science, Section of Pediatrics, University of Naples Federico II, NAPOLI, Italy); Prof. OOSTERVEER, Maaïke H (Department of Pediatrics and Laboratory Medicine, University Medical Center Groningen, University of Groningen, Groningen, The Netherlands); Prof. DERKS, Terry GJ (Section of Metabolic Diseases, Beatrix Children's Hospital, University Medical Centre Groningen, University of Groningen, Groningen, The Netherlands); Prof. PARENTI, Giancarlo (Department of Translational Medical Science, Section of Pediatrics, University of Naples Federico II, NAPOLI, Italy; Telethon Institute of Genetics and Medicine, Pozzuoli, Italy.); Dr. CATERINO, Marianna (Department of Molecular Medicine and Medical Biotechnology, University of Naples Federico II, NAPOLI, Italy; CEINGE Biotecnologie Avanzate Franco Salvatore s.c.a r.l., NAPOLI, Italy.); Prof. RUOPPOLO, Margherita (Department of Molecular Medicine and Medical Biotechnology, University of Naples Federico II, NAPOLI, Italy; CEINGE Biotecnologie Avanzate Franco Salvatore s.c.a r.l., NAPOLI, Italy.)

Presenter(s): Mrs. PIROZZI, Francesca (Department of Molecular Medicine and Medical Biotechnology, University of Naples Federico II, NAPOLI, Italy; CEINGE Biotecnologie Avanzate Franco Salvatore s.c.a r.l., NAPOLI, Italy.)

Contribution ID : 71

Type : **not specified**

The oncogenic role of noncoding single nucleotide variants at adrenergic and mesenchymal neuroblastoma core regulatory circuitries active binding sites

Introduction

Neuroblastoma (NB) is a pediatric malignancy originating from neural crest cells (NCCs) during sympathetic nervous system development. NB is a heterogeneous tumor composed by two distinct cell identities: the most differentiated adrenergic (ADRN) identity, and the most aggressive mesenchymal (MES) one. Perturbations in the activity of transcription factors (TFs) involved in core regulatory circuitries (CRCs), transcriptional networks governing NB-specific gene expression programs, lead to the arising of ADRN and MES phenotypes. Our hypothesis is that somatic single nucleotide variants (SNVs) in CRCs active transcription factor binding sites (aTFBSs) underlie such perturbations, affecting the normal transcriptional activity of CRC TFs, impacting the normal differentiation of NCCs and driving NB onset.

Aim

Our aim is to investigate mutated CRCs aTFBSs, their target-genes and explore the role of selected putative noncoding drivers in NB tumorigenesis.

Methods

We identified aTFBSs analyzing 42 ChIP-seq and 12 ATAC-seq from 7 ADRN and 2 MES NB cell lines. Then, we applied Fisher test to test aTFBSs for the enrichment of SNVs from whole-genome sequencing (WGS) data of 397 NBs. We compared overall survival (OS) and event-free survival (EFS) rates between patients with and without SNVs enriching aTFBSs. Putative drivers affecting CRC TF binding were identified using the FABIAN-variant tool. Next, we identified aTFBSs target-genes through promoter capture Hi-C data of 2 ADRN and 2 MES NB cell lines and correlated their expression with clinical data from 498 NB cases.

Results

We found significantly mutated sets of aTFBSs interacting with 5 ADRN TFs (GATA3, HAND2, ISL1, MYCN, TBX2) and 1 MES TF (FOSL2) ($FDR \leq 0.1$). Patients with SNVs enriching aTFBSs were characterized by lower survival rates compared to wild types, supporting the prognostic significance of these alterations. A total of 689 SNVs impairing CRCs TF binding (Fabian $\neq 0$) were found to interact with genes of neuronal differentiation and MES cell proliferation, highlighting the role of SNVs in defining NB identities. Considering target-genes of aTFBSs with SNVs selected on a more stringent threshold (Fabian ≥ 0.1 or ≤ -0.1), we found several genes (*ROBO2*, *CACNB1*, *PIK3R1*, *MDGA1*, *HES6*, *LDLRAD4*, *DGUOK*, *IRX1*, *SPOCK2*) whose expression correlated with poorer NB outcomes ($FDR \leq 0.05$).

Conclusions

These findings indicate that noncoding SNVs in NB CRC aTFBSs can jointly influence the expression of genes defining NB identities and lead to tumorigenesis.

Recent publications

1. Avitabile M, Bonfiglio F, **Aievola V**, Cantalupo S, Maiorino T, Lasorsa VA, Domenicotti C, Marengo B, Zbyněk H, Vojtěch A, Iolascon A, Capasso M. Single-cell transcriptomics of neuroblastoma identifies chemoresistance-associated genes and pathways. *Comput Struct Biotechnol J*. 2022 Aug 18;20:4437-4445. doi: 10.1016/j.csbj.2022.08.031. PMID: 36051886.

2. Bonfiglio F, Lasorsa VA, Cantalupo S, D'Alterio G, **Aievola V**, Boccia A, Ardito M, Furini S, Renieri A, Morini M, Stainczyk S, Westermann F, Paoella G, Eva A, Iolascon A, Capasso M. Inherited rare variants in homologous recombination and neurodevelopmental genes are associated with increased risk of neuroblastoma. *EBioMedicine*. 2023 Jan;87:104395. doi: 10.1016/j.ebiom.2022.104395. Epub 2022 Dec 6. PMID: 36493725.
3. Bonfiglio F, Lasorsa VA, **Aievola V**, Cantalupo S, Morini M, Ardito M, Conte M, Fragola M, Eva A, Corrias MV, Iolascon A, Capasso M. Exploring the role of HLA variants in neuroblastoma susceptibility through whole exome sequencing. *HLA*. 2024 May;103(5):e15515. doi: 10.1111/tan.15515. PMID: 38747019.

Department

Dip. di Medicina Molecolare e Biotecnologie Mediche, Università degli Studi di Napoli Federico II, Napoli

Primary author(s): Dr. AIEVOLA, Vincenzo (Dip. di Medicina Molecolare e Biotecnologie Mediche, Università degli Studi di Napoli Federico II, Napoli)

Co-author(s): Dr. LASORSA, Vito Alessandro (CEINGE Biotecnologie Avanzate Franco Salvatore s.c.ar.l., Napoli); Ms. MONTELLA, Annalaura (Dip. di Medicina Molecolare e Biotecnologie Mediche, Università degli Studi di Napoli Federico II, Napoli); Dr. BONFIGLIO, Ferdinando (Dip. di Medicina Molecolare e Biotecnologie Mediche, Università degli Studi di Napoli Federico II, Napoli); Dr. AVITABILE, Marianna (Dip. di Medicina Molecolare e Biotecnologie Mediche, Università degli Studi di Napoli Federico II, Napoli); Dr. MAIORINO, Teresa (Dip. di Medicina Molecolare e Biotecnologie Mediche, Università degli Studi di Napoli Federico II, Napoli); Dr. TIRELLI, Matilde (Dipartimento di Ingegneria Chimica, dei Materiali e della Produzione Industriale, Università degli Studi di Napoli Federico II, Napoli); Dr. D'ALTERIO, Giuseppe (CEINGE Biotecnologie Avanzate Franco Salvatore s.c.ar.l., Napoli); Prof. FISCHER, Matthias (Dept. of Experimental Pediatric Oncology, University Children's Hospital of Cologne, Medical Faculty, Cologne); Prof. WESTERMANN, Frank (Hopp Children's Cancer Center, Heidelberg); Prof. IOLASCON, Achille (Dip. di Medicina Molecolare e Biotecnologie Mediche, Università degli Studi di Napoli Federico II, Napoli); Prof. CAPASSO, Mario (Dip. di Medicina Molecolare e Biotecnologie Mediche, Università degli Studi di Napoli Federico II, Napoli)

Presenter(s): Dr. AIEVOLA, Vincenzo (Dip. di Medicina Molecolare e Biotecnologie Mediche, Università degli Studi di Napoli Federico II, Napoli)

Contribution ID : 72

Type : **not specified**

CTpredX: Enhancing Missense Variant Pathogenicity Prediction in Childhood Cancer Predisposition Genes

Effective clinical genome interpretation relies on accurately distinguishing between benign and pathogenic rare variants. Current genome-wide trained variant prioritization tools often lack precision and may overlook key parameters defining gene-disease relationships. We hypothesized that developing predictors based on curated, disease-specific gene sets could significantly enhance the performance of these tools.

We developed CTpredX, a machine learning-based predictor specifically tailored for a curated set of childhood cancer predisposition genes (CCPGs). CTpredX was trained through an Extreme Gradient Boosting algorithm using ClinVar annotations as a ground truth, integrating multiple variant annotations, constraint scores, and existing pathogenicity predictors.

CTpredX outperformed existing genome-wide tools in distinguishing pathogenic from benign variants within CCPGs, achieving an AUC-ROC=0.98 in the testing dataset. Benchmarking against established prediction tools also demonstrated superior performance in terms of accuracy in distinguishing pathogenic from benign variants at high confidence levels. Additionally, CTpredX reclassified 56% of ClinVar's variants of uncertain significance (VUS), with 37.8% of them re-classified as benign and 18.3% as pathogenic.

CTpredX provides a robust tool for pathogenicity prediction of missense variants in childhood cancer, supporting the feasibility of disease-specific variant classifiers. A user-friendly R-shiny interface facilitates broader use in clinical and research settings.

Speaker recent publications:

- Bonfiglio F, Lasorsa VA, Aievola V, Cantalupo S, Morini M, Ardito M, Conte M, Fragola M, Eva A, Corrias MV, Iolascon A, Capasso M. Exploring the role of HLA variants in neuroblastoma susceptibility through whole exome sequencing. *HLA*. 2024 May;103(5):e15515. doi: 10.1111/tan.15515. PMID: 38747019.
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Department

Molecular Medicine and Medical Biotechnology

Primary author(s) : Dr. BONFIGLIO, Ferdinando (University of Naples Federico II)

Co-author(s) : Dr. LASORSA, Vito Alessandro (CEINGE Biotecnologie Avanzate Franco Salvatore s.c.ar.l., Napoli); PIROZZI, Giampiero (Università degli Studi di Napoli "Federico II"); Prof. IOLASCON, Achille (Università degli Studi di Napoli Federico II); Prof. CAPASSO, Mario (Dip. di Medicina Molecolare e Biotecnologie Mediche, Università degli Studi di Napoli Federico II, Napoli)

Presenter(s) : Dr. BONFIGLIO, Ferdinando (University of Naples Federico II)

Contribution ID : 73

Type : **not specified**

Impact of rare synonymous variants on cancer predisposition

Background: Although synonymous variants do not alter protein sequences, they can influence gene regulatory functions like splicing, transcription factor binding, codon optimality, and mRNA stability. Their role in cancer predisposition and rare genetic disease development remains unclear. **Aim:** To evaluate the potential impact of rare synonymous variants in neuroblastoma (NB), a pediatric cancer originating from aberrant neural crest cell development. **Methods:** Whole-exome sequencing was performed on 724 NB patients to identify rare synonymous variants with an allele frequency below 0.01 in non-Finnish European population database. Variants in 675 cancer predisposition genes (CPGs) from five gene lists were analyzed. The identified variants were classified according to their function based on the Cancer Gene Census list of cancer-associated genes. SpliceAI assessed splicing impact using cut-offs (0.8, 0.5, 0.2). Variants were annotated by their distance from the nearest exon-intron boundary and occurrence in the first or last exon. The genes in which variants occurred were subject to gene enrichment analysis for "Disease" and "Reactome" categories. The impact of sSNV on transcriptional factor binding was evaluated building a consensus of open chromatin regions identified through DNaseI, Footprint and ChIP seq data. ATAC-seq data from 23 NB cell lines identified regulatory elements for mesenchymal (MES) and adrenergic (ADRN) NB identities. **Results:** We identified 3923 rare synonymous variants (0.84% of the variants annotated) in 543 CPGs, with a median of 5 mutations per gene. Synonymous variants were enriched in the 'tumor suppressor gene' category (TSG) (26.9%) compared to 'oncogenes' (6.7%). Of the identified genes, 191 (4.86%) had at least a mutation in their last exon, 60 (1.52%) in their first exon, and 28 (0.71%) in both exons. Gene enrichment analysis WebGestalt tool revealed that the 191 genes enriched specifically for NB disease category and DNA repair pathway. Interestingly, this enrichment was observed only with mutations in the last exon, suggesting their role in altering gene expression regulation, mRNA stability, or transcript termination. Most mutations were in tumor suppressor genes across all SpliceAI cutoffs. At the 0.5 cutoff, twenty-two genes, including SMARCA4, ATM, PALB2, FANCA and RTEL1, were identified across multiple gene lists. Synonymous variants in regulatory regions of adrenergic and mesenchymal NB had higher median CADD scores, suggesting their biological significance in altering the gene expression regulation. **Conclusions:** Our findings suggest that synonymous variants can influence splicing, gene regulation and consequently predisposition to NB. Variants in regulatory regions exhibit higher pathogenicity scores, suggesting involvement in gene regulatory mechanisms such as alterations of transcription factor binding sites. Additional studies are ongoing to investigate the role of other types of functional synonymous variants (splicing regulation, transcription factor binding, miRNA binding, codon optimality, and mRNA secondary structure). Further studies are also in progress to assess the potential impact of synonymous variants, on the previously described mechanism, in other pediatric tumors.

Department

University of Naples Federico II, Department of Electrical Engineering and Information Technologies, Naples, Italy

Primary author(s): ESTINTO, GILDA

Co-author(s): BONFIGLIO, Ferdinando (University of Naples Federico II); LASORSA, Vito Alessandro (CEINGE - Biotecnologie Avanzate Scarl); AIEVOLA, Vincenzo (Department of Molecular Medicine and Medical Biotechnologies, University of Naples Federico II, Naples 80131, Italy); Dr. D'ALTERIO, Giuseppe (CEINGE Biotecnologie Avanzate Franco Salvatore s.c.ar.l., Napoli); Prof. IOLASCON, Achille (Dip. di Medicina Molecolare e Biotecnologie Mediche, Università degli Studi di Napoli Federico II, Napoli); Prof. CAPASSO, Mario (Dip. di Medicina Molecolare e Biotecnologie Mediche, Università degli Studi di Napoli Federico II, Napoli)

Presenter(s): ESTINTO, GILDA

Contribution ID : 74

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Proteome and bioinformatic analyses of cellular models of methylmalonic acidemia reveal lysosomal dysregulations

Background. Methylmalonic acidemia (MMA) is the most common form of organic acidemias, an heterogeneous group of rare inherited metabolic disorders that affect amino acid and protein metabolism. As suggested by their name, organic acidemias are characterized by the accumulation of organic acids at toxic concentrations. Isolated methylmalonic acidemia is caused by impaired activity/expression of the enzyme methylmalonyl-CoA mutase (MUT). MUT deficiency determines the increase of methylmalonyl-CoA and methylmalonic acid, causing severe dysfunctions in various metabolic pathways and mitochondrial damage, with significant impacts on organs such as brain, liver, and kidneys. Owing to the complexity of the disorder, many of the systemic dysfunctions in MMA have not been fully mechanistically validated ¹.

Methods. The proteomic landscape of MMA was investigated using diverse cell models. First, a MUT-knockout (MUT-KO) cell line was generated via CRISPR/Cas9 in HEK-293 cells. Also, the expression of a MUT-FLAG protein was rescued in these cells (MUT-Rescue). Finally, dermal fibroblasts derived from MMA patients were collected and cultured. Through the combination of high-resolution proteomics and bioinformatics analysis, the whole cell proteomes and their sub-proteomes were characterized ² to refine and uncover new pathologic mechanisms connected with MUT deficiency.

Results. In this study, a data-independent acquisition (DIA) proteomic approach was used to simultaneously compare the proteomes of the three cell lines: WT, MUT-KO and MUT-Rescue. Profile analysis was performed to select the significant proteins according to their trend of regulation: indeed, two clusters of proteins were highlighted as the most significantly changing (up or down) in MUT-KO compared to WT and MUT-Rescue. Gene Set Enrichment analysis (GSEA) of the whole proteome dataset enriched several terms positively correlated with the MUT-KO condition and which correspond with several known features of MMA pathophysiology, including oxidative phosphorylation and lysosomal dysfunction. However, two of the most interesting dysregulations not yet associated with MUT deficiency occurred for lysosome-associated membrane glycoprotein 2 (LAMP2) and stathmin (STMN1), which both showed decreased signals in MUT-KO cells. To corroborate these findings, we explored the proteome of MMA fibroblasts and found down-regulated proteins common to the MUT-KO model, such as LAMP2. Being LAMP2 a component of the lysosomal membrane, we investigated possible changes in the levels of other lysosomal and autophagy markers in MMA fibroblasts, revealing up-regulation of LAMP1, LC3 and its cleaved form LC3-II, and p62. To elucidate the effects of MUT deficiency on lysosomal and autophagy regulation, we also analyzed the morphology and functionality of MMA-lysosomes that showed deep alterations. At the same time, also the measurement of the autophagic flux in MMA cells resulted strongly impaired. Notwithstanding, the treatment with an anti-propionigenic drug was capable of totally rescuing lysosomal morphology and functional activity in MUT-deficient cells. These results indicate a strict connection between MUT deficiency and lysosomal-autophagy dysfunction.

Conclusions. Our proteomic data ³ show that MUT deficiency is connected with profound proteome dysregulations, revealing molecular actors involved in lysosome and autophagy functioning. In this study, we demonstrate that MUT-deficient cells have defective homeostatic mechanisms in the regulation of autophagy and lysosome functions, demonstrating that MMA triggers such dysfunctions impacting on autophagosome-lysosome fusion and lysosomal activity.

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Department

Department of Molecular Medicine and Medical Biotechnology, University of Naples Federico II, Via S. Pansini 5, 80131 Naples, Italy

Primary author(s): Dr. BIANCO, Sabrina (Department of Molecular Medicine and Medical Biotechnology, University of Naples Federico II, NAPOLI, Italy; CEINGE Biotecnologie Avanzate Franco Salvatore s.c.a r.l., NAPOLI, Italy.); Dr. CEVENINI, Armando (Department of Molecular Medicine and Medical Biotechnology, University of Naples Federico II, NAPOLI, Italy; CEINGE Biotecnologie Avanzate Franco Salvatore s.c.a r.l., NAPOLI, Italy.); Dr. CATERINO, Marianna (Department of Molecular Medicine and Medical Biotechnology, University of Naples Federico II, NAPOLI, Italy; CEINGE Biotecnologie Avanzate Franco Salvatore s.c.a r.l., NAPOLI, Italy.); Dr. COSTANZO, Michele (Department of Molecular Medicine and Medical Biotechnology, University of Naples Federico II, NAPOLI, Italy; CEINGE Biotecnologie Avanzate Franco Salvatore s.c.a r.l., NAPOLI, Italy.); Prof. RUOPPOLO, Margherita (Department of Molecular Medicine and Medical Biotechnology, University of Naples Federico II, NAPOLI, Italy; CEINGE Biotecnologie Avanzate Franco Salvatore s.c.a r.l., NAPOLI, Italy.)

Presenter(s): Dr. BIANCO, Sabrina (Department of Molecular Medicine and Medical Biotechnology, University of Naples Federico II, NAPOLI, Italy; CEINGE Biotecnologie Avanzate Franco Salvatore s.c.a r.l., NAPOLI, Italy.)

Contribution ID : 75

Type : **not specified**

Towards Exabyte-Scale Genomics: Advanced Hardware-Software Solutions for Efficient Read Mapping

DNA analysis has become fundamental to various fields, including *disease treatment* 1, *outbreak surveillance* 1, *forensic investigations* 1, and *evolutionary studies* 1. The rise of large-scale genomics and advanced sequencing technologies, such as Oxford Nanopore Technologies, has led to an exponential increase in data generation, far surpassing *Moore's Law* 1. By 2024-2025, genomic data production is expected to range from exabytes (2^{50}) to zettabytes (2^{60}). This data explosion, coupled with progressively longer sequences constituting the new datasets, also called reads, poses significant challenges in terms of data storage, processing, and analysis. At the heart of these challenges lies the **read mapping** process, which is essential for aligning sequencing reads to a reference genome. The sheer volume of data now demands hours to days of computation, even on powerful servers with optimized tools. Input datasets often exceed hundreds of gigabytes, and peak memory requirements can reach tens of gigabytes, particularly for large genomes like the human genome. This massive computational demand highlights the need for more efficient solutions to handle the growing complexity and scale of genomic data.

Our goal is to tackle these challenges by proposing a hardware-software co-design approach that enhances the efficiency of read mapping in terms of both time and speed. Conventional General Purpose Graphics Processing Units (GPGPUs) and hardware accelerators like Field-Programmable Gate Arrays (FPGAs) are constrained by their limited memory capacity, making them insufficient for handling the entire read mapping workflow given the vast scale of the datasets generated. To overcome this limitation, we have developed a heuristic-based read mapping pipeline that significantly reduces the amount of data requiring computation. This reduction facilitates a dataflow-oriented model, optimizing the entire read mapping process for execution on massively parallel platforms such as GPUs and FPGAs.

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Department

DIETI - Dipartimento di Ingegneria Elettrica e delle Tecnologie dell'Informazione - Università Degli Studi di Napoli Federico II

Primary author(s) : Mr. MERCOGLIANO, Stefano (Università degli Studi di Napoli Federico II)

Co-author(s) : Prof. CILARDO, Alessandro (Università degli Studi di Napoli Federico II)

Presenter(s) : Mr. MERCOGLIANO, Stefano (Università degli Studi di Napoli Federico II)

Contribution ID : 76

Type : **not specified**

Simulation of cell morphology using models derived from cell features and components

Simulation of cell populations can be carried out by using parameters obtained from experimental cell cultures producing cells defined in terms of position, size or growth state. However representation of cell shape is desirable in order to better visualise the results as well as predicting interactions with the culture substrate or between bordering cells. Here we describe a procedure for prediction and visualisation of cell shape according to cell parameters such as volume, attachment status, growth conditions, movement and interaction with other cells. Cells are simulated as “2.5-dimensional” objects, where a relatively detailed two-dimensional footprint is complemented by a volume-dependent thickness to provide the third dimension. Detached cells are modelled as simple spheres freely floating in the medium, but as they become attached, they spread and flatten on the substrate, modifying height and surface, according to a cell specific index that numerically describes the spreading degree. After spreading, cells assume their final morphology (i.e. circular, polygonal or star-shaped), that is modelled by using a polygonal representation where contours are described by vertices connected by Bezier curves. This process causes cells to redistribute their internal volume into a different shape which requires a larger membrane surface, modelled as an internal membrane reservoir which can quickly bring new membrane to the surface. To take movement into account, changes in morphology, normally observed in cultured cells when they move and possibly interact with each other, are obtained modifying the previously defined shape by updating the entire set of vertices and curves following changes in position and formation of contacts between touching cells. The system was integrated within SimulCell, an *in silico* simulation tool developed in-house, where each cell is an independent agent able to interact with the surrounding cells and the external environment. Visualisation techniques, similar to sample staining in fluorescence microscopy, were also introduced to visually highlight structural and molecular aspects of individual cells as well as time-dependent differences.

Department

Department of Molecular Medicine and Medical Biotechnology, University of Naples Federico II, Naples, Italy

Primary author(s): Dr. CIMMINO, Elena (Department of Molecular Medicine and Medical Biotechnology, University of Naples Federico II, Naples, Italy); Dr. TOSCANO, Elvira (Department of Molecular Medicine and Medical Biotechnology, University of Naples Federico II, Naples, Italy); Dr. SEPE, Leandra (Department of Molecular Medicine and Medical Biotechnology, University of Naples Federico II, Naples, Italy); Prof. PAOLELLA, Giovanni (Department of Molecular Medicine and Medical Biotechnology, University of Naples Federico II, Naples, Italy)

Presenter(s): Dr. CIMMINO, Elena (Department of Molecular Medicine and Medical Biotechnology, University of Naples Federico II, Naples, Italy)

Contribution ID : 77

Type : **not specified**

SimulCell: an in silico simulation system which accurately reproduces the behaviour of specific cell populations growing and migrating on culture dish

Simulations are often used to analyse and dissect complex experimental systems where cells modify their behaviour while moving, growing and adapting to internal and external stimuli. A number of procedures and tools have been proposed aimed to model cell behaviour, ranging from whole cell mass simulation to lattice based models, where cells are represented by one or more lattice elements. More recently, simulation systems have been shifting towards models based on individual cell agents where mass, volume and morphology behave according to more or less precise rules and models. Here we present an agent-based simulation system, SimulCell, where individual cells are simulated by using models of cellular processes, such as growth, proliferation and migration, to create synthetic populations which resemble experimental ones. We initially built on a novel motion model, able to describe movement in experimental cell populations using a combination of random, persistence and bias components. The model was extended by adding cell-cell repulsion, movement modifications due to attachment state and mitosis and cell ability to chose a direction by reacting to a field such as that produced by an attractant, among other changes. Within the simulator, in addition to movement features, each cell is also able to individually control its volumetric growth, survival and replication as well as cell cycle transitions following volume changes and external stimuli such as local cell confluence or the presence of growth factors or other drugs in the medium. Support for interactions between cells and their environment was introduced to react to changes in medium composition and other events, such as physical damage or chemical modifications occurring in the culture plate. Integrating all these models and features in SimulCell, and using parameters taken from experimental cell populations, the simulation produces cells that grow, move and undergo cell division modulating their behaviour according to their current state and the surrounding environment. Stochastic changes and combination of many individual cells result in populations which introduce variability in response to different stimuli while preserving the specific features of the original experimental cell population.

Department

Ceinge - Department of Molecular Medicine and Medical Biotechnology, University of Naples Federico II

Primary author(s) : TOSCANO, ELVIRA (Ceinge - University of Naples Federico II); CIMMINO, Elena (<https://indico.unina.it/event/87/registrations/30/?token=fb207e27-d472-4cae-96b3-470f2c961eb9>); Dr. BOCCIA, Angelo (Ceinge - Biotechnologie Avanzate Franco Salvatore, Naples, Italy); Dr. SEPE, Leandra (Department of Molecular Medicine and Medical Biotechnology, University of Naples Federico II, Naples, Italy); Prof. PAOLELLA, Giovanni (Ceinge - University of Naples Federico II)

Presenter(s) : TOSCANO, ELVIRA (Ceinge - University of Naples Federico II)

Contribution ID : 78

Type : **not specified**

Preclinical tumor organoid models in gastric cancer: the missing link for targeted therapy and personalized cancer treatment.

Neoadjuvant chemotherapy (NAC) plays an important role in the therapeutic strategy of locally advanced gastric cancer (GC). Unfortunately, the heterogeneous cellular and molecular nature of GC results in NAC resistance and subsequent loss of benefit in almost 50% of treated patients. Currently, predictive biomarkers to guide perioperative treatment drug selection, are still heterogeneous and hardly applicable to clinical practice. Therefore, it appears crucial to early understand which patients will benefit from NAC, based on reliable predictive factors, in order to personalize the therapeutic approach. It is also relevant to consider that NAC and adjuvant chemotherapy (AC) therapy are related. The aim of this project is to identify pathways and Master Regulator (MRs) associated with NAC efficiency by molecular characterization (various -omics) of patient derived GC fresh-frozen tissues (pGC). In particular, we will investigate whether those biomarkers are intrinsic to the patient or induced by NAC by exploiting the paired pre-NAC biopsies. The secondary aim of the project is to assess whether patient-derived GC organoids (GC-PDOs) are a reliable ex-vivo study model to evaluate and/or predict pharmacological response. GC-PDOs appear promising in addressing this concern. Using GC-PDOs could mimic the complexity of the in vivo situation overcoming the limitations of traditional in vitro and in vivo cancer models. GC-PDOs might enable to properly select patients who could benefit from tailored treatments, optimizing the risk/benefit ratio of chemotherapeutic regimens. Briefly, the pGC analyses may lead to the identification of altered molecular signatures involved in chemoresistance development and to improve the prognosis of patients by predicting the NAC response to therapy and the AC regimen efficacy. Moreover, our proposed GC-PDOs ex-vivo study platform will allow to efficiently test potentially targetable pathways empowering personalized medicine approaches.

Department

Dipartimento di Medicina Molecolare e Biotecnologie Mediche

Primary author(s) : Prof. ZOPPOLI, Pietro (Università degli studi di Napoli Federico II)

Presenter(s) : Prof. ZOPPOLI, Pietro (Università degli studi di Napoli Federico II)

Contribution ID : 79

Type : **not specified**

Strain-resolved metagenomics for human and food microbiome studies

The microbiome plays a critical role in human health and has also become a key focus in the development of food products. Our understanding of these complex microbial communities has been improved thanks to recent advances in metagenomics and computational development that has enabled large-scale integrative analyses. In this talk, we will provide an overview of recent and ongoing research that explores different aspects of strain-resolved metagenomics. Our work includes the development of tools to achieve microbial analysis at the strain level, as well as large-scale studies across diverse environments, with a focus on the intersection between human and food sources. We will also introduce machine learning approaches for predicting host phenotypes from metagenomic data, highlighting the growing potential for integrating computational methods into microbiome research.

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Department

Agricultural Sciences

Primary author(s) : PASOLLI, Edoardo (University of Naples Federico II)

Presenter(s) : PASOLLI, Edoardo (University of Naples Federico II)

Contribution ID : 80

Type : **not specified**

Modelling 2D Nanoflake - Bacterium Interactions in Solutions

Abstract:

Understanding the interaction between nanomaterials and biological membranes is crucial for advancing applications in nanomedicine and antimicrobial therapies. Nanomaterials such as MoS₂ and WS₂ nanoflakes exhibit unique physical properties that could be used for biomedical applications. This study aims to investigate the interaction dynamics between a bacterium such as Staphylococcus aureus (S. aureus), potentially responsible for some important pathologies such as serious forms of pneumonia, and two-dimensional (2D) nanoflakes of MoS₂ and WS₂. The model, based on Molecular Dynamics (MD) simulations, takes into account the material type, its affinity with the bacterial culture, and the concentration of the nanoflakes relative to the bacteria in solution. The study shows that nanoflake material and concentration significantly influence the interactions with and the dynamical approach to the bacterial surface, with MoS₂ and WS₂ displaying distinct behaviours. These insights help potential advance in the use of nanomaterials as antimicrobial agents.

Keywords: Staphylococcus aureus, Molecular Dynamics (MD) Simulations, Nanoflakes, Transition Metal Dichalcogenides (TMDs), Nanomaterials-Bacteria Interaction, LAMMPS

Department

University of Naples Federico II

Primary author(s) : LETO, Nicolas; Dr. ADAM, Jaber; Dr. CHIARIELLO, Andrea Maria (Dipartimento di Fisica Ettore Pancini, Università di Napoli Federico II); Dr. SINGH, Manjot; Dr. VALADAN, Mohammadhassan; Prof. DEL SORBO, Mariarosaria; Dr. BIANCO, Simona; ALTUCCI, CARLO (Dept. of Advanced Biomedical Sciences - Università degli Studi di Napoli Federico II); NICODEMI, MARIO (Università di Napoli "Federico II")

Presenter(s) : LETO, Nicolas; Dr. ADAM, Jaber

Contribution ID : 81

Type : **not specified**

Whole Genome Sequencing Unravels Novel Genomic Variants and Their Impact on Tumor Phenotypes in High-Risk Neuroblastoma

Neuroblastoma (NB) is a pediatric solid tumor, with a median diagnosis age of 18 months. Its presentation varies widely, ranging from low-risk tumors to aggressive disease in high-risk cases with a 5-year survival rate of 50%. Despite numerous identified genomic alterations, the current understanding of NB mutational landscape does not fully explain its heterogeneity. We analyzed Whole Genome Sequencing (WGS) and RNA-seq data from two independent NB cohorts TARGET (n = 136) and EGA (n = 180). We aim to provide a comprehensive overview of NB genomic alterations, focusing on rearrangements (translocation and insertion). We developed pipelines to detect and analyze somatic single nucleotide variants (SNVs), copy-number alterations (CNAs), structural variants (SVs), and germline SNVs. We identified previously unreported SNVs in 3 cancer-related genes: ESR1, MYH9, and SKI. Notably, SKI was overexpressed in the low/intermediate-risk group across both cohorts. We confirmed known CNAs in both high and low/intermediate-risk groups and identified new alterations not previously associated with clinical parameters (chr1 gain, chr2 gain, chr11 loss, chr12 gain, and chr19 loss). The presence of at least one of these aneuploidies predicted survival outcomes, both independently and in multivariate models considering age at diagnosis, INSS stage, MYCN status, and dataset origin. Furthermore, we discovered 5 novel low-frequency SVs in high-risk tumors. These SV breakpoints overlapped with 171 genes, with 12 genes common to both datasets. These genes are involved in synaptic plasticity and in various neurological disorders. Tumors with at least one SV exhibited distinct gene-expression, unique mutational signatures, higher genomic instability and increased tumor mutational burden. Additionally, tumors carrying these SVs were enriched in pathogenic/likely pathogenic germline SNVs in the homologous-recombination (HR) pathway, linking pathway deficiencies to genomic instability. Overall, our analysis identifies novel molecular alterations, define the phenotypes of tumors with SVs, and suggests that rare germline variants in the HR pathway may contribute to genomic instability. These findings could improve NB clinical stratification and our understanding of the genetic predisposition to this tumor.

Department

University of Naples Federico II, Department of Chemical, Materials and Production Engineering, Naples, Italy

Primary author(s) : PIROZZI, Giampiero (Università degli Studi di Napoli "Federico II")

Co-author(s) : Dr. D'ALTERIO, Giuseppe (CEINGE Biotecnologie Avanzate Franco Salvatore s.c.ar.l., Napoli); Dr. LASORSA, Vito Alessandro (CEINGE Biotecnologie Avanzate Franco Salvatore s.c.ar.l., Napoli); BONFIGLIO, Ferdinando (University of Naples Federico II); AIEVOLA, Vincenzo (Department of Molecular Medicine and Medical Biotechnologies, University of Naples Federico II, Naples 80131, Italy); Prof. FISCHER, Matthias (University of Cologne, Children's Hospital and Center for Molecular Medicine, Medical Faculty, Cologne, Germany); Prof. WESTERMANN, Frank (Hopp Children's Cancer Center, Heidelberg, Germany; Division of Neuroblastoma Genomics, German Cancer Research Center,

Heidelberg, Germany); Prof. DISKIN, Sharon (Children's Hospital of Philadelphia, Philadelphia, USA; University of Pennsylvania, Perelman School of Medicine, Philadelphia, USA); IOLASCON, Achille (Università degli Studi di Napoli Federico II); Prof. CAPASSO, Mario (Dip. di Medicina Molecolare e Biotecnologie Mediche, Università degli Studi di Napoli Federico II, Napoli)

Presenter(s): PIROZZI, Giampiero (Università degli Studi di Napoli "Federico II")

Contribution ID : 82

Type : **not specified**

Polymer physics models predict 3D chromatin organization of SARS-CoV-2 infected cells

It has been recently discovered that SARS-CoV-2 alters chromatin 3D structure of the host genome 1 at multiple length scales, ranging from some kbp to entire chromosomes. We use polymer-physics models to investigate the physical mechanisms underlying such re-structuring. In particular, we show that a polymer model with altered chromatin phase-separation properties 1 accurately captures re-arrangements upon viral infection, as emerged from experimental data. Furthermore, Molecular Dynamics (MD) simulations of the model indicate that SARS-CoV-2 infection leads to a peculiar loss of structural specificity and impacts chromatin time dynamics, reducing the stability of the regulatory contact network of key genes involved in the antiviral response. Overall, this study 1 provides the first polymer-physics based 4D reconstruction of SARS-CoV-2 infected genome with mechanistic insights on the consequent gene mis-regulation.

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Department

Dipartimento di Fisica "E. Pancini", Università di Napoli "Federico II"

Primary author(s): Dr. CHIARIELLO, Andrea Maria (Dipartimento di Fisica Ettore Pancini, Università di Napoli Federico II); ABRAHAM, Alex (Dipartimento di Fisica "E. Pancini", Università di Napoli "Federico II"); Dr. ESPOSITO, ANDREA (Università di Napoli Federico II, Dipartimento di Fisica Ettore Pancini); Dr. BIANCO, Simona; FONTANA, Andrea (Università di Napoli "Federico II" and INFN Napoli); VERCELLONE, Francesca (Università degli Studi di Napoli Federico II); Dr. CONTE, Mattia; NICODEMI, MARIO (Università di Napoli "Federico II")

Presenter(s): FONTANA, Andrea (Università di Napoli "Federico II" and INFN Napoli)

Contribution ID : **83**

Type : **not specified**

Prof. Luca Lista (Direttore INFN, Sezione di Napoli)

martedì 22 ottobre 2024 09:43 (8)

Department

Contribution ID : 84

Type : **not specified**

Dr.ssa Valeria Fascione (Assessore alla Ricerca Regione Campania)

martedì 22 ottobre 2024 10:07 (6)

Department

Contribution ID : 85

Type : **not specified**

Prof.ssa Barbara Majello (Delegato del Rettore alla didattica ed alla innovazione didattica)

martedì 22 ottobre 2024 10:19 (6)

Department

Contribution ID : 86

Type : **not specified**

**Dr. Andrea Maria Chiariello (Dipartimento di Fisica
"Ettore Pancini")**

martedì 22 ottobre 2024 10:55 (5)

Department

Contribution ID : 87

Type : **not specified**

**Prof. Stefano Amente (Dipartimento di Medicina
Molecolare e Biotecnologie Mediche)**

martedì 22 ottobre 2024 10:25 (6)

Department

Contribution ID : **88**

Type : **not specified**

Prof. Edoardo Pasolli (Dipartimento di Agraria)

martedì 22 ottobre 2024 11:54 (6)

Department

Contribution ID : **89**

Type : **not specified**

Prof. Gionata De Vico (Direttore Dipartimento di Biologia)

martedì 22 ottobre 2024 09:51 (8)

Department

Contribution ID : **90**

Type : **not specified**

Prof. Alfonso De Simone (Dipartimento di Farmacia)

martedì 22 ottobre 2024 10:39 (8)

Department

Contribution ID : 91

Type : **not specified**

Prof. Antonello Merlino (Dipartimento di Scienze Chimiche)

martedì 22 ottobre 2024 11:38 (8)

Department

Contribution ID : 92

Type : **not specified**

Prof. Massimiliano Fraldi (Dipartimento di Strutture per l'Ingegneria e l'Architettura)

martedì 22 ottobre 2024 10:47 (8)

Department

Contribution ID : 93

Type : **not specified**

Prof. Carlo Altucci (Dipartimento di Scienze Biomediche Avanzate)

martedì 22 ottobre 2024 10:31 (8)

Department

Contribution ID : 94

Type : **not specified**

The Role of Bioinformatics in Plant Genetic Improvement

The study of major biomolecules within cells, such as DNA, RNA, proteins, and metabolites, has led to the emergence of various omics disciplines (genomics, transcriptomics, proteomics, metabolomics) that generate vast volumes of data, known as big omics data. Managing, analyzing, interpreting, sharing, and integrating this data presents significant challenges in bioinformatics. This field leverages interdisciplinary expertise – spanning molecular biology, computer science, genetics, applied mathematics, and statistics – to extract valuable insights and advance our understanding of complex biological systems. Advances in DNA (genomics) and RNA (transcriptomics) sequencing technologies have revolutionized our ability to investigate genome organization and gene expression across a wide range of agriculturally important species. Understanding genomic sequences is vital for basic research, providing access to genes and the regulatory elements that govern their activity. This knowledge is crucial for studying development, adaptation, and stress responses, exploring genetic diversity, and pinpointing the genetic foundations of complex traits. In plant breeding, bioinformatics plays a key role in genome-driven selection, enabling the identification of optimal allele combinations to achieve desired phenotypes (ideotypes). This discipline is at the forefront of the third green revolution, characterized by cutting-edge biotechnologies such as genome editing and knowledge-based breeding by design, all powered by the vast potential of big data.

Department

Agricultural Sciences

Primary author(s) : D'AGOSTINO, NUNZIO (Department of Agricultural Sciences, University of Naples Federico II)

Presenter(s) : D'AGOSTINO, NUNZIO (Department of Agricultural Sciences, University of Naples Federico II)

Contribution ID : 95

Type : **not specified**

8-oxodG is a driver of the transcription machinery

8-Oxo-7,8-dihydro-2'-deoxyguanosine (8-oxodG), a key product of DNA oxidation, has been identified as an epigenetic factor that influences the transcription process. However, the precise role of 8-oxodG in transcription regulation is not fully established. To investigate the involvement of 8-oxodG in global transcription regulation, we applied two complimentary strategies. First, we inhibited RNAPII activity to determine if the presence of 8-oxodG is dependent on RNAPII mobility. Second, we reduced the amount of genomic 8-oxodG to see how it affected RNAPII mobility. Our findings indicate that 8-oxodG actively enhances transcription rather than being a passive participant.

Department

Dept Molecular Medicine and Medicine Biotechnology

Primary author(s) : GORINI, Francesca; SCALA, Giovanni (University Federico II); AMBROSIO, SUSANNA (Federico II); Prof. LANIA, Luigi (University Federico II of Naples); Prof. MAJELLO, Barbara (Dipartimento di Biologia - Università degli studi di Napoli Federico II); AMENTE, Stefano (University Federico II)

Presenter(s) : GORINI, Francesca

Contribution ID : 96

Type : **not specified**

A novel cluster of putative regulatory sequences modulates Tbx1 gene expression

Background: Tbx1 function is involved in cardiac and pharyngeal development. Information regarding the genetic elements and molecular mechanisms that regulate the gene expression is still incomplete. We used in vitro differentiation, single cell biology, and bioinformatic tools to identify and validate regulatory elements of the gene.

Material and methods: We employed simultaneous single cells RNA-seq and ATAC-seq data from mouse ES cells (mESCs) differentiating into precardiac organoids; on these, we correlated chromatin accessibility and Tbx1 gene expression in distinct cell clusters and identified differentially accessible regions. We applied a machine-learning approach to score the probability of being enhancers using logistic regression. Finally, we manipulated putative enhancers by CRISPR-Cas9 to test their requirement for Tbx1 gene expression.

Results and Conclusion: We identified 14 putative regulatory sequences (PRS) on the Tbx1 locus, through integration of scRNAseq with scATACseq datasets. Using ATAC datasets in public repositories, we confirmed that ATAC peaks corresponding to the PRSs were also present in mouse embryo tissues. We focused on a cluster that includes 3 PRSs, named PRS10, 11, and 12, located approx. 10Kb upstream of the gene. PRS10 and PRS12 had a positive predictive score, while PRS11 had a lower score. With CRISPR-Cas9 technology, we generated mESC lines deleted for the entire cluster and we also deleted the 3 PRSs individually. We then differentiated the engineered clones into precardiac organoids to test the Tbx1 gene expression profile. Loss of the entire cluster and of PRS10 and PRS12 individually, led to strong, significant reduction of Tbx1 expression compared to the parental WT line. These results demonstrate that the enhancer cluster is required for Tbx1 gene regulation. Gene expression analyses of clones lacking only PRS11 gave variable results, but for the majority of clones a reduction in Tbx1 expression was observed. In order to determine whether these PRSs are cell-type specific, we performed a scRNA-seq experiments on precardiac organoids derived from deletions of individual PRSs. Preliminary analysis shows that Tbx1 expression is mostly in a distinct cell cluster and shows a significant reduction of Tbx1 expression in cells deleted for PRS10 and PRS12 and a significant increase in PRS11, compared to WT. These results suggest that the enhancer cluster that we have identified has both positive and negative regulatory sequences of the Tbx1 gene.

Department

Department of Molecular Medicine and Medical Biotechnology, University Federico II, Naples, Italy

Primary author(s): ALLEGRETTI, Sara (PhD program in Molecular Medicine and Medical Biotechnology, University Federico II, Naples, Italy)

Co-author(s): LANZETTA, Olga (Institute of Genetics and Biophysics, National Research Council, Naples, Italy); FERRENTINO, Rosa (Institute of Genetics and Biophysics, National Research Council, Naples, Italy); AURIGEMMA, Ilaria (Department of Chemistry e Biology, University of Salerno, Fisciano, Italy); BALDINI, Antonio (PhD program in Molecular Medicine and Medical Biotechnology, University

Federico II, Naples, Italy)

Presenter(s): ALLEGRETTI, Sara (PhD program in Molecular Medicine and Medical Biotechnology, University Federico II, Naples, Italy)

Contribution ID : **107**

Type : **not specified**

Prof.ssa Franca Esposito (Direttrice del Dipartimento di Medicina Molecolare e Biotecnologie Mediche)

martedì 22 ottobre 2024 09:59 (8)

Department

Contribution ID : **108**

Type : **not specified**

Prof. Alfredo Nicosia (Dip.to di Medicina Molecolare e Biotecnologie Mediche)

martedì 22 ottobre 2024 11:46 (8)

Department

Contribution ID : **109**

Type : **not specified**

The Role of Bioinformatics in Plant Genetic Improvement

martedì 22 ottobre 2024 12:00 (9)

Department

Presenter(s): D'AGOSTINO , Nunzio

Contribution ID : 110

Type : **not specified**

Understanding Epigenetics of Sex Bias in Immune reactions by X chromosome inactivation

martedì 22 ottobre 2024 12:36 (9)

Department

Presenter(s) : CANTONE, Irene

Contribution ID : 111

Type : **not specified**

**Functional Genomics in biomedicine: an integrative
approach dealing with energetic metabolism,
innate immune regulation and calcium (Ca²⁺⁺)
signaling**

martedì 22 ottobre 2024 12:09 (9)

Department

Presenter(s) : ZOLLO, Massimo

Contribution ID : 112

Type : **not specified**

Preclinical tumor organoid models in gastric cancer: the missing link for targeted therapy and personalized cancer treatment

martedì 22 ottobre 2024 12:18 (9)

Department

Presenter(s) : ZOPPOLI, Pietro

Contribution ID : 113

Type : **not specified**

Force-biased nuclear import sets nuclear-cytoplasmic volumetric coupling by osmosis.

martedì 22 ottobre 2024 12:27 (9)

Department

Presenter(s) : MAIURI, Paolo

Contribution ID : 114

Type : **not specified**

From Research to Services and back: integrative comparative approaches and open resources while overcoming scientific silos

martedì 22 ottobre 2024 12:45 (9)

Department

Presenter(s) : CHIUSANO, Maria Luisa

Contribution ID : 115

Type : **not specified**

CTpredX: Enhancing Missense Variant Pathogenicity Prediction in Childhood Cancer Predisposition Genes

martedì 22 ottobre 2024 12:54 (6)

Department

Presenter(s) : BONFIGLIO, Ferdinando

Contribution ID : 116

Type : **not specified**

AI-based Design Workflow of De-Novo Antigens by Epitope Scaffolding

martedì 22 ottobre 2024 14:46 (9)

Department

Presenter(s) : ALTIERO, Francesco

Contribution ID : 117

Type : **not specified**

Mathematical and numerical modeling of hyperthermia-triggered drug delivery

martedì 22 ottobre 2024 14:55 (9)

Department

Presenter(s) : ADABBO, Gabriele

Contribution ID : 118

Type : **not specified**

Serum multi-omics approach may help redefine management guidelines for patients with Glycogen storage disease type Ia

martedì 22 ottobre 2024 15:04 (9)

Department

Presenter(s) : PIROZZI, Francesca

Contribution ID : **119**

Type : **not specified**

Strain-resolved metagenomics for human and food microbiome studies

martedì 22 ottobre 2024 14:37 (9)

Department

Presenter(s) : CAVALIERE, Sara

Contribution ID : **120**

Type : **not specified**

MiDNE: Multi-omics genes and Drugs Network Embedding

martedì 22 ottobre 2024 15:13 (9)

Department

Presenter(s) : BRANDI, Aurora

Contribution ID : **121**

Type : **not specified**

Simulation of cell morphology using models derived from cell features and components

martedì 22 ottobre 2024 15:31 (9)

Department

Presenter(s) : CIMMINO, Elena

Contribution ID : 122

Type : **not specified**

SimulCell: an in silico simulation system which accurately reproduces the behaviour of specific cell populations growing and migrating on culture dish

martedì 22 ottobre 2024 15:22 (9)

Department

Presenter(s) : TOSCANO, Elvira

Contribution ID : 123

Type : **not specified**

The oncogenic role of noncoding single nucleotide variants at adrenergic and mesenchymal neuroblastoma core regulatory circuitries active binding sites

martedì 22 ottobre 2024 14:28 (9)

Department

Presenter(s) : AIEVOLA, Vincenzo

Contribution ID : 124

Type : **not specified**

Impact of rare synonymous variants on cancer predisposition

martedì 22 ottobre 2024 14:19 (9)

Department

Presenter(s) : ESTINTO, Gilda

Contribution ID : 125

Type : **not specified**

Whole Genome Sequencing Unravels Novel Genomic Variants and Their Impact on Tumor Phenotypes in High-Risk Neuroblastoma

martedì 22 ottobre 2024 15:40 (9)

Department

Presenter(s) : PIROZZI, Giampiero

Contribution ID : 126

Type : **not specified**

8-oxodG is a driver of the transcription machinery

martedì 22 ottobre 2024 15:49 (9)

Department

Presenter(s) : GORINI, Francesca

Contribution ID : 127

Type : **not specified**

A novel cluster of putative regulatory sequences modulates Tbx1 gene expression

martedì 22 ottobre 2024 15:58 (9)

Department

Presenter(s) : ALLEGRETTI, Sara

Contribution ID : **128**

Type : **not specified**

Proteome and bioinformatic analyses of cellular models of methylmalonic acidemia reveal lysosomal dysregulations

martedì 22 ottobre 2024 14:10 (9)

Department

Presenter(s) : BIANCO, Sabrina

Contribution ID : **129**

Type : **not specified**

The contribution of DNA methylation studies to the diagnosis and prognosis of rare genetic disease

martedì 22 ottobre 2024 16:07 (9)

Department

Presenter(s) : DE RISO, Giulia

Contribution ID : **130**

Type : **not specified**

Polymer physics models predict 3D chromatin organization of SARS-CoV-2 infected cells

martedì 22 ottobre 2024 16:16 (9)

Department

Presenter(s) : FONTANA, Andrea

Contribution ID : 131

Type : **not specified**

Impact of Sleep Deprivation on Chromatin Organization in Mouse Hippocampus Cells

martedì 22 ottobre 2024 16:25 (5)

Department

Presenter(s) : DI PIERNO, Florinda

Contribution ID : 132

Type : **not specified**

Multicellular PID Control of Gene Expression in Microbial Consortia

martedì 22 ottobre 2024 17:00 (9)

Department

Presenter(s) : MARTINELLI, Vittoria

Contribution ID : 133

Type : **not specified**

Modelling 2D Nanoflake - Bacterium Interactions in Solutions

martedì 22 ottobre 2024 17:09 (9)

Department

Presenter(s) : LETO NICOLAS & JABER ELIA

Contribution ID : 134

Type : **not specified**

Multi-omics data integration methods for cancer-subtyping, drug discovery and tumor-model alignment

martedì 22 ottobre 2024 17:18 (9)

Department

Presenter(s) : SCALA, Giovanni

Contribution ID : 135

Type : **not specified**

A new docking protocol to predict metal/DNA interactions

martedì 22 ottobre 2024 17:27 (9)

Department

Presenter(s) : TITO, Gabriella

Contribution ID : 136

Type : **not specified**

Binding of $[V(IV)O(8-HQ)(H_2O)]^+$ to the model protein lysozyme: structural and computational studies

martedì 22 ottobre 2024 17:36 (9)

Department

Presenter(s) : PAOLILLO, Maddalena

Contribution ID : 137

Type : **not specified**

A biomolecular circuit for high-performance in vivo biosensing: monitoring of copper levels in Wilson Disease

martedì 22 ottobre 2024 17:45 (9)

Department

Presenter(s) : POSTIGLIONE, Lorena

Contribution ID : 138

Type : **not specified**

Towards Exabyte-Scale Genomics: Advanced Hardware-Software Solutions for Efficient Read Mapping

martedì 22 ottobre 2024 17:54 (9)

Department

Presenter(s) : MERCOGLIANO, Stefano

Contribution ID : 139

Type : **not specified**

Prostate tumors laser ablation: mathematical model and protocol multi-objective optimization framework establishment.

martedì 22 ottobre 2024 18:03 (9)

Department

Presenter(s) : NAPOLI, Giovanni

Contribution ID : 140

Type : **not specified**

Multiscale Modeling in Magnetic Hyperthermia: From Thermal Model Assessment to Tumor Microenvironment Simulation

martedì 22 ottobre 2024 18:12 (8)

Department

Presenter(s) : CAFARCHIO, Andrea

Contribution ID : **141**

Type : **not specified**

Dr.ssa Lorena Postiglione (TIGEM)

martedì 22 ottobre 2024 11:30 (8)

Department

Contribution ID : 142

Type : **not specified**

Prof.ssa Maura Striano (Assessore all'Istruzione Comune di Napoli)

martedì 22 ottobre 2024 10:13 (6)

Department