**Biosketch:**

Graduated in Medicine and Surgery at Federico II of Naples in 1980, he worked first as a researcher in Naples at the Faculty of Medicine and after carried out two periods of study at the Pathology department of the University of Oxford. He also spent a long period of study at the European Molecular Biology Laboratory in Heidelberg.

Giovanni Paolella has been Professor of Biochemistry since 1994, first at the University of Molise and, from 2006 onwards, at the University of Naples Federico II.

From 2011 to 2019 he led the Degree course in Biotechnology for Health, first as President and then as Coordinator.

At CEINGE he coordinated, since the first establishment of the research center, and still coordinates, the work group that carries out research in the field of computational analysis of genomic and transcriptomic data and of data coming from dynamic microscopy.

**CV:** Vedi file

**Linee di ricerca:**

1. Development of computational tools to manage, analyse and share big biological data volumes.

The activity in this field is aimed to generate modules and programs that implement advanced algorithms to analyse large data volumes coming from investigation in the genomic/transcriptomic field but also from numerical elaborations of data contained in biological images.

2. Computational analysis and modelling of movement and proliferation of cultured mammalian cells observed in time-lapse microscopy.

Migration and proliferation of cultured cells are studied in vitro by complementing dynamic microscopy with image analysis and with quantitative and statistical evaluations. Experimental studies are associated to an effort in developing analysis tools useful to support investigation.

3. Simulation of migratory and proliferative behaviour of in vitro cultured cells

The work in this field produced a simulation system able to predict the behaviour of eukaryotic cell populations cultured in vitro. The system has been developed with a specific emphasis on the reproduction of wound repair experiments, but works by simulating cells as single entities by using models of cellular process such as growth, proliferation and migration; this make the simulator useful for the production of synthetic populations in different experimental contexts.

4. Mammalian genome analysis and de novo assembly.

The activity in this field is focused on the analysis of “high-throughput” sequencing data aimed to assemble de novo mammalian genomes and analyse variants among the obtained sequences. This work led to the development of new tools able to support the comparative evaluation of eukaryotic genomes and the graphical visualisation of the alignment of long chromosomes.

**Abstract sulle ricerche eseguite al CEINGE:**

Research activity is directed to study the behaviour of normal and pathological eukaryotic cells in culture, in terms of migration patterns and proliferation rates. In vitro cultured cells are studied by complementing dynamic microscopy with image analysis and quantitative and statistical evaluation. Experimental studies are associated with an effort to develop advanced analysis tools, useful to support investigation. Computational analysis of experimental data is combined with molecular and cellular approaches aimed to identify the characteristics of the biological phenomena and numerically describe and predict the involved processes. With this approach, a new model was developed, which describes cell movement as a combination of three components, a randomly directed vector, an intrinsic directional persistence and an optional bias vector, typically generated in response to external factors such as chemioattractant gradients or a wound stimulus. Using the model to described the movement of a set of experimental cultures, moving under different conditions, led to the understanding that most cell lines and populations tend to adhere to movement patterns which characterise them enough to differentiate them from each other.

This model, extended to predict the movement of cells in a range of experimental conditions and combined with a cell cycle model, was used as a base for the development of a simulation system, SimulCell, which can predict the behaviour of eukaryotic cell populations cultured in vitro. The simulation system works by simulating cells as single entities which individually use models of growth, proliferation and migration to determine the behaviour of each of them. This approach makes SimulCell able to produce synthetic populations, which strongly resemble their experimental counterpart and react similarly in different experimental contexts.

Another line focuses on the analysis of “high-throughput” sequencing data, and recently produced a de novo assembled mammalian genome (Bubalus bubalis), with depth and quality that surpass the current reference assembly for this species. Also in this case, the work led to the development of a new tool, able to support comparative evaluation of eukaryotic genomes and graphical visualisation of the alignment of long chromosomes.

**Composizione del gruppo di ricerca:**

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**SCOPUS link:** <https://www.scopus.com/authid/detail.uri?authorId=6603960879>

**pubblicazioni più rilevanti:**

- Toscano E, Cimmino E, Boccia A, Sepe L, Paolella G. Cell populations simulated in silico within SimulCell accurately reproduce the behaviour of experimental cell cultures. NPJ Syst Biol Appl. 2025 May 17;11(1):48. doi: 10.1038/s41540-025-00518-w. PMID: 40379622; PMCID: PMC12084383.

- Toscano E, Cimmino E, Pennacchio FA, Riccio P, Poli A, Liu YJ, Maiuri P, Sepe L, Paolella G. Methods and computational tools to study eukaryotic cell migration in vitro. Front Cell Dev Biol. 2024 Jun 3;12:1385991. doi: 10.3389/fcell.2024.1385991. PMID: 38887515; PMCID: PMC11180820.

- Toscano E, Sepe L, Del Giudice G, Tufano R, Paolella G. A three component model for superdiffusive motion effectively describes migration of eukaryotic cells moving freely or under a directional stimulus. PLoS One. 2022 Aug 2;17(8):e0272259. doi: 10.1371/journal.pone.0272259. PMID: 35917375; PMCID: PMC9345344.

- Boccia A, Tufano R, Ferrucci V, Sepe L, Bianchi M, Pascarella S, Zollo M, Paolella G. SARS-CoV-2 Pandemic Tracing in Italy Highlights Lineages with Mutational Burden in Growing Subsets. Int J Mol Sci. 2022 Apr 9;23(8):4155. doi: 10.3390/ijms23084155. PMID: 35456974; PMCID: PMC9029933.

- Sepe, L., Candia, U., Sasso Del Verme, D., Toscano, E., Toriello, M., Sodaro, G., Rapuano, R., Romano, S., Grosso, M., Paolella, G., Lupo, A., Costanzo, P., & Cesaro, E. (2025). ZNF224 enhances the oncogenic function of p21 via p53 and AKT pathways in melanoma. The FEBS journal, 292(15), 3986–4005. https://doi.org/10.1111/febs.70114

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