OMB No. 0925-0001 and 0925-0002 (Rev. 10/2021 Approved Through 01/31/2026)

BIOGRAPHICAL SKETCH

NAME: Stathis Megas

POSITION TITLE: Assistant Professor, Department of Medicine III, Medical University of Vienna

EDUCATION/TRAINING

INSTITUTION AND LOCATION	DEGREE	Period	FIELD OF STUDY
Mani Bhaumik Institute of Theoretical Physics and University of California, Los Angeles	PhD	2016-2021	Mathematical Physics (GPA 4.0/4.0) Supervised by Per Kraus
University of California, Los Angeles	MSc	2015-2016	Theoretical Physics (GPA 4.0/4.0) Supervised by Per Kraus
University of Athens (National and Kapodistrian)	BSc	2010-2014	Nuclear and Particle Physics (GPA 9.74/10, highest grade in recent history) Supervised by Paris Sphicas

A. Biographical Summary

As an assistant professor in AI/ML for Biomedicine and with a PhD background in string theory, topological quantum gravity, and topological quantum field theory, I lead research that leverages mathematics to design better machine learning algorithms, and then use these machine learning algorithms to drive discoveries and applications in biomedicine.

B. Positions, Leadership, and Honors

Positions and Employment

2025 – now Assistant Professor, Department of Medicine III, Medical University of Vienna.
2025 – now Group Leader, Center of AI in Medicine, Medical University of Vienna.
2025 – now Adjunct Key Researcher, MetAGE Cluster of Excellence
2024 – 2025 Schmidt Accelerate Science Postdoctoral Fellow, Cambridge Stem Cell Institute, supervised by Sarah Teichmann.
2023 – 2024 Postdoc, Cambridge Center for AI in Medicine (CCAIM), University of Cambridge
2023 – 2024 Postdoc Fellow, Wellcome Sanger Institute, Hinxton, UK

2021 – 2023 Postdoc, EMBL-EBI and Gurdon Institute, Cambridge, UK, supervised by John Marioni

Grants

As Assistant Professor at Meduni Vienna

	Amount of funding	Source
ESPRIT fellowship for Silvia Weiss	376.506 EUR	FWF
Anthropic AI for Science Grant	~44.000 EUR	Anthropic
Onassis Single Project Grant	20.000 EUR	Onassis Foundation
Total:	440.506 EUR	

Leadership

2025 – Now Supervising postdoc, PhD, MSc, BSc students at MEdical University of Vienna.
2023 – 2025 Supervised students for their Masters degrees at the University of Cambridge.
June 2024 Attended EMBO leadership workshop.
2023 – 2024 Wellcome Genome startup school, team leader.

Awards, Prizes & Honors

Feb-Jun 2026 Invited long residency at Isaac Newton Institute for Math, Cambridge, UK.
2024 – 2025 Funding from Schmidt Sciences for Accelerate Science Program.
2015 – 2019 Onassis Doctoral Scholarship.
2016 – 2017 Mavroyiannis Doctoral Scholarship.
2015 – 2021 UCLA Tuition and Stipend Doctoral Scholarship.
2010 – 2014 IKY Distinction Scholarships for highest GPA every year of my BSc.
2010 – 2014 IKY Excellence Scholarships for high (>8.0/10.0) GPA every year of my BSc.
2010 – 2014 Papadakis Undergraduate Fellowship.
2015 Ranked 4th/42 at the PhD comprehensive exams (taken as 0-year student, normally taken after year 1).
2010 Bronze medal at the Hellenic Mathematical Olympiad 2010 (15000 participants).
2010 Valedictorian Prize.

D. Contributions to Science, Teaching, Supervision, Talks, Engagement

Teaching

Six full years of teaching assistant experience in graduate and undergraduate classes at UCLA. Responsibilities included leading lectures, compiling notes and problem sets for discussion sessions, writing solutions to weekly homework, and grading and proctoring for exams.Selection of classes taught:

Graduate classes: Quantum Field Theory I, Complex Analysis, Continuous Group Theory.

Undergraduate Classes: Analytical Mechanics I (Upper Division), Electromagnetism I (Upper Division), Electromagnetism laboratories I&II, Classical Mechanics (Lower Division), Physics for Pre-meds, Laboratories for Pre-meds, Physics for students from Human, Social and Political Sciences.

Invited Talks

NSF-Simon Center Theory and Mathematics of Biology, Chicago, USA, October 2026.
Uncovering Hidden Biology organised by Carol Robinson, University of Oxford, Sept 2025.
Cambridge AI club, University of Cambridge, November 2024.
CCAIM at the University of Cambridge, Boehringer Ingelheim visit, October 2024.
Front Line Genomics, Webinar on multi-omic integration, July 2024.
Alan Turing Institute, Conference on The Role of Generative AI for Omics, May 2024.
IBM, Zurich, Seminar, April 2024.
Yale Inference Workshop, December 2023, New Haven, https://shorturl.at/ckoHr.
Athens School of Fine Arts, Journal Club, 2021.

Engagement

2 April 2022, The Great BioQuest, Cambridge, UK, riddle master for scientific treasure hunt.
15 March 2022, Cambridge Festival, UK, demo of algebraic topology applications in biology.
17-22 March 2015, 2nd Athens Science Festival, volunteer at the CERN CMS experiment booth.
September 2013, CERN Open Days, volunteer at the CERN CMS experiment booth.

Contributions in Research

First-author publications (**five most important papers listed at the top**):
On papers in pure mathematics, authors are **listed alphabetically by last name**.
* denotes equal contribution.

Throughout my scientific career, I **established a research portfolio as one of few scientists in the world to combine expertise** in (1) advanced physical mathematics, (2) GenAI for models of Virtual Cells and Virtual Tissues, (3) methods development for single-cell multiomic data, which together make this project feasible. I strived to forge my own path, as shown by my

first/corresponding authorship on nearly all my papers, including in top journals[27,28] and leading ML conferences[15].

During my career, **I conducted research spanning literally all scales**. According to theories of quantum gravity, at the so-called "Planck scale", the quantum fluctuations of spacetime are so volatile that the notions of space and time lose their meaning, so there cannot be a smaller scale. In [9], I used quantum gravity calculations at this scale to derive results in conformal field theories (CFTs) and contribute to the classification program of all possible phase transitions – which are described by CFTs.

At the other extreme, to resolve Hawking's Information Paradox, we need to consider our universe in the context of a multiverse, which is the largest scale used in science. In [4], I developed the world's first rigorous theory of quantum gravity with non-trivial non-gravitational forces. I included mutli-universe effects to mathematically show how this 2d theory is equivalent to a distribution of 1d theories, or conversely how being agnostic about the parameters of 1d theories can literally create space and time and gravity. This is an example of an emergent property, like how tissue architecture arises from molecular interactions.

During my postdoc **I leveraged the mathematical tools I developed for** emergent phenomena, causality, and **physical spacetime, and used them to study biological spacetime** [1,2,3,5], profiled using spatial transcriptomics across time points.

At the cell level, my work introduced new notions for methods for single cell data, leading to cell type discoveries. CellDISECT [3] is a GenAI model that can disentangle the intertwined effects of covariates on gene expression, and then predict the effect of perturbations. CellDISECT introduced the idea of using the model's own synthetic data during training to achieve state of the art perturbation predictions. CellDISECT's multifaceted view of the data was instrumental in enabling our discovery of a new type of megakaryocyte with immune characteristics.

At the tissue scale, my work **laid the foundations for generalizing perturbation models of virtual cells to Virtual Tissue Perturbation Models by leveraging spatial genetic screens [1,2]**. Celcomen is a GenAI model that learns and disentangles intra-cellular gene regulation from intercellular cell communication. It can then be prompted with perturbations such as spatially localised gene knock outs to predict the response of the cell, its neighbors and the entire tissue, offering insights into disease causality. To our knowledge it is the first learning model to be benchmarked on spatial genetic screens.

Representative publications in the last 5 years

#corresponding author, *Equal contribution.

1. S. Megas*#, D. G. Chen*, K. Polanski, H. Asadollahzadeh, M. Eliasof, C. Schonlieb, S. A. Teichmann# (2024). Celcomen: spatial causal disentanglement for single-cell and tissue perturbation modeling. Nature Communications. 2026 Mar 18;17(1):4126. doi: 10.1038/s41467-026-69856-5.

2. S. Megas*#, D. G. Chen*, K. Polanski, M. Eliasof, C. Schonlieb, S. A. Teichmann#. Estimation of single-cell and tissue perturbation effect in spatial transcriptomics via Spatial Causal Disentanglement. ICLR 2025, main conference, https://openreview.net/forum?id=Tqdsruwyac.
In thse co-first and co-corresponding author works, we make a first step towards creating a model of a virtual tissue at single-cell resolution powered by causal generative AI and string-theory-inspired mathematics. We mathematically analyze and prove our GenAI's causal identifiability, and then test it using synthetic and real data. Using Celcomen's generative abilities we can perform spatial counterfactuals to answer fundamental questions on the interface of oncology and immunology.

3. S. Megas*, A. Amani*, A. Rose*, O. Dufva, K. Shamsaie, H. Asadollahzadeh, K. Polanski, M. Haniffa#, S.A. Teichmann#, M. Lotfollahi#. Integrating multi-covariate disentanglement with counterfactual analysis on synthetic data enables cell type discovery and counterfactual predictions. bioRxiv https://doi.org/10.1101/2025.06.03.657578. Under review at Nature Methods.
This study introduces a computational framework combining multi-covariate disentanglement with counterfactual analysis to identify previously unrecognized cell types and predict cellular responses to perturbations. Using synthetic data with known ground truth, it demonstrates how separating biological and technical sources of variation can improve cell type discovery and enable interpretable counterfactual predictions.

4. J. Gardiner*# and **S. Megas***#, "2d TQFTs and Baby-Universes", JHEP 10 (2021) 052, arXiv:2011.06137, https://doi.org/10.1007/JHEP10(2021)052.
In this co-first and co-corresponding author work, we sought to leverage correlations between parallel universes to resolve Hawking's black hole information paradox. Much of the formalism is directly relevant to counterfactual reasoning in Judea Pearl's parallel world diagrams, which are the basis of my causal GenAI models.
More specifically, in this work, we defined rigorous and analytically exactly solvable models of 2d quantum gravity endowed with any Atiyah open/closed topological quantum field theory and then resolved Hawking's paradox in this rigorous context. Our findings demonstrated that the signatures Hawking interpreted as information loss (such as mixed states) can arise naturally in well-defined quantum gravity theories due to the superposition of topologies.

5. S. Megas, V. Lorenzi and J.C. Marioni, J.C. EmptyDropsMultiome discriminates real cells from background in single-cell multiomics assays. Genome Biol 25, 121 (2024), https://doi.org/10.1186/s13059-024-03259-x.
A major bottleneck in analyzing high-throughput single-cell data is deciding which droplets contain cells and which only contain soup, a task referred to as cell/nuclei calling. For multiome datasets, where gene expression and genome accessibility are measured in the same nucleus,

there currently exists no method that leverages both modalities to distinguish nuclei from empty droplets. EmptyDropsMultiome fills this gap and in both simulations and real data outperforms RNA-only methods such as EmptyDrops and the default cell calling method in CellRanger-arc. EmptyDropsMultiome has found widespread applications such as in studying gene regulation in the thymus, building a fetal skeletal atlas (in press at Nature), a skin atlas, and more.

6. To et al, A multiomic atlas of human embryonic skeletal development (2024), Nature 635, 657–667 (2024), https://www.nature.com/articles/s41586-024-08189-z
In this work, I leveraged EmptyDropsMultiome to do optimal cell calling and enhance the potential for new cell-type discoveries. Thanks to EmptyDropsMultiome, we identified several new cell types in skeletal development.

7. S. Megas, N. Yayon, K. Meyer, S.A. Teichmann, (2024). Molecular Connectomics: placing cells into morphological tissue context. PLOS Biology 22(8): e3002803, https://journals.plos.org/plosbiology/article?id=10.1371/journal.pbio.3002803
In this opinion article, we proposed the term "Molecular Connectomics" for all research in tissues that aims to 1) provide in-depth profiling of molecular features of the cell as well as its 3D micro and macro environment, and 2) link molecular and morphological features using novel computational methods. We propose that, as we study the molecular interactions of cells at increasing scales, new "emergent" properties will give insights into whole-body function.

8. S. Megas*, A. Wilbrey-Clark*, A. Maartens, S.A. Teichmann, K.B. Meyer (2024). Spatial Transcriptomics of the Respiratory System. Annual Reviews of Physiology, Vol. 87, https://pubmed.ncbi.nlm.nih.gov/39353142/
Over the last decade, single-cell genomics has revealed remarkable heterogeneity and plasticity of cell types in the lungs, and the challenge now is to understand how these cell types interact in 3D space to perform lung functions. Here, we reviewed the most commonly used spatial analysis workflows and recent and coming developments in foundation models that will augment how we interpret spatial data, and we showcase studies in lung development, COVID-19, lung cancer, and fibrosis where spatially resolved transcriptomics is already providing novel insights.

9. P. Kraus*, **S. Megas*** and A. Sivaramakrishnan* (alphabetical order), "Anomalous Dimensions from Thermal AdS Partition Functions", JHEP 10 (2020) 149, https://arxiv.org/abs/2004.08635.
Here we sought to classify all possible phase transitions across biology and physics. To perform this classification, we developed a new mathematical formalism that unexpectedly relied on quantum gravity.
More specifically, we contributed to the Conformal Bootstrap program which aims to classify all possible conformal field theories (CFTs), i.e. the theories that govern phase transitions, using their axiomatic definition. Our idea was to use dualities to gravitational theories and aim to

classify only some of the defining constants of CFTs instead of all of them at once. This resulted in perhaps the simplest formula to calculate corrections to anomalous dimensions.