Christoph Gorgulla, Ph.D.

Harvard University

Contact Information

Christoph Gorgulla
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Current Positions

Research Associate (February 2021 - Current)
Harvard Medical School, Boston, USA
Mentor: Gerhard Wagner

Associate (August 2018 - Current)
Physics Department, Harvard University, Cambridge, USA
Mentor: Arthur Jaffe

Education

IMPRS-CBSC (Graduate school – parallel to PhD at the FU Berlin), 2016-2018
International Max Planck Research School for Computational Biology and Scientific Computing, Max Planck Institute for Molecular Genetics, Berlin, Germany
Joint graduate program with the FU Berlin, Focus on computational drug discovery.

BMS Phase II (Graduate school – parallel to PhD at the FU Berlin), 2014-2018
Berlin Mathematical School (BMS), Berlin, Germany
Joint graduate program with the FU Berlin, Focus on quantum chemistry

PhD in Mathematics, 2014-2018, Freie Universität Berlin, Germany
Focus on quantum chemistry and computational drug discovery

BMS Phase I (Graduate school – parallel to MSc in Mathematics), 2012-2014
Berlin Mathematical School (BMS), Germany
Focus on quantum physics, GPA: A+ (*Summa cum laude*)

MSc in Mathematics, Freie Universität Berlin, Germany, 2012-2014
Focus on quantum physics, GPA: A+ (*Summa cum laude*)

BSc in Mathematics, Freie Universität Berlin, Germany, 2010-2012
Focus on analysis, GPA: A+ (*Summa cum laude*)

BSc in Molecular Biology, Westphaelian University of Applied Sciences, Germany, 2004-2009, Focus on bioinformatics, GPA: A (*Summa cum laude*)

Research Experience

Postdoctoral Research, Harvard University, 2018-2022

- Mentors: Gerhard Wagner (Harvard), Arthur Jaffe (Harvard), Haribabu Arthanari (Harvard/DFCI), Alan Aspuru-Guzik (University of Toronto)
- Application of the ultra-large virtual screening platform VirtualFlow to multiple drug targets, such as eIF4E, eIF4A, HIV capsid protein, NOX5 (collaboration with U. of. Pavia), KRAS (collaboration with AWS and DFCI), BCL11A (collaboration with Boston Children's Hospital), COVID 19 (collaboration with Abbvie and Google, https://vf4covid19.hms.harvard.edu/), and other targets. Supervision and management of the experimental validation of the predicted drug candidates of several of these projects.
- Further development of VirtualFlow as open source project. Lead developer, supervision of a global team of more than 15 contributors/members of the project. Active collaborations with Google and AWS regarding cloud-versions of VirtualFlow. Homepage: https://virtual-flow.org/

- Development and implementation of new quantum chemical free-energy prediction methods for biomolecular systems (collaboration with TU Berlin, ZIB Berlin, University of Cambridge)
- Development of new methods and tools for quantum chemistry and computational drug discovery based on quantum computing

Visiting PhD Student, Harvard Medical School, 1/2017-8/2017

- Application of the ultra-large virtual screening method to multiple drug targets of the Harvard Medical School, such as SREBP

PhD Project, Computational Drug Design and Quantum Chemistry, 2014-2018

- Primary PhD Advisor: Christoph Schütte, Biocomputing Group
  Additional PhD Advisors: Konstantin Fackeldey, Petra Imhof
- Ultra-large virtual screenings: Theoretical studies, development and implementation of an ultra-large virtual screening platform "VirtualFlow"
- Development and implementation of new quantum-mechanical free-energy prediction methods including nuclear and electronic structure effects for predicting protein-ligand binding affinities based on the path integral formalism of quantum mechanics
- Development and implementation of new quantum mechanics/molecular mechanics (QM/MM) methods for biomolecular systems
- Application of the ultra-large virtual screening method to multiple drug targets (some in collaboration), such KEAP1, EBP1, and the peptidoglycan (collaboration with Charite Berlin)

Master Project, B.Sc. in Mathematics (with Quantum Physics), 2013-2014

- Theoretical and numerical studies of squeezed states of spherical quantum pendula
- In the Burkhard Schmidt Group, Institute for Mathematics and and Computer Science, Freie Universität Berlin

Bachelor Project, B.Sc. in Molecular Biology (with Bioinformatics), 2009

- Small angle X-Ray scattering of the bacterial MukEF complex
- Research visit (5 months) at POSTECH, Structural Biology Lab (Prof. Kyung-Ha Oh), Pohang, South Korea

Bachelor Project, B.Sc. in Mathematics, 2011

- Theoretical studies about the differentiation of signed and complex measures
- In the Dirk Werner Group, Institute for Mathematics and and Computer Science, Freie Universität Berlin

Research Interests

Virtual Screening Approaches

- Development of state-of-the-art virtual screening methods and tools/software for discovering new small molecule drug candidates for given target proteins.
- Using the worlds largest ligand libraries with billions of compounds, cloud computing, and artificial intelligence approaches.
- Combination with quantum chemistry, quantum computing, and (quantum) machine learning (see below).
- Project director and lead developer of the *VirtualFlow* open-source project (www.virtual-flow.org, Gorgulla et al., 2020). Managing and supervising an international team of contributors to the open-source project (over 10 active members).

Applied Drug Discovery

- Application of the new method and tools which I am developing to real drug discovery projects, which if successful go all the way up to human clinical trials.
- Multiple active international collaborations on drug discovery projects.
- Past/current projects include multiple cancer drug discovery projects, neuro-degenerative diseases, and antiviral drug discovery (COVID-19, herpes, HIV).
- In particular I am interested in challenging target classes such as protein-protein interaction and allosteric sites.

(Classical) Quantum Chemistry

- Development of new methods and tools for quantum chemistry on classical computers. This includes the development of novel QM/MM (Quantum Mechanics/Molecular Mechanics) methods to model electronic quantum effects, path integral molecular dynamics to model nuclear quantum effects, and free energy simulation methods for predicting the free energy of binding.

Quantum Computing and Quantum Machine Learning for Drug Discovery

- Theoretical development of new quantum algorithms for computational chemistry and drug discovery, based on quantum machine learning and simulation-based approaches for near-term quantum computers.
- Implementation of the new methods in quantum software.

Awards and Fellowships

Google Cloud Research Innovator (mentor status), Google, 2022-2023

Konrad-Zuse Fellow, Zuse Institute Berlin, 2021-2023

Google Cloud Research Innovator, Google, 2021-2022

Google Cloud Customer Award Winner - Healthcare & Life Sciences, 2021

HPCwire Readers' Choice Award, jointly awarded with Google, 2020

Fellowship of e-fellows.net, 2014-2018

Doctoral Scholarship
Max Planck Institute for Molecular Genetics, Berlin, Germany, 2017

Doctoral Fellowship,
ECMath (Einstein Center for Mathematics), Berlin, Germany, 2014-2017

Young Researcher, Heidelberg Laureate Forum (HLF), Germany, 2016

Digital Future Scholarship, Deutsche Telekom, Tagesspiegel Berlin, Germany, 2016

Graduation Scholarship for Bachelor Thesis, Freie Universität Berlin, Germany, 2011

Grants

AWS Award, 2021-2022
1.6 million USD for computing time in the AWS cloud, 2021.
Grant jointly awarded to Haribabu Arthanari and myself for cancer drug discovery.

Google Cloud Research Innovator Program, 2021-2023
~100,000 USD awarded directly to me for research in the Google Cloud.

Google Cloud Award, 2020-2021
1.1 million USD for computing time for the Google Cloud, 2020.
Jointly awarded to H. Arthanari and myself for COVID-19 therapeutics research.

AWS Cloud Credit for Research, 2019
20,000 USD for computing time for the AWS Cloud.

Google Cloud Research Credits, 2019
20,000 USD for computing time for the Google Cloud.

HLRN Supercomputing Center Germany, 2015-2016
A total of 125 000 NPL of computing time was granted to me worth of a market price of more than 30,000 Euro.

Publications

12. Olivet, J., Maseko, S.B., Volkov, A.N., Salehi-Ashtiani, K., Das, K., Calderwood, M.A., Twizere, J.C. and **Gorgulla, C.***, 2022. A systematic approach to identify host targets and rapidly deliver broad-spectrum antivirals. *Molecular Therapy,* 30(5), pp.1797-1800. https://doi.org/10.1016/j.ymthe.2022.02.015
    * Corresponding author

11. **Gorgulla, C.***, Jayaraj, A., Fackeldey, K. and Arthanari, H., 2022. Emerging frontiers in virtual drug discovery: From quantum mechanical methods to deep learning approaches. *Current Opinion in Chemical Biology*, 69, p.102156. https://doi.org/10.1016/j.cbpa.2022.102156
    * Corresponding author

10. Rossetti, G.G., Ossorio, M.A., Rempel, S., Kratzel, A., Dionellis, V. S., Barriot, S., Tropia, L., **Gorgulla, C.**, Arthanari, H., Thiel, V., Mohr, P., Gamboni, R., Halazonetis, T.D., 2022. Non-covalent SARS-CoV-2 Mpro inhibitors developed from in silico screen hits. *Scientific Reports*, 12(1), pp.1-9. https://doi.org/10.1038/s41598-022-06306-4

9. Fischer, P. D., Papadopoulos, E., Dempersmier, J. M., Wang, Z.-F., Nowak, R. P., Donovan, K. A., Kalabathula, J., **Gorgulla, C.**, Junghanns, P. P. M., Kabha, E., Dimitrakakis, N., Petrov, O. I., Mitsiades, C., Ducho, C., Gelev, V., Fischer, E. S., Wagner, G., & Arthanari, H., 2021. A biphenyl inhibitor of eIF4E targeting an internal binding site enables the design of cell-permeable PROTAC-degraders. *European Journal of Medicinal Chemistry*, 219, p.113435. https://doi.org/10.1016/j.ejmech.2021.113435

8. Maseko, S., Van Molle, I., Blibek, K., **Gorgulla, C.**, Olivet, J., Blavier, J., Vandermeulen, C., Skupiewski, S., Saha, D., Ntombela, T. and Lim, J., 2021. Interactome and structural basis for targeting the human T-cell leukemia virus Tax oncoprotein. *BioRxiv*. https://doi.org/10.1101/2021.08.25.457680

7. Fackeldey, K., **Gorgulla, C.**, Weber, M., 2021. *Neue Medikamente dank Supercomputern. Spektrum der Wissenschaft*, (11), pp.40-46.
    Notes: All authors contributed equally

6. **Gorgulla, C*.**, Padmanabha Das, K. M., Leigh, K. E., Cespugli, M., Fischer, P. D., Wang, Z.-F., Tesseyre, G., Pandita, S., Shnapir, A., Calderaio, A., Gechev, M., Rose, A., Lewis, N., Hutcheson, C., Yaffe, E., Luxenburg, R., Herce, H. D., Durmaz, V., Halazonetis, T. D., … Arthanari, H.*, 2021. A multi-pronged approach targeting SARS-CoV-2 proteins using ultra-large virtual screening. *iScience*, 2(7), p.102021. https://doi.org/10.1016/j.isci.2020.102021
    * Corresponding author

5. Zhang, M., Gui, M., Wang, Z.-F., **Gorgulla, C.**, Yu, J., Wu, H., Sun, Z.-Y. J., Klenk, C., Merkinger, L., Morstein, L., Hagn, F., Plueckthun, A., Brown, A., Nasr, M.L., Wagner, G., 2021. Cryo-EM structure of an activated GPCR-G protein complex in lipid nanodiscs. *Nature Structural & Molecular Biology*, 28(3), pp.258-267. https://doi.org/10.1101/2020.06.11.145912

4. **Gorgulla, C*.**, Çınaroğlu, S. S., Fischer, P. D., Fackeldey, K., Wagner, G., & Arthanari, H., 2021. VirtualFlow Ants—Ultra-Large Virtual Screenings with Artificial Intelligence Driven Docking Algorithm Based on Ant Colony Optimization. *International Journal of Molecular Sciences*, 22(11), p.5807. https://doi.org/10.3390/ijms22115807

* Corresponding author
Special Issue: AI & Deep Learning Approaches for Structural Bioinformatics

3. **Gorgulla, C***., Fackeldey, K., Wagner, G., & Arthanari, H.*, 2020. Accounting of Receptor Flexibility in Ultra-Large Virtual Screens with VirtualFlow Using a Grey Wolf Optimization Method. *Supercomputing Frontiers and Innovations*, 7(3), pp.4–12. https://doi.org/10.14529/jsfi200301
* Corresponding author
Notes: One of the leading journal in the field of supercomputing

2. **Gorgulla, C***., Boeszoermenyi, A., Wang, Z., Fischer, P. D., Coote, P. W., Padmanabha Das, K. M., Malets, Y. S., Radchenko, D. S., Moroz, Y. S., Scott, D. A., Fackeldey, K., Hoffmann, M., Iavniuk, I., Wagner, G., & Arthanari, H.*, 2020. An open-source drug discovery platform enables ultra-large virtual screens. *Nature*, 580(7805), pp.663–668. https://doi.org/10.1038/s41586-020-2117-z
* Corresponding author

1. Shin, D., **Gorgulla, C.**, Boursier, M. E., Rexrode, N., Brown, E. C., Arthanari, H., Blackwell, H. E., & Nagarajan, R. (2019). N-Acyl homoserine lactone analog modulators of the Pseudomonas aeruginosa RhlI quorum sensing signal synthase. *ACS Chemical Biology*, 14(10), pp.2305-2314. https://doi.org/10.1021/acschembio.9b00671

Publications in preparation

Boeszoermenyi A, Zhu C, Nishikawa J, Padmanabha Das KM, Dempersmier JM, **Gorgulla C**, Wu S, Buhrlage SJ, Papagiannidis D, Chhabra S, Leigh K, Hoffmann K, Naar A, Wagner G, Arthanari H. Inhibiting de novo lipid biosynthesis reveals a major vulnerability in cancer.

Olivet J, Choi SG, Sierra S, O'Grady TM, de la Fuente Revenga M, Laval F, Botchkarev Jr. V, **Gorgulla C**, Coote PW, Blavier J, Geffken EA, Lakhani J, Song K, Yeoh CZ, Hu B, Varca AC, Richardson A, Yue H, Wang Y, Bruyr J, Calonghi N, Stefan A, Spirohn K, Vertommen D, Baietti MF, Lemmens I, Seo HS, Dozmorov MG, Willems L, Tavernier J, Leucci E, Hochkoeppler A, Sun J, Calderwood MA, Hao T, Hill DE, Boeszoermenyi A, Arthanari H, Buhrlage SJ, Dequiedt F, González-Maeso J, Dhe-Paganon S, Twizere JC, and Vidal M. Locus-specific inhibition of histone deacetylase complexes by targeting scaffolding protein interactions.

A M, Wales TE, Zhou H,Mittenbühler MJ, Kim CR, **Gorgulla C**, Draga-Coleta SV, Blackmore KA, Wang Z, Jedrychowski MP, Seo HS, Song K, Xu AZ, Sebastian L, Bogoslavski D, Gygi SP, Griffin PR, Dhe-Paganon S, Engen JR, and Spiegelman BM. Irisin acts through integrin receptor in a twp-step process.

Multiple authors, including **Gorgulla C.** and others. JEDI: Results of the Billion Molecules against Covid19 Grand Challenge.

Chen H, Lye MF, **Gorgulla C**, Cuny G, Ficarro S, Wang S, Rothlauf PF, Scott DA, Wu F, Marto J, Arthanari H, Hogle JM, Coen DM. Small molecule targeting of the human cytomegalovirus nuclear egress complex for antiviral activity.

Gorgulla C*. Virtual Screening in Drug Discovery – A Comprehensive Review. Invited Review. To be submitted to Annual Review of Biomedical Data Sciences.
* Corresponding author

Gorgulla C*, Fackeldey K, Imhof P, Fackeldey K, Kapil V*. A novel QM/MM method combining electronic and nuclear quantum effects for biomolecular systems.
* Corresponding author

Behera S, Jayaraj A, Wagner G, Arthanari H, **Gorgulla C***. Preventing off-target binding via inverse virtual screenings using the AlphaFold Structure Database. To be submitted to Nature Computational Science.
* Corresponding author

Gorgulla C*, Kapil V, Arthanari H, Wagner G. Development of a novel alchemical free energy simulation method for protein-ligand binding prediction including nuclear quantum effects.
* Corresponding author

Theses

Gorgulla, C. *Free Energy Methods Involving Quantum Physics, Path Integrals, and Virtual Screenings: Development, Implementation and Application in Drug Discovery,* PhD Thesis (Mathematics/Computational Drug Discovery), Freie Universität Berlin, 2018. http://dx.doi.org/10.17169/refubium-11597

Gorgulla, C. *Quantum Dynamics and Squeezed States of Generalized Spherical Pendula*, Master Thesis (Mathematics/Quantum Physics), Freie Universität Berlin, 2014

Gorgulla, C. *Differentiation of Measures*, Bachelor Thesis (Mathematics), Freie Universität Berlin, 2011

Gorgulla, C. *Small Angle X-ray Scattering Studies of the Bacterial MukEF Complex*, Bachelor Thesis (Molecular Biology with Bioinformatics), Westphaelian University of Applied Sciences, 2009

Project Websites

VirtualFlow project homepage: https://virtual-flow.org/

COVID-19 project homepage: https://vf4covid19.hms.harvard.edu/

Presentations

Harvard Medical School, BCMP Department, 4/29/2022
Presentation in the Data Club Seminar Series

QuEra Computing (quantum computing company), Boston, 3/3/2022
Presentation within the science division

Broad Institute, Chemical Biology and Therapeutics Science Program, 2/23/2022
Presentation in the Seminar Series

University of Toronto, Matter Lab (Alan Aspuru-Guzik Lab), 2/23/2022
Group meeting presentation

AWS re:Invent 2021, Las Vegas. 11/30/2021.
Presentation and Discussion

Leipzig University, Institute for Biophysics and Medical Physics, 10/29//2021
Presentation in the Seminar Series

AWS Healthcare & Life Sciences Virtual Symposium, Presentation, 5/27/2021

NIH Computational Genomics Conference, Presentation, 4/28/2021

Cornell Cloud Forum, Presentation, 3/12/2021

ASF Roundtable, Keynote Presentation jointly with Google, 2/17/2021.

Google, HPC Days Digital, Presentation and Discussion, 7/22/2020

Mathematical Picture Language Seminar, Harvard, Physics Department, 10/16/2018

EPFL, COSMO Group (Michelle Ceriotti), Group Meeting Presentation, 10/25/2016

Media Coverage (selection)

CNN/WarnerMedia, Short film featuring VirtualFlow and myself. 2022

Google, Feature video, 2020

Harvard Medical School**,** Animation video and blog post, 3/2020.

HPCwire Readers' Choice Awards 2020**,** Feature video, HPCWire, 2020.

Public Sector Summit Welcome & Opening Keynote**,** Feature video, Google, 2020 (our segment is starting at position 9:50)

Blog post/Case study, Google for Education, 2020

Teaching

Harvard Macy Institute, 2021
Lecture about discovering hit and lead compounds via ultra-large virtual screenings

Physics Department, Freie Universität Berlin, 2016
Teaching Assistant for the course "Computer Physics"

Mentoring and Supervision of Student/Postdoc Research

Supervision of members within the VirtualFlow open source project:

- Tanner Marsh (Master student at Harvard)
- Juan Castillo (Bachelor student at Harvard)
- Xiaoyu Yu (PhD student at Scripps Research Institute)
- Soumya Prakash Behera (PhD student at John Hopkins)
- Dr. Sorin Draga (PhD student at University of Bucharest)
- Dr. Anita Nivedha (Postdoc at City of Hope)
- Jadadish Mahendra (VirtualFlow Consortium)
- Anthony Calderaio (VirtualFlow Consortium)
- Dr. Amr Alhossary (Postdoc at Nanyang Technological University, Singapore)
- Süleyman Selim (PhD student at Oxford university)
- Anna My Nguyen (Bachelor student at Saint Benedict & Saint John's University)
- Ella Rajaonson (PhD student at at the University of Toronto)
- Dr. Matt Coop (Programmer at AWS)
- Aditya Kumar (Master student at the Technical University Berlin)

Service

Peer reviews for articles in the following journals:

- iScience
- Biophysical Journal
- Current Topics in Medicinal Chemistry
- ACS Infectious Diseases

Founded Companies

Based on my academic research, I have co-founded two companies in the USA, although I do not have any current active roles in either company:

- **Virtual Discovery, Inc.** Founded in March 2020 with Prof. Gerhard Wagner. The company provides computational drug discovery services, including virtual screenings using VirtualFlow.
- **Quantum Therapeutics, Inc.** Founded in June 2021 with Prof. Anders Näär (UC Berkeley, Prof. Gerhard Wagner (Harvard), Prof. Haribabu Arthanari (Harvard), Prof. Arthur Jaffe (Harvard), Dr. Dan Barry, and myself. The company develops novel therapeutics using a VirtualFlow-based platform.

References

Arthur Jaffe
Landon T. Clay Professor of Mathematics and Theoretical Science, Department of Physics, Harvard University, Cambridge, MA, USA
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Gerhard Wagner
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Anders Näär
Professor of Metabolic Biology and Vice Chair of the Dept. of Nutritional Sciences & Toxicology, UC Berkeley, Berkeley, CA, USA
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Haribabu Arthanari
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Petra Imhof (one of my PhD mentors**)**
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