

Seminar “Physics of Viruses”
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Summer term 2021

This seminar will introduce approaches from physics and mathematics to analyze viruses and viral infections. Participants are expected to select one of the topics listed below based on the corresponding papers. They should also further research the subject on their own for more papers of this kind. The different topics should be presented ideally in teams of two in a 30 min talk with a clear focus on the most important concepts and results. Please avoid unnecessary details and focus on the main messages. The topics comprise different aspects of the viral life cycle and the infection dynamics, including characterizing viral structure, the kinetics of virus assembly, entry, exit, spread, mitigation strategies and viral evolution.

| Nr. | Topic |
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| 1. | <p>Early work on capsids</p> <p>(a) Crick, Francis HC, and James D. Watson. "Structure of small viruses." <i>Nature</i> (1956): 473-75</p> <p>(b) Caspar, Donald LD, and Aaron Klug. "Physical principles in the construction of regular viruses." <i>Cold Spring Harbor Symposia on Quantitative Biology</i>. Vol. 27. Cold Spring Harbor Laboratory Press, 1962</p> |
| 2. | <p>Symmetry of virus capsids</p> <p>(a) Zandi, Roya, et al. "Origin of icosahedral symmetry in viruses." <i>Proceedings of the National Academy of Sciences</i> 101.44 (2004): 15556-60</p> <p>(b) Lorman, V. L., and S. B. Rochal. "Landau theory of crystallization and the capsid structures of small icosahedral viruses." <i>Physical Review B</i> 77.22 (2008): 224109</p> <p>(c) Twarock, Reidun, and Antoni Luque. "Structural puzzles in virology solved with an overarching icosahedral design principle." <i>Nature communications</i> 10.1 (2019): 1-9.</p> |
| 3. | <p>Assembly - energy considerations</p> <p>(a) Perlmutter, Jason D., and Michael F. Hagan. "Mechanisms of virus assembly." <i>Annual review of physical chemistry</i> 66 (2015): 217-239.</p> <p>(b) Zlotnick, Adam. "To build a virus capsid: an equilibrium model of the self assembly of polyhedral protein complexes." <i>Journal of Molecular Biology</i> 241.1 (1994): 59-67</p> <p>(c) Bruinsma, Robijn F., et al. "Viral self-assembly as a thermodynamic process." <i>Physical review letters</i> 90.24 (2003): 248101.</p> <p>(d) Zandi, Roya, et al. "Classical nucleation theory of virus capsids." <i>Biophysical journal</i> 90.6 (2006): 1939-1948.</p> |
| 4. | <p>Assembly - computer simulations</p> <p>(a) Hagan, Michael F., and David Chandler. "Dynamic pathways for viral capsid assembly." <i>Biophysical Journal</i> 91.1 (2006): 42-54</p> <p>(b) Rapaport, D. C. "Self-assembly of polyhedral shells: a molecular dynamics study." <i>Physical Review E</i> 70.5 (2004): 051905.</p> <p>(c) Baschek, Johanna E., Heinrich CR Klein, and Ulrich S. Schwarz. "Stochastic dynamics of virus capsid formation: direct versus hierarchical self-assembly." <i>BMC biophysics</i> 5.1 (2012): 22.</p> |

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| 5. | <p>Assembly – experiments</p> <p>(a) Kler, Stanislav, et al. "RNA encapsidation by SV40-derived nanoparticles follows a rapid two-state mechanism." <i>Journal of the American Chemical Society</i> 134.21 (2012): 8823-8830.</p> <p>(b) Van Rosmalen, Mariska GM, et al. "Revealing in real-time a multistep assembly mechanism for SV40 virus-like particles." <i>Science advances</i> 6.16 (2020): eaaz1639.</p> |
| 6. | <p>Genome organization</p> <p>(a) Purohit, Prashant K., Jané Kondev, and Rob Phillips. "Mechanics of DNA packaging in viruses." <i>Proc of the Nat. Acad. Of Sci.</i> 100.6 (2003): 3173-78.</p> <p>(b) Kindt, James, et al. "DNA packaging and ejection forces in bacteriophage." <i>Proceedings of the National Academy of Sciences</i> 98.24 (2001): 13671-13674.</p> <p>(c) Speir, Jeffrey A., and John E. Johnson. "Nucleic acid packaging in viruses." <i>Current opinion in structural biology</i> 22.1 (2012): 65-71.</p> |
| 7. | <p>Virus entry by endocytosis</p> <p>(a) Deserno, Markus. "Elastic deformation of a fluid membrane upon colloid binding." <i>Physical Review E</i> 69.3 (2004): 031903</p> <p>(b) Frey, Felix, Falko Ziebert, and Ulrich S. Schwarz. "Stochastic Dynamics of Nanoparticle and Virus Uptake." <i>Physical review letters</i> 122.8 (2019): 088102</p> <p>(c) Frey, Felix, Falko Ziebert, and Ulrich S. Schwarz. "Dynamics of particle uptake at cell membranes." <i>Physical Review E</i> 100.5 (2019): 052403</p> |
| 8. | <p>Virus entry by fusion</p> <p>(a) Chernomordik, Leonid V., and Michael M. Kozlov. "Mechanics of membrane fusion." <i>Nature structural & molecular biology</i> 15.7 (2008): 675-683.</p> <p>(b) White, Judith M., et al. "Structures and mechanisms of viral membrane fusion proteins: multiple variations on a common theme." <i>Critical reviews in biochemistry and molecular biology</i> 43.3 (2008): 189-219.</p> <p>(c) Ryham, Rolf J., et al. "Calculating transition energy barriers and characterizing activation states for steps of fusion." <i>Biophysical journal</i> 110.5 (2016): 1110-1124.</p> |
| 9. | <p>Stoichiometry of HIV-uptake</p> <p>(a) Magnus C, Rusert P, Bonhoeffer S, Trkola A, Regoes RR. "Estimating the stoichiometry of human immunodeficiency virus entry." <i>J Virol.</i> 2009 Feb;83(3):1523-31</p> <p>(b) Brandenburg, Oliver F., et al. "The HIV-1 entry process: a stoichiometric view." <i>Trends in Microbiology</i> 23.12 (2015): 763-74</p> |
| 10. | <p>Structure of SARS-CoV-2</p> <p>(a) Turoňová, Beata, et al. "In situ structural analysis of SARS-CoV-2 spike reveals flexibility mediated by three hinges." <i>Science</i> 370.6513 (2020): 203-208.</p> <p>(b) Ke, Zunlong, et al. "Structures and distributions of SARS-CoV-2 spike proteins on intact virions." <i>Nature</i> 588.7838 (2020): 498-502.</p> <p>(c) Klein, Steffen, et al. "SARS-CoV-2 structure and replication characterized by in situ cryo-electron tomography." <i>Nature communications</i> 11.1 (2020): 1-10.</p> <p>(d) Yao, Hangping, et al. "Molecular architecture of the SARS-CoV-2 virus." <i>Cell</i> 183.3 (2020): 730-738.</p> <p>(e) Casalino, Lorenzo, et al. "Beyond shielding: the roles of glycans in the SARS-CoV-2 spike protein." <i>ACS Central Science</i> 6.10 (2020): 1722-1734.</p> <p>(f) Sikora, Mateusz, et al. "Computational epitope map of SARS-CoV-2 spike</p> |

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| | protein." PLoS computational biology 17.4 (2021): e1008790. |
| 11. | <p>Introduction to viral spread and epidemics</p> <p>(a) Kumberger, Peter, et al. "Multiscale modeling of virus replication and spread." <i>FEBS letters</i> 590.13 (2016): 1972-1986</p> <p>(b) Matt J Keeling and Pejman Rohani, Modeling infectious diseases in humans and animals, Princeton University Press 2008</p> <p>(c) Hethcote, Herbert W. "The basic epidemiology models: models, expressions for R0, parameter estimation, and applications." <i>Mathematical understanding of infectious disease dynamics</i>. 2009. 1-61.</p> |
| 12. | <p>SIR-modelling for influenza dynamics</p> <p>(a) Perelson, Alan S. "Modelling viral and immune system dynamics." <i>Nature Reviews Immunology</i> 2.1 (2002): 28-36</p> <p>(b) Smith, Amber M., and Alan S. Perelson. "Influenza A virus infection kinetics: quantitative data and models." <i>Wiley Interdisciplinary Reviews: Systems Biology and Medicine</i> 3.4 (2011): 429-445.</p> <p>(c) Canini, Laetitia, and Alan S. Perelson. "Viral kinetic modeling: state of the art." <i>Journal of pharmacokinetics and pharmacodynamics</i> 41.5 (2014): 431-443.</p> <p>(d) Baccam, Prasith, et al. "Kinetics of influenza A virus infection in humans." <i>Journal of virology</i> 80.15 (2006): 7590-7599</p> |
| 13. | <p>SIR-modelling for spatial spread of HIV</p> <p>(a) Imle, Andrea, et al. "Experimental and computational analyses reveal that environmental restrictions shape HIV-1 spread in 3D cultures." <i>Nat. Commun.</i> (2019): 1-18</p> <p>(b) Bracq, Lucie, et al. "Mechanisms for cell-to-cell transmission of HIV-1." <i>Frontiers in immunology</i> 9 (2018): 260.</p> <p>(c) Fackler, Oliver T., et al. "Adding new dimensions: towards an integrative understanding of HIV-1 spread." <i>Nature Reviews Microbiology</i> 12.8 (2014): 563-574.</p> |
| 14. | <p>SIR-modelling for SARS-CoV-2 pandemic</p> <p>(a) Dehning, Jonas, et al. "Inferring change points in the spread of COVID-19 reveals the effectiveness of interventions." <i>Science</i> 369.6500 (2020).</p> <p>(b) Neher, RA., et al. "Impact of seasonal forcing on a potential SARS-CoV-2 pandemic." <i>Swiss Med. Weekly</i> (2020)</p> <p>(c) Liu, Xiaoyue, et al. "The role of seasonality in the spread of COVID-19 pandemic." <i>Environmental research</i> 195 (2021): 110874.</p> <p>(d) Kuhl, Ellen. "Data-driven modeling of COVID-19—Lessons learned." <i>Extreme Mechanics Letters</i> (2020): 100921.</p> |
| 15. | <p>Forecasting global pandemics and effective strategies</p> <p>(a) Hufnagel, Lars, Dirk Brockmann, and Theo Geisel. "Forecast and control of epidemics in a globalized world." <i>Proceedings of the National Academy of Sciences</i> 101.42 (2004): 15124-15129</p> <p>(b) Ferguson, Neil M., et al. "Strategies for mitigating an influenza pandemic." <i>Nature</i> 442.7101 (2006): 448-452</p> <p>(c) Ferguson, Neil, et al. "Report 9: Impact of non-pharmaceutical interventions (NPIs) to reduce COVID19 mortality and healthcare demand." (2020).</p> <p>(d) Davies, Nicholas G., et al. "Effects of non-pharmaceutical interventions on COVID-19 cases, deaths, and demand for hospital services in the UK: a modelling study." <i>The</i></p> |

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| | <p><i>Lancet Public Health</i> (2020).</p> <p>(e) Kucharski, Adam J., et al. "Early dynamics of transmission and control of COVID-19: a mathematical modelling study." <i>The lancet infectious diseases</i> 20.5 (2020): 553-558.</p> |
| 16. | <p>Modelling vaccination effects in COVID-19 pandemics</p> <p>(a) Ke, Ruian, et al. "Estimating the reproductive number R0 of SARS-CoV-2 in the United States and eight European countries and implications for vaccination." <i>Journal of theoretical biology</i> 517 (2021): 110621.</p> <p>(b) Saad-Roy, Chadi M., et al. "Immune life history, vaccination, and the dynamics of SARS-CoV-2 over the next 5 years." <i>Science</i> 370.6518 (2020): 811-818.</p> <p>(c) Lavine, Jennie S., Ottar N. Bjornstad, and Rustom Antia. "Immunological characteristics govern the transition of COVID-19 to endemicity." <i>Science</i> 371.6530 (2021): 741-745.</p> |
| 17. | <p>Epidemics in social contact networks and superspreading</p> <p>(a) Lloyd-Smith, James O., et al. "Superspreading and the effect of individual variation on disease emergence." <i>Nature</i> 438.7066 (2005): 355-359.</p> <p>(b) Leventhal GE, Hill AL, Nowak MA, Bonhoeffer S. "Evolution and emergence of infectious diseases in theoretical and real-world networks." <i>Nat Commun.</i> 2015 Jan 16;6:6101</p> <p>(c) Endo, Akira, et al. "Estimating the overdispersion in COVID-19 transmission using outbreak sizes outside China." <i>Wellcome Open Research</i> 5.67 (2020): 67.</p> |
| 18. | <p>Mapping influenza evolution</p> <p>(a) Smith DJ, Lapedes AS, de Jong JC, Bestebroer TM, Rimmelzwaan GF, Osterhaus AD, Fouchier RA. "Mapping the antigenic and genetic evolution of influenza virus." <i>Science.</i> 2004 16;305(5682):371-6.</p> <p>(b) Lapedes A, Farber R. "The geometry of shape space" <i>J. of Theo. Biol.</i> 2001, 7;212(1):57-69</p> <p>(c) Petrova, Velislava N., and Colin A. Russell. "The evolution of seasonal influenza viruses." <i>Nature Reviews Microbiology</i> 16.1 (2018): 47-60.</p> <p>(d) Krammer, Florian, et al. "Influenza (Primer)." <i>Nature Reviews: Disease Primers</i> (2018).</p> |
| 19. | <p>Predicting influenza evolution</p> <p>(a) Łuksza, Marta, and Michael Lässig. "A predictive fitness model for influenza." <i>Nature</i> 507.7490 (2014): 57-61</p> <p>(b) Peck, Kayla M., and Adam S. Lauring. "Complexities of viral mutation rates." <i>Journal of virology</i> 92.14 (2018).</p> |
| 20. | <p>Phylogenetics for viral evolution</p> <p>(a) Neher, Richard A., et al. "Prediction, dynamics, and visualization of antigenic phenotypes of seasonal influenza viruses." <i>Proceedings of the National Academy of Sciences</i> 113.12 (2016): E1701-E1709</p> <p>(b) Hadfield, James, et al. "Nextstrain: real-time tracking of pathogen evolution." <i>Bioinformatics</i> 34.23 (2018): 4121-23</p> <p>(c) Gorbalenya, Alexander E., and C. Lauber. "Phylogeny of viruses." <i>Reference Module in Biomedical Sciences</i> (2017)</p> |