



UvA-DARE (Digital Academic Repository)

Complex networks and agent-based models of HIV epidemic

Zarrabi, N.

Publication date
2013

[Link to publication](#)

Citation for published version (APA):

Zarrabi, N. (2013). *Complex networks and agent-based models of HIV epidemic*. [Thesis, fully internal, Universiteit van Amsterdam].

General rights

It is not permitted to download or to forward/distribute the text or part of it without the consent of the author(s) and/or copyright holder(s), other than for strictly personal, individual use, unless the work is under an open content license (like Creative Commons).

Disclaimer/Complaints regulations

If you believe that digital publication of certain material infringes any of your rights or (privacy) interests, please let the Library know, stating your reasons. In case of a legitimate complaint, the Library will make the material inaccessible and/or remove it from the website. Please Ask the Library: <https://uba.uva.nl/en/contact>, or a letter to: Library of the University of Amsterdam, Secretariat, Singel 425, 1012 WP Amsterdam, The Netherlands. You will be contacted as soon as possible.

References

- [1] Overview of the global aids epidemic. Technical report, Joint United Nations Programme on HIV/AIDS, 2006.
- [2] *Global report: UNAIDS report on the global AIDS epidemic 2012*. WHO Library Cataloguing in Publication Data, Joint United Nations Programme on HIV/AIDS (UNAIDS), 2012.
- [3] T. B. Achacoso and W. S. Yamamoto. CRC-Press, 1992.
- [4] A. Adamatzky, M. H. Lees, and P. M. A. Sloot. Bio-development of motorway networks in the netherlands: A slime mould approach. *Advances in Complex Systems*, 15(4):1250034+28, 2012.
- [5] R. Albert and A.-L. Barabási. Statistical mechanics of complex networks. *Reviews of Modern Physics*, 74(January), 2002.
- [6] R. Albert, H. Jeong, and A.-L. Barabasi. Internet: Diameter of the World-Wide Web. *Nature*, 401(6749):130–131, 1999.
- [7] I. Altintas, M. Bubak, C. Boucher, P. M. A. Sloot, and A. Tirado-Ramos. From molecule to man: Decision support in individualized e-health. volume 39, pages 40–46. IEEE Computer Society, 2006.

-
- [8] A. Anglemyer, G. W. Rutherford, R. C. Baggaley, M. Egger, and N. Siegfried. Antiretroviral therapy for prevention of hiv transmission in hiv-discordant couples. *Cochrane database of systematic reviews*, 8(CD009153), 2011.
- [9] N. Arhel, A. Genovesio, K. Kim, S. Miko, E. Perret, J. Olivo-Marin, S. Shorte, and P. Charneau. Quantitative four-dimensional tracking of cytoplasmic and nuclear hiv-1 complexes. *Nature Methods*, 3(10):817–827, 2006.
- [10] S. Attia, M. Egger, M. Muller, M. Zwahlen, and N. Low. Sexual transmission of hiv according to viral load and antiretroviral therapy: systematic review and meta-analysis. *AIDS*, 23(11):1397–1404.
- [11] S. Y. Auyang. *Foundations of complex-system theories: in economics, evolutionary biology, and statistical physics*. Cambridge University Press, 1999.
- [12] V. Baldazzi, F. Castiglione, and M. Bernaschi. An enhanced agent based model of the immune system response. *Cellular Immunology*, 244(2):77–79, 2006.
- [13] M. Balmer, N. Cetin, K. Nagel, and B. Raney. Towards truly agent-based traffic and mobility simulations. In *Proceedings of the Third International Joint Conference on Autonomous Agents and Multiagent Systems Volume 1*, volume 1pp, pages 60–67. IEEE Computer Society Washington, DC, USA, 2004.
- [14] Y. Bar-Yam. Addison-Wesley, 1997.
- [15] A.-L. Barabási, R. Albert, and H. Jeong. Mean-field theory for scale-free random networks. *Physica A: Statistical Mechanics and its Applications*, 272(1-2):173–187, Oct. 1999.
- [16] P. Barbosa, P. Charneau, N. Dumey, and F. Clavel. Kinetic analysis of hiv-1 early replicative steps in a coculture system. *AIDS Research and Human Retroviruses*, 10(1):53–59, 1994.

-
- [17] S. Barcherini, M. Cantoni, P. Grossi, and A. Verdecchia. Reconstruction of human immunodeficiency virus (hiv) sub-epidemics in italian regions. *International Journal of Epidemiology*, 28:122–9, 1999.
- [18] I. Benenson, K. Martens, and S. Birfir. PARKAGENT: An agent-based model of parking in the city. *Computers Environment and Urban Systems*, 32(6):431–439, 2008.
- [19] L. Bettencourt and G. West. A unified theory of urban living. *Nature*, 467:912–913, 2010.
- [20] S. Boccaletti, V. Latora, Y. Moreno, M. Chavez, and D. Hwang. Complex networks: Structure and dynamics. *Physics Reports*, (424):175–308, 2006.
- [21] S. Boccaletti, V. Latora, Y. Moreno, M. Chavez, and D. U. Hwang. Complex networks: Structure and dynamics. *Physics Reports*, 424:175–308, 2006.
- [22] G. Bogle and P. R. Dunbar. Agent-based simulation of T-cell activation and proliferation within a lymph node. *Immunology and Cell Biology*, 88(2):172–179, 2010.
- [23] E. Bonabeau. Agent-based modeling: methods and techniques for simulating human systems. *Proceedings of the National Academy of Sciences of the United States of America*, 99 Suppl 3:7280–7, May 2002.
- [24] J. Borgdorff, J. L. Falcone, Lorenz, C. Bona-Casas, B. Chopard, and A. Hoekstra. Foundations of distributed multiscale computing: Formalization, specification, and analysis. *Journal of Parallel and Distributed Computing*, 73(4):465–483, 2013.
- [25] G. Brancato, G. Brancato, P. Pezzotti, E. Rapiti, C. A. Perucci, and et al. Multiple imputation method for estimating incidence of hiv infection. the multicenter prospective hiv study. *International Journal of Epidemiology*, 26:1107–1114, 1997.

- [26] B. G. Brenner, M. Roger, and et. al. High rates of forward transmission events after acute/early hiv-1 infection. *The Journal of Infectious Diseases*, 195:951–9, 2007.
- [27] P. C. Bressloff and J. M. Newby. Stochastic models of intracellular transport. *Rev. Mod. Phys.*, 85(1):135–196, 2013.
- [28] A. Brown, R. J. Gifford, J. P. Clewley, C. Kucherer, B. Masquelier, and et al. Phylogenetic reconstruction of transmission events from individuals with acute hiv infection: toward more-rigorous epidemiological definitions. *Journal of Infectious Diseases*, 199:427–431, 2009.
- [29] A. L. Brown, S. Lycett, L. Weinert, G. Hughes, E. Fearnhill, and et al. Analysis of the degree distribution of hiv transmission networks inferred from viral sequence data. In *17th Conference on Retrovirology and Opportunistic Infection*, 2010.
- [30] A. Brussel and P. Sonigo. Analysis of early human immunodeficiency virus type 1 dna synthesis by use of a new sensitive assay for quantifying integrated provirus. *Journal of Virology*, 77(18):10119–10124, 2003.
- [31] E. Bullmore and O. Sporns. Complex brain networks: graph theoretical analysis of structural and functional systems. *Nature reviews. Neuroscience*, 10(3):186–98, 2009.
- [32] C. J. Burrell, L. Karageorgos, and P. Li. Stepwise analysis of reverse transcription in a cell-to-cell human immunodeficiency virus infection model: kinetics and implications. *General Virology*, 76:1675–1686, 1995.
- [33] A. Canals. Knowledge diffusion and complex networks: a model of high-tech geographical industrial clusters. pages 1–21, 2005.
- [34] K. Carley and Z. Lin. Proactive or Reactive : An Analysis of the Effect of Agent Style on Organizational Decision- making Performance. *Intelligent systems in accounting finance and management*, 2(March):271–287, 1993.

- [35] A. Casal, C. Sumen, T. E. Reddy, M. S. Alber, and P. P. Lee. Agent-based modeling of the context dependency in t cell recognition. *Journal of Theoretical Biology*, 236:376–391, 2005.
- [36] C. Castellano and R. Pastor-Satorras. Competing activation mechanisms in epidemics on networks. *Nature Scientific Reports*, 2:371, 2012.
- [37] J. Castilla, J. Del Romero, V. Hernando, B. Marincovich, S. Garcia, and C. Rodriguez. Effectiveness of highly active anti-retroviral therapy in reducing heterosexual transmission of hiv. *AIDS*, 40(1):96–101, 2005.
- [38] L. Chen, P. Jha, B. Stirling, S. K. Sgaier, T. Daid, and et al. Sexual risk factors for hiv infection in early and advanced hiv epidemics in sub-saharan africa: Systematic overview of 68 epidemiological studies. *PLoS ONE*, 2(1), 2007.
- [39] S. Y. Chu, T. A. Peterman, L. S. Doll, J. W. Buehler, and J. W. Curran. Aids in bisexual men in the united states: epidemiology and transmission to women. *American Journal of Public Health*, 82(2):220–224, 1992.
- [40] A. Clauset, C. R. Shalizi, and M. E. J. Newman. Power-law distributions in empirical data. *SIAM Review*, (51):661–703, 2009.
- [41] M. S. Cohen, Y. Q. Chen, M. McCauley, T. Gamble, and M. C. Hosseinipour. Prevention of hiv-1 infection with early antiretroviral therapy. *New England Journal of Medicine*, 365:1–13, 2011.
- [42] V. Colizza and A. Vespignani. The flu fighters. *Physics World*, 23(2):26–30, 2010.
- [43] G. Csardi and T. Nepusz. The igraph software package for complex network research. *InterJournal Journal of Complex Systems*, page 1965, 2006.
- [44] P. Davidsson. Agent Based Social Simulation : A Computer Science View. *Journal of Artificial Societies and Social Simulation*, 5(1):4–8, 2002.

- [45] R. J. De Boer, R. M. Ribeiro, and A. S. Perelson. Current estimates for hiv-1 production imply rapid viral clearance in lymphoid tissues. *PLoS Computational Biology*, 6(9):e1000906, 2010.
- [46] R. Dean, M. G. Dov, A. H. Cliff, P. Thagard, and J. Woods. Econophysics and the complexity of financial markets. In *Philosophy of Complex Systems*, pages 531–565. North-Holland, Amsterdam, 2011.
- [47] R. DeBoer, A. S. Perelson, and K. D. E. Dynamics of hiv infection of cd4+ t cells. *Journal of Math Bioscience*, 114:81–125, 1993.
- [48] V. DeGruttola and R. T. Schooley. Antiretroviral therapy as prevention: linking the mainframe to main street. *Clinical Infectious Diseases*, 52(8):1050–1052, 2011.
- [49] Z. Dezsó and A.-L. Barabási. Halting viruses in scale-free networks. *Physical Review E*, 65(5):1–4, May 2002.
- [50] D. V. Dijk, G. Ertaylan, C. A. B. Boucher, and P. M. A. Sloot. Identifying potential survival strategies of hiv-1 through virus-host protein interaction networks. *BMC Systems Biology*, 4(1):96+17, 2010.
- [51] A. T. Dinh, T. Theofanous, and S. Mitragotri. Understanding intracellular transport processes pertinent to synthetic gene delivery via stochastic simulations and sensitivity analyses. *Biophysical Journal*, 92(3):831–846, 2005.
- [52] P. J. Dodd, G. P. Garnett, and T. B. Hallett. Examining the promise of hiv elimination by 'test and treat' in hyperendemic settings. *AIDS*, 24(5):729–35, 2010.
- [53] A. J. Drummond and A. Rambaut. Beast: Bayesian evolutionary analysis by sampling trees. *BMC Evolutionary Biology*, 7:214, 2009.
- [54] R. C. Edgar. Muscle: multiple sequence alignment with high accuracy and high throughput. *Nucleic Acids Research*, 32(5):1792–1797, 2004.

- [55] P. A. M. Ehlert and L. J. M. Rothkrantz. Microscopic traffic simulation with reactive driving agents. *ITSC 2001 2001 IEEE Intelligent Transportation Systems Proceedings Cat No01TH8585*, pages 860–865, 2001.
- [56] J. M. Epstein. Modelling to contain pandemics. *Nature*, 460(7256):687, Aug. 2009.
- [57] G. Ertaylan and P. M. A. Sloot. A complex automata model of hiv-1 co-receptor tropism: Understanding mutation rate pressure. In *Reviews in Antiretroviral Therapy*, 2007.
- [58] J. Felsenstein. Inferring phylogenies. *Sinauer Associates*, 266:418–27.
- [59] N. Ferguson. Capturing human behaviour. *Nature*, 446(7137):733, 2007.
- [60] N. L. Fleischer and A. V. Diez Roux. “using directed acyclic graphs to guide analyses of neighbourhood health effects: an introduction. *Journal of Epidemiology and Community Health*, 62(9):842–846, 2008.
- [61] T. Fruchterman and E. Reingold. Graph drawing by force-directed placement. *Software Practice and Experience*, 21:1129–1164, 1991.
- [62] M. T. Gastner and M. E. J. Newman. Shape and efficiency in spatial distribution networks. *Disordered Systems and Neural Networks*, 424:175–308, 2004.
- [63] E. Girardi. Epidemiological aspects of transmitted hiv drug resistance. *Scandinavian Journal of Infectious Diseases*, 35(s106):17–20, 2003.
- [64] G. R. M. Giuliani, A. Di Carlo, G. Palamara, M. Dorrucchi, A. Latini, and et al. Increased hiv incidence among men who have sex with men in rome. *AIDS*, 19:1429–31, 2005.

- [65] J. Gomez-Gardenes, V. Latora, Y. Moreno, and E. Profumo. Spreading of sexually transmitted diseases in heterosexual populations. *PNAS*, 105:1399–1404, 2008.
- [66] R. M. Granich, C. F. Gilks, C. Dye, K. M. De Cock, and B. G. Williams. Universal voluntary hiv testing with immediate anti-retroviral therapy as a strategy for elimination of hiv transmission: a mathematical model. *Lancet*, 373:48–57, 2009.
- [67] V. Grimm and S. F. Railsback. *Individual-based modeling and ecology*. Princeton series in theoretical and computational biology. Princeton University Press, 2005.
- [68] V. Grimm, E. Revilla, U. Berger, F. Jeltsch, W. M. Mooij, S. F. Railsback, H.-H. Thulke, J. Weiner, T. Wiegand, and D. L. DeAngelis. Pattern-oriented modeling of agent-based complex systems: lessons from ecology. *Science (New York, N.Y.)*, 310(5750):987–91, Nov. 2005.
- [69] Z. Guo and J. Tay. A comparative study of modeling strategies of immune system dynamics under hiv-1 infection. In *Lecture Notes in Computer Science*, pages 220–233. Springer-Verlag Banff, 2005.
- [70] H. K. Han, J. C. Tay, and Z. Guo. Sufficiency verification of hiv-1 pathogenesis based on multi-agent simulation. In *In Proceedings of the Genetic and Evolutionary Conference*, volume 1, pages 305–312, 2005.
- [71] M. S. T. Hansen, F. D. Bushman, and S. L. Butler. A quantitative assay for hiv dna integration in vivo. *Nature Medicine*, 7:631–634, 2001.
- [72] A. L. Hartman, S. H. Swerdlow, and P. A. Angermeier. Nuclear morphology of follicular center cell-associated t-cells: an immunoultrastructural study of follicular hyperplasia and follicular center cell lymphoma. *Modern pathology*, 1(4):268–273, 1988.

- [73] C. Haub. World population highlights: Key findings from prb's 2007 world population data sheet. volume 62. Population bulletin. Washington, DC: Population Reference Bureau, 2007.
- [74] S. Heckbert. Experimental economics and agent-based models. In *18th World IMACS/MODSIM Congress*, number July, pages 2997–3003, 2009.
- [75] A. G. Hoekstra, J. Kroc, and P. M. A. Sloot. *Introduction to Modeling of Complex Systems Using Cellular Automata*. Springer, 2010.
- [76] A. G. Hoekstra, J. Kroc, and P. M. A. Sloot. *Simulating Complex Systems by Cellular Automata*. Springer, 2010.
- [77] P. W. Holland and S. Leinhardt. Transitivity in structural models of small groups. *Comparative Group Studies*, 2:107–124, 1971.
- [78] Y. Hongyong, L. Lan, and Z. Siying. Consensus of synchronization-preferential scale-free networks. *Physics Procedia*, 3(5):1913–1920, 2010.
- [79] S. Hue, J. Clewley, P. Cane, and D. Pillay. Hiv-1 pol gene variation is sufficient for reconstruction of transmissions in the era of antiretroviral therapy. *AIDS*, 18:719–728, 2004.
- [80] G. J. Hughes, E. Fearnhill, D. Dunn, S. J. Lycett, A. Rambaut, and et al. Molecular phylodynamics of the heterosexual hiv epidemic in the united kingdom. *PLoS Pathogenes*, 5(9):e1000590, 2009.
- [81] D. H. Huson, R. Rupp, and C. Scornavacca. *Phylogenetic Networks*. Cambridge University Press, UK, 2010.
- [82] S. M. Jenness, A. Neaigus, H. Hagan, C. S. Murrill, and T. Wendel. Heterosexual hiv and sexual partnerships between injection drug users and noninjection drug users. *AIDS Patient Care and STDs*, 24(3):175–181, 2010.
- [83] H. Jeong, S. P. Mason, Z. N. Oltvai, and A.-L. Barabási. Lethality and centrality in protein networks. *Nature*, 411:41, May 2001.

- [84] W.-S. Jung, H.-T. Moon, and H. Eugene Stanley. Dynamics of clustered opinions in complex networks. *Journal of Economic Interaction and Coordination*, 3(1):81–88, 2008. 1860-711.
- [85] M. Kennedy and L. S. Doll. Male bisexuality and hiv risk. *Journal of Bisexuality*, 1:109–135, 2001.
- [86] S. Khan, R. Makkena, F. McGeary, K. Decker, W. Grills, and C. Schmidt. A multi-agent system for quantitative simulation of biological networks. In *AAMAS*, pages 385–392, 2003.
- [87] M. Kitsak, L. Gallos, S. Havlin, F. Liljeros, L. Muchnik, H. Stanley, and H. Makse. Identification of influential spreaders in complex networks. *Nature Physics*, 6:888–893, 2010.
- [88] J. Kroc and P. M. A. Sloot. *Complex Systems Modeling by Cellular Automata*. Information Science Reference, 2010.
- [89] S. Leclerc-Madlala. Age-disparate and intergenerational sex in southern africa: the dynamics of hypervulnerability. *AIDS*, 22:17–25, 2008.
- [90] P. Lemey, A. Rambaut, A. J. Drummond, and M. A. Suchard. Bayesian phylogeography finds its roots. *PLoS Computational Biology*, 5(9):e1000520, 2009.
- [91] P. Lemey, A. Rambaut, and O. G. Pybus. Hiv evolutionary dynamics within and among hosts. *AIDS Reviews*, 8:125–140, 2006.
- [92] F. Lewis, G. J. Hughes, A. Rambaut, A. Pozniak, and A. J. Leigh Brown. Episodic sexual transmission of hiv revealed by molecular phylodynamics. *PLoS Medicine*, 5(3):e50, 2008.
- [93] S. Li, J. Wang, X. Luo, and X. Guan. A new framework of consensus protocol design for complex multi-agent systems. *Systems & Control Letters*, 60(1):19–26, 2011.

-
- [94] Z. Li, Z. Duan, G. Chen, and L. Huang. Consensus of Multiagent Systems and Synchronization of Complex Networks: A Unified Viewpoint. *IEEE Transactions on Circuits and Systems I: Regular Papers*, 57(1):213–224, Jan. 2010.
- [95] F. Liljeros, C. R. Edling, L. A. Nunes Amaral, H. E. Stanley, and Y. Aberg. The web of human sexual contacts. *Nature*, 411:907–908, 2001.
- [96] J. Litorco, L. Lee, and C. Jacob. Agent-based simulations of the human immune system. In *Proceedings of 3rd International Conference on Artificial Immune Systems*, volume 3239, pages 400–412. Springer-Verlag GmbH, 2004.
- [97] J. O. Lloyd-Smith, S. J. Schreiber, P. E. Kopp, and W. M. Getz. Superspreading and the effect of individual variation on disease emergence. *Nature*, 438:355–359, 2005.
- [98] L. Luo, S. Zhou, W. Cai, M. Lees, and M. Low. Modeling human-like decision making for virtual agents in time-critical situations. In *Cyberworlds (CW), 2010 International Conference on*, pages 360–367, oct. 2010.
- [99] M. Lurgi and D. Robertson. Simple ecological rules yield complex agent networks. In *Proceedings of the 2010 conference on Artificial Intelligence Research and Development: Proceedings of the 13th International Conference of the Catalan Association for Artificial Intelligence*, pages 39–48, Amsterdam, The Netherlands, The Netherlands, 2010. IOS Press.
- [100] S. Maloy. Multiplicity of infection (moi). Technical report, College of Sciences, San Diego State University, November 2003.
- [101] E. Mancini, F. Castiglione, M. Bernaschi, A. de Luca, and P. M. A. Sloom. Hiv reservoirs and immune surveillance evasion cause the failure of structured treatment interruptions: A computational study. *PLoS ONE*, 7(4):e36108, 2012.

- [102] A. Massimo, C. A. Perucci, and T. Spadea. The epidemic dynamics of hiv-1 in italy: Modelling the interaction between intravenous drug users and heterosexual population. *Statistics in Medicine*, 11(13):1657–1684, 1992.
- [103] D. McDonald, V. M. A, G. Lucero, T. M. Svitkina, G. G. Borisy, M. Emerman, and T. J. Hope. Visualization of the intracellular behavior of hiv in living cells. *Journal of Cell Biology*, 159(3):441–452, 2002.
- [104] S. Mei, R. Quax, D. V. D. Vijver, Y. Zhu, and P. M. A. Sloot. Increasing risk behaviour can outweigh the benefits of antiretroviral drug treatment on the hiv incidence among men-having-sex-with-men in amsterdam. *BMC Infectious Diseases*, 11(1):118, 2011.
- [105] S. Mei, P. Sloot, R. Quax, Y. Zhu, and W. Wang. Complex agent networks explaining the hiv epidemic among homosexual men in amsterdam. *Mathematics and Computers in Simulation*, 80(5):1018–1030, 2010.
- [106] S. Mei, D. van de Vijver, L. Xuan, Y. Zhu, and P. Sloot. Quantitatively evaluating interventions in the influenza A (H1N1) epidemic on China campus grounded on individual-based simulations. *Procedia Computer Science*, 1(1):1675 – 1682, 2010.
- [107] S. Mei, X. Zhou, Y. Zhu, Z. Zhu, T. Zheng, A. V. Boukhanovsky, and P. M. A. Sloot. Simulating city-level airborne infectious diseases. *Computers, Environment and Urban Systems*, 2012.
- [108] V. T. Metzger, J. O. Lloyd-Smith, and L. S. Weinberger. Autonomous targeting of infectious superspreaders using engineered transmissible therapies. *PLoS Computational Biology*, 7(12):e1002015, 2011.
- [109] J. P. Montgomery, E. D. Mokotoff, A. C. Gentry, and J. M. Blair. The extent of bisexual behaviour in hiv-infected men and implications for transmission to their female sex partners. *AIDS Care*, 15(6):829–837, 2003.

-
- [110] A. Mordvintsev, V. Krzhizhanovskaya, M. Lees, and P. Sloot. Simulation of city evacuation coupled to flood dynamics. In *Pedestrian Evacuation Dynamics*, 2012.
- [111] P. W. Nelson, J. D. Murray, and A. S. Perelson. Mathematical analysis of delay differential equation models of hiv-1 infection. *Mathematical Biosciences*, 163(2):201–215, 2000.
- [112] M. E. J. Newman. Assortative mixing in networks. *Physics Review Letters*, 89:208701, 2002.
- [113] M. E. J. Newman. The Structure and Function of Complex Networks. *SIAM Review*, 45(2):167, 2003.
- [114] M. E. J. Newman. Power laws, pareto distributions and zipf’s law. *Contemporary Physics*, 46:323–351, 2005.
- [115] M. E. J. Newman. Finding community structure in networks using the eigenvectors of matrices. *Physical Review E*, 74:036104, 2006.
- [116] M. E. J. Newman, D. J. Watts, and S. H. Strogatz. Random graph models of social networks. *Proceedings of the National Academy of Sciences of the United States of America*, 99 Suppl 1:2566–72, 2002.
- [117] W. Ni and D. Cheng. Leader-following consensus of multi-agent systems under fixed and switching topologies. *Systems & Control Letters*, 59(3-4):209–217, 2010.
- [118] J. M. Oakes, J. S. Kaufman, and M. M. Glymour. Methods in social epidemiology. In *Methods in Social Epidemiology*, volume 7, pages 393–428. Jossey-Bass Inc Pub, 2006.
- [119] T. Okamoto and F. Wong-Staal. Demonstration of virus-specific transcriptional activator(s) in cells infected with htlv-iii by an in vitro cell-free system. *Cell Press*, 47(1):29–35, 1986.

- [120] A. O’Leary, D. W. Purcell, R. H. Remien, H. E. Fisher, and P. S. Spikes. Characteristics of bisexually active men in the seropositive urban mens’ study (sums). *AIDS Care*, 19(7):940–946, 2007.
- [121] J. B. Park, J. Won Lee, J.-S. Yang, H.-H. Jo, and H.-T. Moon. Complexity analysis of the stock market. *Physica A: Statistical Mechanics and its Applications*, 379(1):179–187, 2007.
- [122] C. E. Parker, M. A. Nowak, and D. J. Stekel. A model of lymphocyte recirculation. *Immunology Today*, 18:216–221, 1997.
- [123] R. Pastor-Satorras and A. Vespignani. Immunization of complex networks. *Physical Review E*, 65, 2002.
- [124] R. Pastor-Satorras and A. Vespignani. Complex networks: Patterns of complexity. *Nature Physics*, 6:480–481, 2010.
- [125] A. S. Perelson and P. W. Nelson. Mathematical analysis of hiv-1 dynamics in vivo. *SIAM Review*, 41(1):3–44, 1999.
- [126] K. D. Phillips. Protease inhibitors: a new weapon and a new strategy against hiv. *Journal of the Association of Nurses in AIDS Care*, 7(5):57–71, 1992.
- [127] J. J. Potterat, L. Phillips-Plummer, S. Q. Muth, R. B. Rothenberg, D. E. Woodhouse, T. S. Maldonado-Long, H. P. Zimmerman, and J. B. Muth. Risk network structure in the early epidemic phase of hiv transmission in colorado springs. *Sexually Transmitted Infections*, 78:i159–i163, 2002.
- [128] R. Prabhu, D. L. Owen, K. Folger, and W. McFarland. The bisexual bridge revisited: sexual risk behavior among men who have sex with men and women, san francisco, 1998-2003. *AIDS*, 18(11):1604–1606, 2004.
- [129] M. N. Price, P. S. Dehal, and A. P. Arkin. Fasttree 2 – approximately maximum-likelihood trees for large alignments. *PLoS ONE*, 5(3):e9490, 2010.

- [130] M. C. F. Prosperi, M. Ciccozzi, I. Fanti, F. Saladini, M. Pecorari, and et al. A novel methodology for large-scale phylogeny partition. *Nature Communications*, 2(321), 2011.
- [131] S. R. Proulx, D. E. Promislow, and P. C. Phillips. Network thinking in ecology and evolution. *TRENDS in Ecology and Evolution*, 20(6):345–353, Nov. 2005.
- [132] G. Qiu, B. D. Kandhai, N. F. Johnson, and P. M. A. Sloom. Understanding complex dynamics in derivatives finance: Why do options markets smile? *Advances in Complex Systems*, 15:1250050–69, 2012.
- [133] R. Quax, A. Apolloni, and P. M. A. Sloom. Information processing reveals how microscopic components affect the macroscopic system-state in complex networks. *CoRR*, abs/1111.5483, 2011.
- [134] E. Qwarnstrom, M. Holcombe, M. Pogson, and R. Smallwood. Formal agent-based modelling of intracellular chemical interactions. *BioSystems*, 85:37–45, 2006.
- [135] C. Rademacher. Reconstructing spatiotemporal dynamics of Central European natural beech forests: the rule-based forest model BEFORE. *Forest Ecology and Management*, 194(1-3):349–368, 2004.
- [136] L. Ratner, W. Haseltine, R. Patarca, and et al. Complete nucleotide sequence of the aids virus, htlv-iii. *Nature*, 313(6000):277–284, 1985.
- [137] B. Reddy and J. Yin. Quantitative intracellular kinetics of hiv type-1. *AIDS Research and Human Retroviruses*, 15(3):273–283, 1999.
- [138] S. Resik, P. Lemey, L. H. Ping, V. Kouri, J. Joanes, J. Perez, A. M. Vandamme, and R. Swanstrom. Limitations to contact tracing and phylogenetic analysis in establishing hiv type 1 transmission networks in cuba. *AIDS Research and Human Retroviruses*, 23(3):347–356, 2007.

- [139] G. Rezza, A. Nicolosi, M. Zaccarelli, L. Sagliocca, M. Nespoli, and et al. Understanding the dynamics of the hiv epidemic among italian intravenous drug users: a cross-sectional versus a longitudinal approach. *AIDS*, 7:500–503, 1992.
- [140] D. W. Roberts. The mosaic-cycle concept of ecosystems, 1991.
- [141] M. N. Rosario and H. S. Eugene. *An Introduction to Econophysics: Correlations and Complexity in Finance*. Cambridge University Press, 2000.
- [142] R. B. Rothenberg, J. J. Potterat, D. E. Woodhouse, S. Q. Muth, W. W. Darrow, and a. S. Klovdahl. Social network dynamics and HIV transmission. *AIDS (London, England)*, 12(12):1529–36, Aug. 1998.
- [143] A. Sabbatini, B. Carulli, M. Villa, M. L. Correa Leite, and A. Nicolosi. Recent trends in the hiv epidemic among injecting drug users in northern italy, 1993-1999. *AIDS*, 15(16):2181–5, 2001.
- [144] L. Scherer, J. J. Rossi, and M. S. Weinberg. Progress and prospects: Rna-based therapies for treatment of hiv infection. *Gene Therapy*, 14:1057–1064, 2007.
- [145] A. Schneeberger, C. H. Mercer, S. A. J. Gregson, N. M. Ferguson, C. A. Nyamukapa, R. M. Anderson, A. M. Johnson, and G. P. Garnett. Scale-free networks and sexually transmitted diseases: a description of observed patterns of sexual contacts in Britain and Zimbabwe. *Sexually Transmitted Diseases*, 31(6):380–387, 2004.
- [146] F. Schweitzer. *Modeling Complexity in Economics and Social Systems*. World Scientific Publishing Co. Pte. Ltd., 2002.
- [147] A. R. Sedaghat, J. B. Dinoso, L. Shen, C. O. Wilkem, and R. F. Ciliciano. Decay dynamics of hiv-1 depend on the inhibited stages of the viral life cycle. *PNAS*, 105(12), 2008.
- [148] P. Sloot. Virolab: A virtual laboratory for decision support in viral deisease treatment.

- [149] P. M. A. Sloot, F. Chen, and C. Boucher. Cellular automata model of drug therapy for hiv infection. In *5th International Conference on Cellular Automata for Research and Industry*, volume 2493, pages 282–293. Proceedings, in series Lecture Notes in Computer Science, 2002.
- [150] P. M. A. Sloot, P. V. Coveney, G. Ertaylan, V. Muller, C. A. B. Boucher, and M. T. Bubak. Hiv decision support: From molecule to man. *Philosophical Transactions of the Royal Society A*, 367:2691–2703, 2009.
- [151] P. M. A. Sloot and C. G. Figdor. Elastic light scattering from nucleated bloodcells: Rapid numerical analysis. *Applied Optics*, 25:3559, 1986.
- [152] P. M. A. Sloot, S. V. Ivanov, A. V. Boukhanovsky, V. D. V. D, and C. Boucher. Stochastic simulation of hiv population dynamics through complex network modelling. *International Journal of Computer Mathematics*, 85(8):1175–1187, 2008.
- [153] P. M. A. Sloot, B. J. Overeinder, and A. Schoneveld. Self-organized criticality in simulated correlated systems. *Computer Physics Communications*, 142(1-3):76–81, 2001.
- [154] P. M. A. Sloot and R. Quax. Information processing as a paradigm to model and simulate complex systems. *Journal of Computational Science*, 3(5):247 – 249, 2012.
- [155] D. Smith, S. J. May, S. Tweeten, L. Drumright, M. Pacold, S. Kosakovsky Pond, R. Pesano, Y. Lie, D. Richman, S. Frost, C. Woelk, and S. Little. A public health model for the molecular surveillance of hiv transmission in san diego, california. *AIDS*, 23:225–32, January 2009.
- [156] D. M. D. Smith, J. P. Onnela, C. F. LEE, M. D. Fricker, and N. F. Johnson. Network automata: Coupling structure and function in dynamic networks. *Advances in Complex Systems*, 14(03):317–339, 2011.

- [157] R. J. Smith, J. T. Okano, J. S. Kahn, E. N. Bodine, and S. Blower. Evolutionary dynamics of complex networks of hiv drug-resistant strains: the case of san francisco. *Science*, 327(5966):697–701, 2010.
- [158] S. W. Sorensen, S. L. Sansom, J. T. Brooks, G. Marks, E. M. Begier, and et al. A mathematical model of comprehensive test-and-treat services and hiv incidence among men who have sex with men in the united states. *PLoS ONE*, 7(2):e29098, 2012.
- [159] O. Sporns, D. R. Chialvo, M. Kaiser, and C. C. Hilgetag. Organization, development and function of complex brain networks. *Trends in Cognitive Sciences*, 8(8):418–25, 2004.
- [160] M. Steel. *The Phylogenetic Handbook: A Practical Approach to Phylogenetic Analysis and Hypothesis Testing*. Cambridge University Press, 2010.
- [161] D. J. Stekel, C. E. Parker, and M. A. Nowak. A model of lymphocyte recirculation. *Immunology Today*, 18:216–221, 1997.
- [162] S. H. Strogatz. Exploring complex networks. *Nature*, 410(6825):268–76, 2001.
- [163] C. Sumen, T. E. Reddy, M. S. Alber, P. P. Lee, and A. Casal. Agent-based modeling of the context dependency in t cell recognition. *Journal of Theoretical Biology*, 236(4):376–391, 2005.
- [164] J. Summersy, R. Srivastavawz, L. Youw, and J. Yin. Stochastic vs. deterministic modeling of intracellular viral kinetics. *Journal of Theoretical Biology*, 218:309–321, 2002.
- [165] S. Suo and Y. Chen. The dynamics of public opinion in complex networks. *Journal of Artificial Societies and Social Simulation*, 11, 2008.
- [166] K. Tamura, J. Dudley, M. Nei, and S. Kumar. Mega4: Molecular evolutionary genetics analysis (mega) software version 4.0. *Molecular Biology and Evolution*, 24:1596–1599, 2007.

- [167] P. Taxonomy. A Review On Natural Stand Dynamics In Beechwoods Of East Central Europe. *Applied Ecology and Environmental Research*, 1(1):19–46, 2003.
- [168] J. C. Tay and Z. Guo. A comparative study on modeling strategies for immune system dynamics under hiv-1 infection. *Lecture Notes in Computer Science*, 3627:220–233, 2005.
- [169] K. Thulasiraman and M. N. S. Swamy. Wiley-Interscience, 1992.
- [170] J. Vercauteren, A. M. Wensing, D. V. D. Vijver, J. Albert, and C. Balotta. Transmission of drug-resistant hiv-1 is stabilizing in europe. *Journal of Infectious Diseases*, 200:1503–1508, 2009.
- [171] J. Verdasca, M. Da Gama, A. Nunes, N. R. Bernardino, J. M. Pacheco, and et al. Recurrent epidemics in small world networks. *Journal of Theoretical Biology*, 233:553–561, 2005.
- [172] A. Vespignani. Predicting the behavior of techno-social systems. *Science (New York, N.Y.)*, 325(5939):425–8, July 2009.
- [173] A. Vespignani. Modelling dynamical processes in complex socio-technical systems. *Nature Physics*, 8:32–39, 2012.
- [174] D. V. D. Vijver, A. M. J. Wensing, and C. A. B. Boucher. The epidemiology of transmission of drug resistant hiv-1. *Epidemiology*, pages 17–36, 2006.
- [175] I. Vragović, E. Louis, and A. Díaz-Guilera. Efficiency of informational transfer in regular and complex networks. *Phys. Rev. E*, 71(3):036122, 2005.
- [176] R. P. Walensky, A. D. Paltiel, E. Losina, B. L. Morris, C. A. Scott, and et al. Test and treat dc: forecasting the impact of a comprehensive hiv strategy in washington dc. *Clinical Infectious Diseases*, 51(4):392–400, 2010.
- [177] D. J. Watts. Collective dynamics of small-world networks. *The Structure and Dynamics of Networks*, 393(6684):440–442, 2006.

- [178] D. J. Watts and S. H. Strogatz. Collective dynamics of ‘small-world’ networks. *Natur*, 393:440–442, june 1998.
- [179] G. Weng, U. S. Bhalla, and R. Iyengar. Complexity in biological signaling systems. *Science*, 284(5411):92–96, 1999.
- [180] D. B. West. Prentice-Hall, Englewood Cliffs, NJ, 1995.
- [181] T. White and K. Webb. Cell modeling using agent-based formalisms. In *Proceedings of the Third International Joint Conference on Autonomous Agents and Multiagent Systems*, volume 3, pages 1190–1196. IEEE Computer Society, 2004.
- [182] D. Wodarz and M. A. Nowak. Mathematical models of hiv pathogenesis and treatment. *Bioessays*, 24(12):1178–87, 2002.
- [183] F. Xiao, L. Wang, and A. Wang. Consensus problems in discrete-time multiagent systems with fixed topology. *Journal of Mathematical Analysis and Applications*, 322(2):587–598, 2006.
- [184] J. Yu and L. Wang. Group consensus in multi-agent systems with switching topologies and communication delays. *Systems & Control Letters*, 59(6):340–348, 2010.
- [185] N. Zarrabi, M. Mancini, J. C. Tay, S. Shahand, and P. M. A. Sloor. Modeling hiv-1 intracellular replication: two simulation approaches. 1:555–564, 2010.
- [186] N. Zarrabi, M. Prospero, R. G. Belleman, M. Colafigli, A. De Luca, and P. M. A. Sloor. Combining epidemiological and genetic networks signifies the importance of early treatment in hiv-1 transmission. *PLoS ONE*, 7(9):e46156+15, 2012.
- [187] Y. H. Zheng, N. Lovsin, and B. M. Peterlin. Newly identified host factors modulate hiv replication. *Immunol. Lett.*, 97(2):225–34, 2005.