Related work:

Duffy, S. et al. (2008) Rates of evolutionary change in viruses: patterns and determinants. Nat. Rev. Genet, .9, 267–276, Lauring, A.S. and Andino, R. (2010) Quasispecies theory and the behavior of RNA viruses. PLoS Pathog., 6, e1001005., Rozera, G. et al. (2014) Quasispecies tropism and compartmentalization in gut and peripheral blood during early and chronic phases of HIV-1 infection: possible correlation with immune activation markers. Clin. Microbiol. Infect., 20, O157-O166., Tsibris, A.M.N. et al. (2009) Quantitative deep sequencing reveals dynamic HIV-1 escape and large population shifts during CCR5 antagonist therapy in vivo. PLoS One, 4, e5683., Vignuzzi, M. et al. (2006) Quasispecies diversity determines pathogenesis through cooperative interactions in a viral population. Nature, 439, 344–348. Kuroda, M. et al. (2010) Characterization of quasispecies of pandemic 2009 influenza A virus (A/H1N1/2009) by de novo sequencing using a next-generation DNA sequencer. PLoS One, 5, e10256., Nowak, M.A. et al. (1991) Antigenic diversity thresholds and the development of AIDS. Science, 254, 963–969. Gaschen, B. (2002) Diversity considerations in HIV-1 vaccine selection. Science, 296, 2354–2360. Mason, S. et al. (2018) Comparison of antiviral resistance across acute and chronic viral infections. Antiviral Res., 158, 103-112. Barzon, L. et al. (2013) Next-generation sequencing technologies in diagnostic virology. J. Clin. Virol., 58, 346–350, Capobianchi, M.R. et al. (2013) Next-generation sequencing technology in clinical virology. Clin. Microbiol. Infect., 19, 15–22., Goodwin, S. et al. (2016) Coming of age: ten years of next-generation sequencing technologies. Nat. Rev. Genet., 17, 333–351. Beerenwinkel, N. et al. (2012) Challenges and opportunities in estimating viral genetic diversity from next-generation sequencing data. Front Microbiol, 3, 329. Eliseev, A. et al. (2020) Evaluation of haplotype callers for next-generation sequencing of viruses. Infect. Genet. Evol., 82, 104277. Posada-Ce'spedes, S. et al. (2017) Recent advances in inferring viral diversity from high-throughput sequencing data. Virus Res., 239, 17-32. Ho, T. and Tzanetakis, I.E. (2014) Development of a virus detection and dis2covery pipeline using next generation sequencing. Virology, 471–473, 54–60. Li, Y. et al. (2016) VIP: an integrated pipeline for metagenomics of virus identi@fication and discovery. Sci. Rep., 6, 237, Wan, Y. et al. (2015) VirAmp: a galaxy-based viral genome assembly pipeline. Gigascience, 4, 19., Howison, M. et al. (2019) Measurement error and variant-calling in deep Illumina sequencing of HIV. Bioinformatics, 35, 2029–2035, Jayasundara, D. et al. (2015) ViQuaS: an improved reconstruction pipeline for viral quasispecies spectra generated by next-generation sequencing. Bioinformatics, 31, 886-896. Lee, E.R. et al. (2020) Performance comparison of next generation sequencing analysis pipelines for HIV-1 drug resistance testing. Sci Rep, 10, 1634. Archer, J. et al. (2010) The evolutionary analysis of emerging low frequency HIV-1 CXCR4 using variants through time—an ultra-deep approach. PLoS Comput. Biol., 6, e1001022., (Posada-Ce'spedes et al., 2017) Recent advances in inferring viral diversity from high-throughput sequencing data. Virus Res., 239, 17-32. Di Giallonardo, F. et al. (2014) Full-length haplotype reconstruction to infer the structure of heterogeneous virus populations. Nucleic Acids Res., 42, e115. Zanini, F. et al. (2015) Population genomics of intrapatient HIV-1 evolution. eLife, 4, e11282.