

Cumming School of Medicine



Evolution of variable mutative organisms Summary of Literature

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1 Project Outline

A project proposal may or may not appear here. It depends on how private the material should be.

2 References Discussion

This section is intended for me to write notes connecting the material in the references with observations and comments.

References

- [1] ; on behalf of the ACMG Laboratory Quality Assurance Committee, S. Richards, N. Aziz, S. Bale, D. Bick, S. Das, J. Gastier-Foster, W. W. Grody, M. Hegde, E. Lyon, E. Spector, K. Voelkerding, and H. L. Rehm, "Standards and guidelines for the interpretation of sequence variants: a joint consensus recommendation of the American College of Medical Genetics and Genomics and the Association for Molecular Pathology," *Genetics in Medicine*, vol. 17, no. 5, pp. 405–423, may 2015. [Online]. Available: <http://www.nature.com/articles/gim201530>

This is the guidelines for assessing the pathogeneity of a genetic variant by the ACMG. These guidelines are fairly exustive but are currently a bit out of date in my opinion with regard to in silico methods. The go

through an exhaustive list of impacts. These impacts are ranked as supporting, moderate, strong, and very strong when evaluating pathogeneticity and stand alone, strong, and supporting with regard to benign evidence. To list the impacts and evidence is not useful, but there are some select quotes highlighted in the text about population genetics and the use of in silico solutions.

- [2] S. Balsamo and A. Marin, “Separable solutions for Markov processes in random environments,” *European Journal of Operational Research*, vol. 229, no. 2, pp. 391–403, sep 2013. [Online]. Available: <https://linkinghub.elsevier.com/retrieve/pii/S0377221713002191>

NOT CLEAR YET.

- [3] E. Domingo and C. Perales, “Viral quasispecies,” *PLOS Genetics*, vol. 15, no. 10, p. e1008271, oct 2019. [Online]. Available: <https://dx.plos.org/10.1371/journal.pgen.1008271>

A comprehensive review of support for Quasi-Species theory. This paper covers the historical basis and gives a comprehensive coverage of evidence for viral QS. It also discusses the following topics, Error-prone replication and mutant spectra, phenotypic reservoir, adaptive parameters, intra-mutant spectrum quasispecies memory, sequence space, population bottleneck, biological constraints, connections with viral pathogenesis, and QS and long term evolution.

- [4] J. Frazer, P. Notin, M. Dias, A. Gomez, J. K. Min, K. Brock, Y. Gal, and D. S. Marks, “Disease variant prediction with deep generative models of evolutionary data,” *Nature*, vol. 599, no. 7883, pp. 91–95, nov 2021. [Online]. Available: <https://www.nature.com/articles/s41586-021-04043-8>

This paper covers a neural network that uses the amino acid sequence of different proteins to produce an evolutionary index. The evolutionary index is then used to produce a distribution of different sequences and make a prediction of Benign, unknown, and Pathogenic. The distribution allows for an estimate of the confidence of the prediction. They used unsupervised learning and were able to achieve an avg AUC = 0.92

- [5] P. G. Harrison, “Reversed processes, product forms and a non-product form,” *Linear Algebra and its Applications*, vol. 386, pp. 359–381, jul 2004. [Online]. Available: <https://linkinghub.elsevier.com/retrieve/pii/S0024379504001089>

NOT CLEAR YET.

- [6] E. C. Holmes and A. Moya, “Is the Quasispecies Concept Relevant to RNA Viruses?” *Journal of Virology*, vol. 76, no. 1, pp. 460–462, jan 2002. [Online]. Available: <https://journals.asm.org/doi/10.1128/JVI.76.1.460-462.2002>

This is a letter to the editor, discussing the issues of applying quasi-species to viral RNA. It starts by critisizing the lack of formal definitions of QS. This letter addresses, critisims (lack of def, lack of drift), and evidence (strong theoretic basis?) it makes arguments but many seem flimsy now.

- [7] M. A. Huynen, P. F. Stadler, and W. Fontana, “Smoothness within ruggedness: the role of neutrality in adaptation,” *Proceedings of the National Academy of Sciences*, vol. 93, no. 1, pp. 397–401, 1996. [Online]. Available: <https://www.pnas.org/content/93/1/397>

This paper is fascianting. It used a simulation to show the importance of nutral mutation on secondary structure evolution. This was achived by simulationg mtation using a diffution model with imperically derived hyper params. This paper then shows that nutral mutation allows for nutral movement to new wells of fitness, that are otherwise unreachable f selective forces are too strong. Worth Re-reading. :)

- [8] M. Kimura, “Evolutionary Rate at the Molecular Level,” *Nature*, vol. 217, no. 5129, pp. 624–626, feb 1968. [Online]. Available: <https://www.nature.com/articles/217624a0>

A paper on the early scuttle butt of how to compute mutation rates. It draws its own conclusion, which has been since refuted but has realted neutral theory with molecular evolution which is molecular clock theory.

- [9] S. Matuszewski, L. Ormond, C. Bank, and J. D. Jensen, “Two sides of the same coin: A population genetics perspective on lethal mutagenesis and mutational meltdown ,” *Virus Evolution*, vol. 3, no. 1, 03 2017. [Online]. Available: <https://doi.org/10.1093/ve/vex004>

An exellent review paper. It goes through and cites many of the ideas and evidence for and against many of them. This paper also makes some unfair assumptions in my opinion. Mainly that if mean fitness is less than 1, the population will go extinct, this seems like a gross over assumption. The population will certainly decrease, but depending of the facorts which drive the change in fitness must be considered when making such a statement.

- [10] A. Moya, E. C. Holmes, and G.-C. Fernando, “The population genetics and evolutionary epidemiology of RNA viruses,” *Nature Reviews Microbiology*, vol. 2, no. 4, pp. 279–288, apr 2004. [Online]. Available: <http://www.nature.com/articles/nrmicro863>

This paper reviews viral RNA mechanisms and some quantifications around the variables of mutation. Then it discusses how studies are struc-tred for wet lab research of mutation and evolution studies. Helps to give a large overview of the topic of viral RNA without discussing Quasi-Species.

- [11] on behalf of the ClinGen Sequence Variant Interpretation Working Group (ClinGen SVI), S. V. Tavtigian, M. S. Greenblatt, S. M. Harrison, R. L. Nussbaum, S. A. Prabhu, K. M. Boucher, and L. G. Biesecker, “Modeling the ACMG/AMP

variant classification guidelines as a Bayesian classification framework,” *Genetics in Medicine*, vol. 20, no. 9, pp. 1054–1060, sep 2018. [Online]. Available: <http://www.nature.com/articles/gim2017210>

This paper uses naive bayes method to develop a classifier for pathogeneity of a genetic variant. This method is okay, it is not very strong, but is laying the ground work for future studies. It does a good job of relating the ACMG guidelines to a mathematical framework.

- [12] A. Wagner, “Information theory, evolutionary innovations and evolvability,” *Philosophical Transactions of the Royal Society B: Biological Sciences*, vol. 372, no. 1735, p. 20160416, Oct 2017. [Online]. Available: <https://doi.org/10.1098/rstb.2016.0416>

This paper looked at the idea of applying information theory to the mapping between Phenotype space and genotype space. The model selected had significant restrictions for simplicity, but did allow for the establishing of some interesting results, like the fact that “The complexity increase is generally lower if the old site had high information content, which shows that phenotypic information change can depend on ancestral phenotypes and are thus contingent on evolution theory.” These results are based on the understanding of the amount of information stuck in a given molecular structure.

- [13] C. O. Wilke, “Molecular clock in neutral protein evolution,” *BMC Genetics*, vol. 5, no. 1, p. 25, 2004. [Online]. Available: <http://bmcbgenet.biomedcentral.com/articles/10.1186/1471-2156-5-25>

An interesting paper discussing the impact of population size and mutation rate on the interpretation of molecular clock theory. This was an attempt to show that neutral theory could be used to help answer the disconnect of empirical results and molecular clock theory, called “overdispersed molecular clock”. They were able to help account for overdispersion when mutation is low and population is reasonably low.

- [14] —, “Quasispecies theory in the context of population genetics,” *BMC Evolutionary Biology*, vol. 5, no. 1, p. 44, dec 2005. [Online]. Available: <https://bmcevolbiol.biomedcentral.com/articles/10.1186/1471-2148-5-44>

This paper is wonderful, it describes and relates the equations from quasispecies and the concepts from evolutionary theory. It shows how the QS equations can be derived from the principals mutation-selection equations.