METAGENOMIC ART: A FAMILY PORTRAIT

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Abstract

Metagenomics now makes available not only the genome of a single organism, but that of a community of species sampled from the environment. Namely, metagenomic research has been used to analyze and characterize the human microbiome – the collection of microorganisms living on the body and inside of it. In this paper, I present a framework for metagenomic art. I then show how this approach can be applied to generate metagenomic family portraits.

Microbial genomics traditionally aimed at sequencing, assembling and annotating the genome of a single organism cultured in the lab. However, the so-called *great plate count anomaly* revealed that the vast majority of bacteria present in nature will not grow on cultured media. That implies that extant genomic data are highly biased and only represent a small percentage of the genomes of microbial species sampled from the environment [1]. Metagenomics is the discipline that enables the study of genomic data from uncultured microbial communities, sometimes containing more than 10,000 species represented by millions of new genomic sequences.

Metagenomic studies have been successful at revealing patterns in community genome variation across geographic and vertical profiles of the ocean and many other important microbial habitats [2]. The *Human Microbiome Project* aims at applying the same metagenomic approach to sample different regions of the human body [3]. By sequencing a sample of DNA directly from the environment, human metagenomic studies have revealed that less than 10% of the cells that comprise our bodies are human cells. The remaining 90% are bacterial cells. The description of this *human microbiome* [4] is of great interest and importance for several reasons. For one, *Homo sapiens* as we know it is now best described as a *superorganism*, an organism in which a large number of different species coexist [5]. It implies that the human genome is only one of the many genomes that affect *Homo sapiens*. More importantly, human biology can no longer deal only with human cells. The human microbiome is a plastic metagenome that changes according to body site, environment, and health status. It varies within and between individuals, to such a degree that the metagenomes at each body site (e.g., skin, gut) are more similar across the human population than they are to metagenomes present at other sites in the same individual [6].

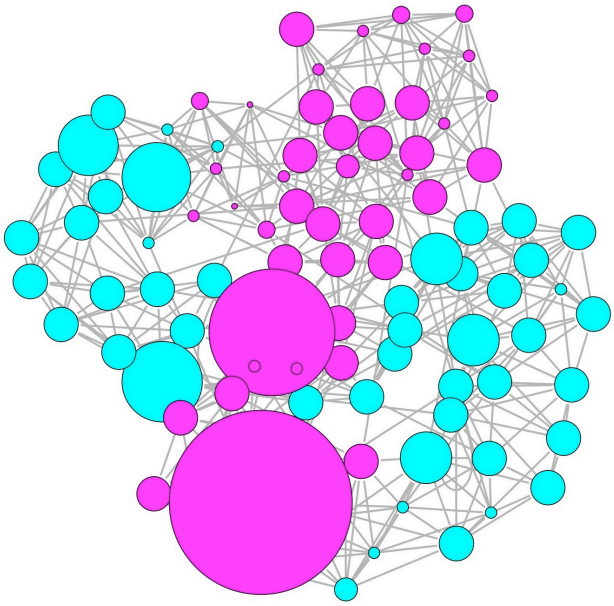
A framework for metagenomic art

Our bodies grow old, they change in time, but our DNA remains the same. Contrary to our genome, our microbiome is multiple and dynamic; it varies from body site to body site and evolves at any given site from day to day. Consequently, one cannot contemplate capturing our true essence with metagenomic data. The microbiome landscape is ever changing. How to picture it is a daunting task for any given artist. How to define it remains a challenge, even for the most gifted scientist. As an "artscientist", I want to tackle this problem through various experiments. I will use meteganomic data and network analysis to generate family portraits, an artscience project focusing on the microbiomes of real-life couples.

One can safely assume that two adults from the same household are probably sharing a large part of their microbiomes. Moreover, one could also postulate that the microbiomes of two lovers are more likely to be similar than the microbiomes of two strangers. This is the type of scientific hypothesis that metagenomic art can actually put to the test [7]. Hundreds of microbiomes have already been sequenced across age, gender and geography [8]. According to our prediction, it is expected that pairs of metagenomes sampled at random from different individuals will be more different than metagenomes obtained from a real-life couple. In other words, two lovers who are constantly exchanging microbes are very likely to have similar metagenomes, whereas total strangers should exhibit different metagenomes.

My wife enters the picture. What if we match our metagenomes? What does it say about our love life? Analyzing our respective microbiomes reveals inner-body differences and similarities. The corresponding network (Fig. 1), displayed as a *metagenomic family portrait*, provides a testimony of the intricate relationships among the metagenomes of individuals sharing microbes on a daily basis

Fig. 1. Metagenomic family portrait of a real-life couple. Male and female microbiomes are respectively depicted by the nodes in blue and pink.



References and Notes

1. J. C. Wooley, A. Godzik and I. Friedberg, "A primer on metagenomics," *PloS Computational Biology* **6,** No. 2 (2010) p. e1000667.

2. V. Iverson, R. M. Morris, C. D. Frazar, C. T. Berthiaume, R. L. Morales and E. V. Armbrust, "Untangling genomes from metagenomes: Revealing an uncultured class of marine Euryarchaeota," *Science* **335** (2012) pp. 587-590.

3. Human Microbiome Project Consortium, "Structure, function and diversity of the healthy human microbiome," *Nature* **486** (2012) pp. 207-214.

4. P. J. Turnbaugh, R. E. Ley. M. Hamady, C. M. Fraser-Liggett, R. Knight and J. I. Gordon, "The human microbiome project," *Nature* **449** (2007) pp. 804-810.

5. R. D, Sleator, "The human superorganism – of microbes and men," *Medical Hypotheses* **74** (2010) pp. 214-215.

6. K. J. Pflughoeft and J. Versalovic, "Human microbiome in health and disease," *Annual Review of Pathology: Mechanisms of Disease* **7** (2012) pp. 99-122.

7. Human Microbiome Project Consortium, "A framework for human microbiome research," *Nature* **486** (2012) pp. 215-221.

8. I. Cho and M. J. Blaser, "The human microbiome: At the interface of health and disease," *Nature Review Genetics* **13** (2012) pp. 260-270.