VIROLIEGY < HTTPS://VIROLIEGY.COM/>

Exposing the lies of Germ Theory and virology using their own sources.

The Human “Virome”

“Viruses are microscopic parasites, generally much smaller than bacteria. **They lack the capacity to thrive and reproduce outside of a host body.**

https://www.google.com/amp/s/www.livescience.com/amp/53272-what-is-a-virus.html < https://www.google.com/amp/s/www.livescience.com/amp/53272-what-is-a-virus.html>

When most people think of “viruses,” they think of invisible floating invaders from

outside which find a way to inhabit the body taking over host cells and multiplying out of control until disease occurs. They are under the false assumption that what are referred to as "viruses" do not belong to our own bodies (endogenous) but must come from some outside source (exogenous). However, this is clearly not the case according to the newest scientific evidence as it is claimed that the human body is full of what virologists call "viruses." In fact, when you look at the evidence presented to us today, the human genome is primarily made up of "viruses:"

The non-human living inside of you

"The human genome contains billions of pieces of information and around 22,000 genes, but not all of it is, strictly speaking, human. **Eight percent of our DNA consists of remnants of ancient viruses, and another 40 percent is made up of repetitive strings of genetic letters that is also thought to have a viral origin."**

"For many years, biologists had little understanding of how that connection worked—so little that they came to refer to the viral part of our DNA as dark matter within the genome. "They just meant they didn't know what it was or what it did," explains Molly Gale Hammell, an associate professor at Cold Spring Harbor Laboratory."

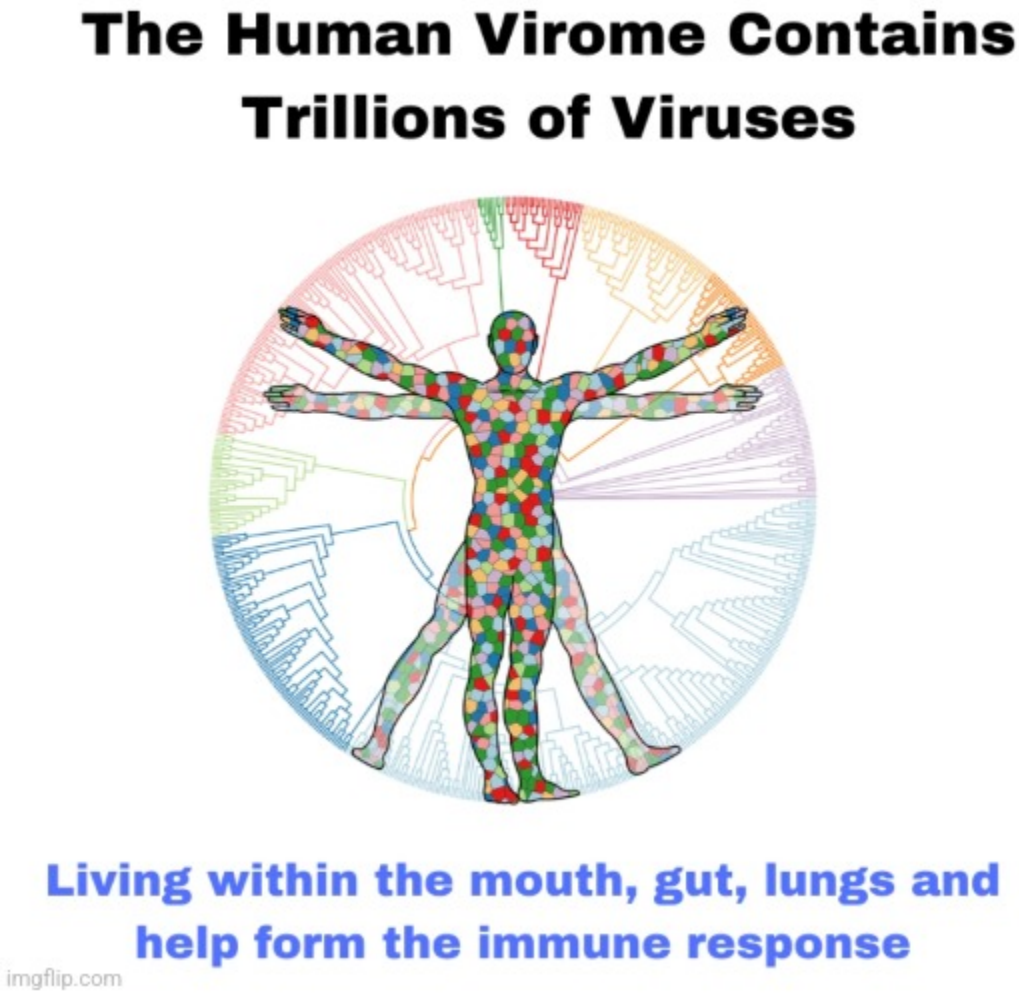
Due to the power of metagenomic sequencing, it has been determined that at least 48% of our genome is made up of “viruses.” Gramted, they have no understanding of what this genetic “dark matter” is nor whether it is even “viral” at all. However, the discovery of these vast amounts of repetitive strings of RNA/DNA assumed to be of “viral” origin has given way to what has now become known as the human “virome:”

Virology: a scientific discipline facing new challenges

“Many host districts of the human body and its mucous membranes are heavily ‘colonized’ by viruses that are not associated with any disease. This has led to

the concept of the virome, which can be considered as the set of all viruses, eukaryotic and prokaryotic, present in the human body. The virome includes viruses that infect host cells, viruses that infect the majority of other types of microorganisms harboured by the body, and virus-related genetic elements in our chromosomes [[1] < https://www.clinicalmicrobiologyandinfection.com/article/S1198-743X(18)30775-4/fulltext#bib1>]. Viruses, which can no longer be invariably considered pathogens, interact with the host and other members of the microbial communities (Archaea, bacteria and eukaryotes) in a variety of complex and meaningful ways. These complex interactions have just begun to be investigated but it is common opinion that they profoundly affect health status [**[2] < https://www.clinicalmicrobiologyandinfection.com/article/S1198-743X(18)30775-4/fulltext#bib2>**]. **Due to the existence of commensal viruses, we should probably redefine chronic viral infections and focus our attention on the host rather than on infectious agents to dissect disease determinants.”**

https://www.clinicalmicrobiologyandinfection.com/article/S1198-743X(18)30775-4/fulltext < https://www.clinicalmicrobiologyandinfection.com/article/S1198-743X(18)30775-4/fulltext>



The explosion of genomic sequencing in the early 2000’s gave way to numerous sequences of unknown origin. As genomic databases were in their infancy and just starting to be built, anything that did not fit with already existing references were set aside. Rather than assuming that these strings of DNA were of human origin, it was decided that they must be either bacterial or “viral.” While the bacterial side of the microbiome has been studied extensively, the “viral” side has been neglected and thus very little is actaully known about it. In fact, they do not know whether the sequences belong to bacteriophages (“viruses” of bacteria) or other “virus” types. Essentially, they have a massive amount of data with no idea what to do with it as there are no references avaliable to compare these sequences to, so assumptions were made and stories were built to justify the collection of meaningless data:

The human virome: assembly, composition and host interactions

"The human body hosts vast microbial communities, termed the microbiome. Less well known is the fact that the human body also hosts vast numbers of different viruses, collectively termed the 'virome'. **Viruses are believed to be the most abundant and diverse biological entities on our planet, with an estimated 10^{31} particles on Earth. The human virome is similarly vast and complex, consisting of approximately 10^{13} particles per human individual, with great heterogeneity.** In recent years, studies of the human virome using metagenomic sequencing and other methods have clarified aspects of human virome diversity at different body sites, the relationships to disease states and mechanisms of establishment of the human virome during early life. **Despite increasing focus, it remains the case that the majority of sequence data in a typical virome study remain unidentified, highlighting the extent of unexplored viral 'dark matter'."**

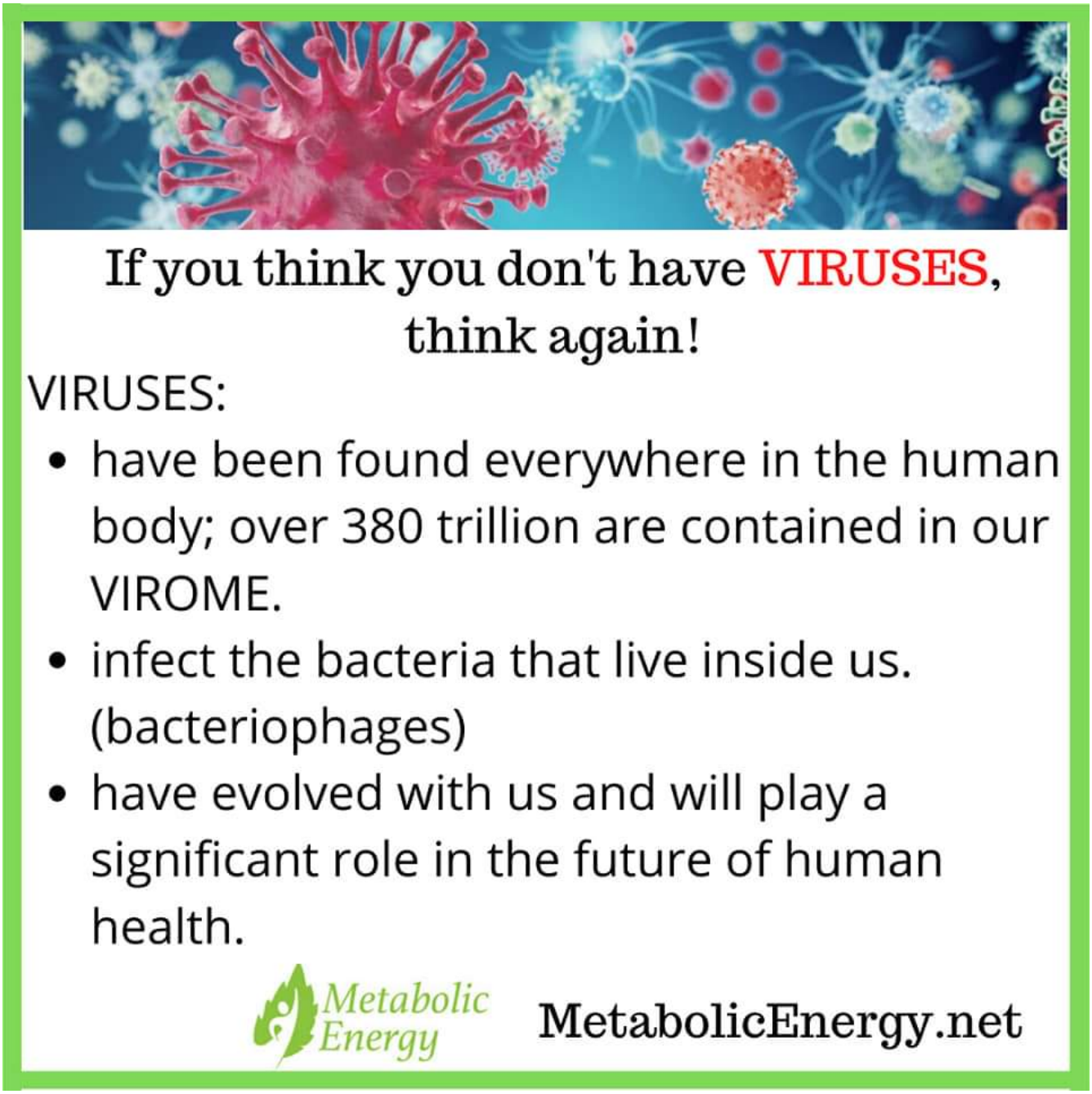
"We are becoming accustomed to the idea that healthy humans are colonized by a rich diversity of microorganisms — the microbiome. However, less well known is that healthy humans are also colonized by a remarkable diversity of viruses — the virome. **The human virome comprises bacteriophages (phages) that infect bacteria, viruses that infect other cellular microorganisms such as archaea, viruses that infect human cells and viruses present as transients in food."**

"Centuries of medical research have linked infection by specific viruses with characteristic disease states; however, **the nature and importance of whole viral populations were mostly not appreciated until the development of advanced DNA sequencing methods that could report the structures of whole communities.** Untargeted sequencing of purified viral samples, termed 'shotgun sequencing', was first applied to environmental viral populations in 2002 by Breitbart et al. Viral particles were prepared from seawater, and then shotgun metagenomic sequencing was employed to characterize the viral communities present[8 < https://www.nature.com/articles/s41579-021-00536-5#ref-CR8>], revealing highly abundant and diverse phage genomes, **as well as a large proportion of viral 'dark matter' (that is, sequences that looked like nothing in available databases)."**

“Most constituents of the human virome are **inferred to be phages.** This is an inference because, in most cases, **the majority of sequences uncovered in a virome metagenomic sequencing experiment do not align with any information present in existing databases (Box 1 < https://www.nature.com/articles/s41579-021-00536-5#Sec3>), so it is unknown whether they are phages or some other virus types.”**

“However, within a healthy adult**, the virome is usually relatively stable over time,** paralleling stability in the cellular microbiome. For example, one study found that ~**80% of viral contigs < https://www.nature.com/articles/s41579-021-00536-5#Glos2> present persisted over a span of 2.5 years** in the gut of one individual[6 < https://www.nature.com/articles/s41579-021-00536-5#ref-CR6>]. Another recent study tracked the gut virome of 10 individuals and found that **>90% of recognizable viral contigs persisted in each individual over 1 year**[39 < https://www.nature.com/articles/s41579-021-00536-5#ref-CR39>]**.** Studies on the oral virome **revealed similar stability**[40 < https://www.nature.com/articles/s41579-021-00536-5#ref-CR40> ,41 < https://www.nature.com/articles/s41579-021-00536-5#ref-CR41>]**.”**

https://www.nature.com/articles/s41579-021-00536-5 < https://www.nature.com/articles/s41579-021-00536-5>



These “viruses” that make up our virome are not considered pathogenic, are said to be integrated elements within our genome, and are believed to interact with the body in complex and **MEANINGFUL** ways. It has been estimated that while our microbiome is made up of 38 trillion bacteria, our “virome” contains 380 trillion “viruses.” Essentially, we are walking, talking “viruses.” With that many of these “microscopic parasites” living inside of us, you would think we would be in a perpetual state of sickness. However, that is obviously not the case. Still, as with

most of science it seems, much is unknown about the virome as it remains a vastly understudied area. Study of the "virome" lags far behind bacteria as there is a lack of standardized technology necessary to decipher what it all means. Still, this hasn't stopped scientists from assuming that these strings of genetic material show that we have "viruses" in every part of our body:

Meet the trillions of viruses that make up your virome

'If you think you don't have viruses, **think again.**

It may be hard to fathom, but the human body is occupied by large collections of microorganisms, commonly referred to as our microbiome, that have evolved with us since the early days of man. Scientists have only recently begun to quantify the microbiome, and discovered it is inhabited by at least **38 trillion bacteria < http://doi.org/10.1371/journal.pbio.1002533>** . **More intriguing, perhaps, is that bacteria are not the most abundant microbes that live in and on our bodies. That award goes to viruses.**

It has been estimated that there are over 380 trillion viruses < http://doi.org/10.1016/j.coviro.2011.12.004> inhabiting us, a community collectively known as the human virome. But these viruses are not the dangerous ones you commonly hear about, like those that cause the flu or the common cold, or more sinister infections like Ebola or dengue. Many of these viruses infect the bacteria that live inside you and are known as bacteriophages, or phages for short. **The human body is a breeding ground for phages, and despite their abundance, we have very little insight into what all they or any of the other viruses in the body are doing.**

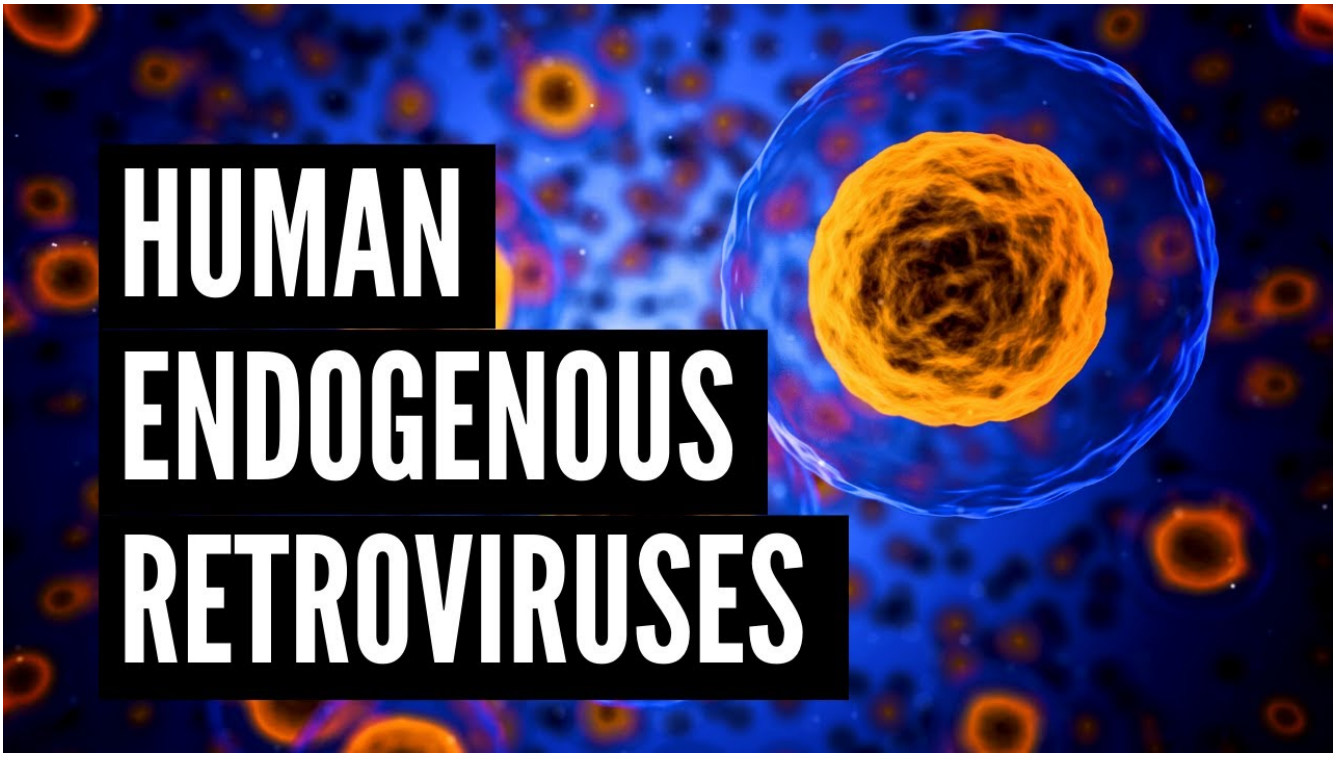
I am a physician-scientist studying the human microbiome by focusing on viruses, because I believe that harnessing the power of bacteria's ultimate natural predators will teach us how to prevent and combat bacterial infections. **One might rightly assume that if viruses are the most abundant microbes in the body, they would**

be the target of the majority of human microbiome studies. But that assumption would be horribly wrong. The study of the human virome lags so far behind the study of bacteria that we are only just now uncovering some of their most basic features. This lag is due to it having taken scientists much longer to recognize the presence of a human virome, **and a lack of standardized and sophisticated tools to decipher what's actually in your virome."**

"Viruses may inhabit all surfaces both inside and outside of the body. Everywhere researchers have looked in the human body, viruses have been found. Viruses in the blood? Check. Viruses on the skin? Check. Viruses in the lungs? Check. Viruses in the urine? Check. And so on. **To put it simply, when it comes to where viruses live in the human body, figuring out where they don't live is a far better question than asking where they do < http://doi.org/10.1016/j.jmb.2014.07.002> ."**

"So the race is on to find those viruses in our viromes **that have already figured out how to protect us from the bad guys**, while leaving the good bacteria intact."

Many people believe that these “viruses” must come from the outside the body and invade us, integrating into our cells and DNA. However, seeing as the RNA making up the “virome” is found within humans, the logical conclusion would be that this genetic material must come from us and be human in nature. Take, for instance, **ENDOGENOUS** (internal origin) “retroviruses.” These are “viruses” that are said to be a part of our genetic makeup. While a story was concocted stating that they must be remnants of ancient “viruses” that ended up mixed into our genetic code, the case could easily be made that these were never “viruses” and that the assumed “viral” sequences were in fact human all along:



"About 8% of our genome is composed of sequences with viral origin, namely human Endogenous Retroviruses (HERVs). HERVs are relics of ancient infections that affected the primates' germ line along the last 100 million of years, **and became stable elements at the interface between self and foreign DNA."**

https://www.frontiersin.org/articles/10.3389/fimmu.2018.02039/full < https://www.frontiersin.org/articles/10.3389/fimmu.2018.02039/full>

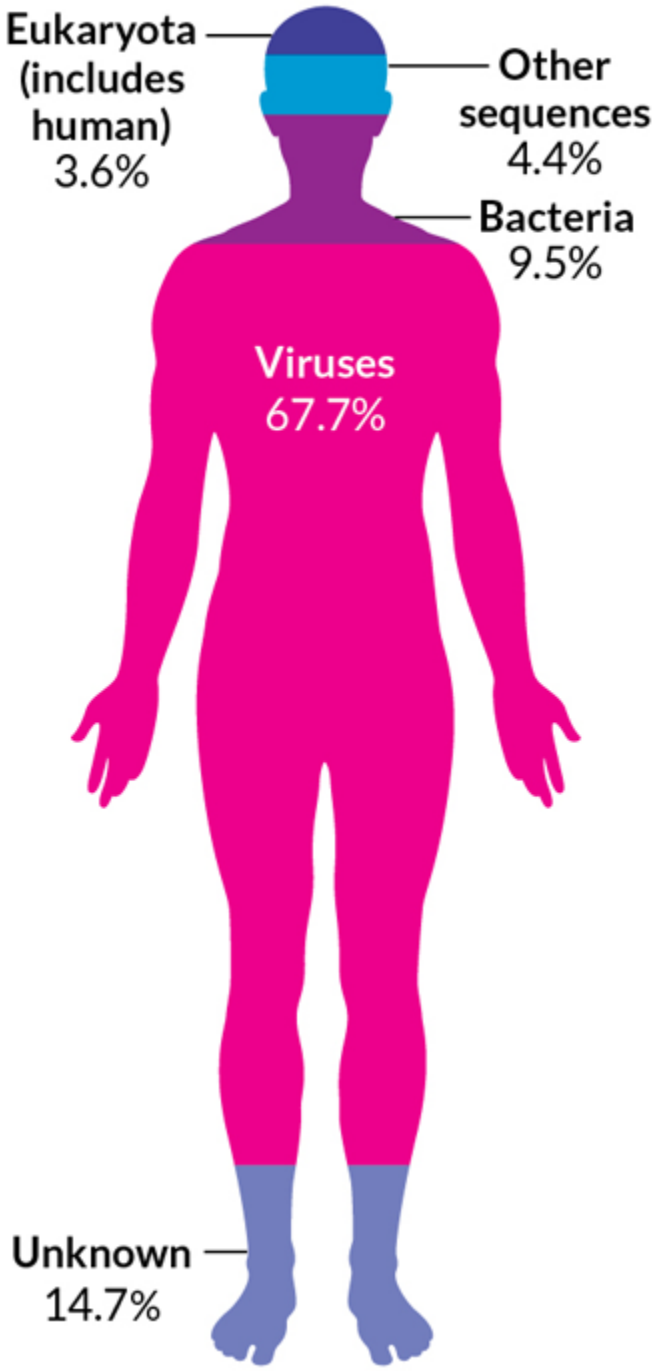
"The viral component of the human microbiome is referred to as the "human virome." The human virome (also referred to as the "viral metagenome") is the collection of all viruses that are found in or on humans, including viruses causing acute, persistent, or latent infection, **and viruses integrated into the human genome, such as endogenous retroviruses."**

https://www.ncbi.nlm.nih.gov/labs/pmc/articles/PMC3701101/ < https://www.ncbi.nlm.nih.gov/labs/pmc/articles/PMC3701101/>

"Although there are exceptions, **the vast majority of ERVs (particularly the ancient**

ERVs) is not closely related to known exogenous retroviruses, is no longer capable of expressing virus, and has no other associated biological or phenotypic properties to facilitate classification.”

https://www.sciencedirect.com/topics/medicine-and-dentistry/endogenous-retrovirus < https://www.sciencedirect.com/topics/medicine-and-dentistry/endogenous-retrovirus>



As can be seen by the above three sources, endogenous “retroviruses” are a part of us and make up about 8% of our genome. They are said not to be related to exogenous “retroviruses” and can not express “virus.” These sequences *are of human origin.* They have been labelled as “viral” when that obviously is not the case. How many other sequences claimed to be “virus” are in fact nothing but

human genetic material incorrectly labelled as such?

It is becoming clearer to scientists that "viruses" are an integral part of human biology. It is now theorized that many of these "viruses" are beneficial to us and actually promote health, which doesn't really sound like the classical definition of a "virus," now does it? In fact, "viruses" thought pathogenic and seen as causes of the common cold have been found in completely healthy children. Thus, it is now being considered that "viruses," or at least the strings of non-classifiable RNA claimed to be them, are in fact a part of us rather than something that lives in or on us:

The vast virome

"The most abundant inhabitants of what many researchers are calling "the human ecosystem" are the viruses. So Pérez-Brocal reasoned they were worth a closer look.

Viruses are deceptively simple organisms consisting of genetic material packed in a protein shell. They are tiny and can't replicate on their own, relying on human or other cells to reproduce.

And yet, scientists estimate that 10 quintillion virus particles populate the planet. That's a one followed by 31 zeros. They outnumber bacteria 10-to-1 in most ecosystems. **And they're ubiquitous in and on humans.**

Pérez-Brocal and others are learning that viruses, once seen only as foreign invaders that make people sick, are an integral part of human biology. Some cause major diseases, including influenza, AIDS and some cancers. **Others, conversely, may promote health. Some may even help us gauge how well the human immune system works."**

"We know a lot about the bacteria that inhabit humans," says David Pride, an infectious disease doctor at the University of California, San Diego. **In comparison,**

"we know absolutely nothing about the viruses."

"Not that scientists haven't been interested in viruses. **Until recently there was just no good way to identify them, an important first step toward understanding the biology of health and disease. As a consequence, virome research is in its infancy."**

"Virus hunters aren't so lucky. There is no analogous virus-identification tag. Instead, to look for viruses, **researchers must sequence hundreds of thousands of bits of DNA from a sample** — skin swabs, saliva, feces or mucus, for example. **Scientists have gotten really good at generating these DNA sequences; the trick is figuring out what they are.**

Some of these DNA bits come from human cells, some from bacteria and other microbes that occupy the body, such as archaea and fungi. Some bits may come from viruses, but it is hard to tell for sure, says Pérez-Brocal, because scientists have a limited set of characterized viruses to use as a guide for spotting new ones."

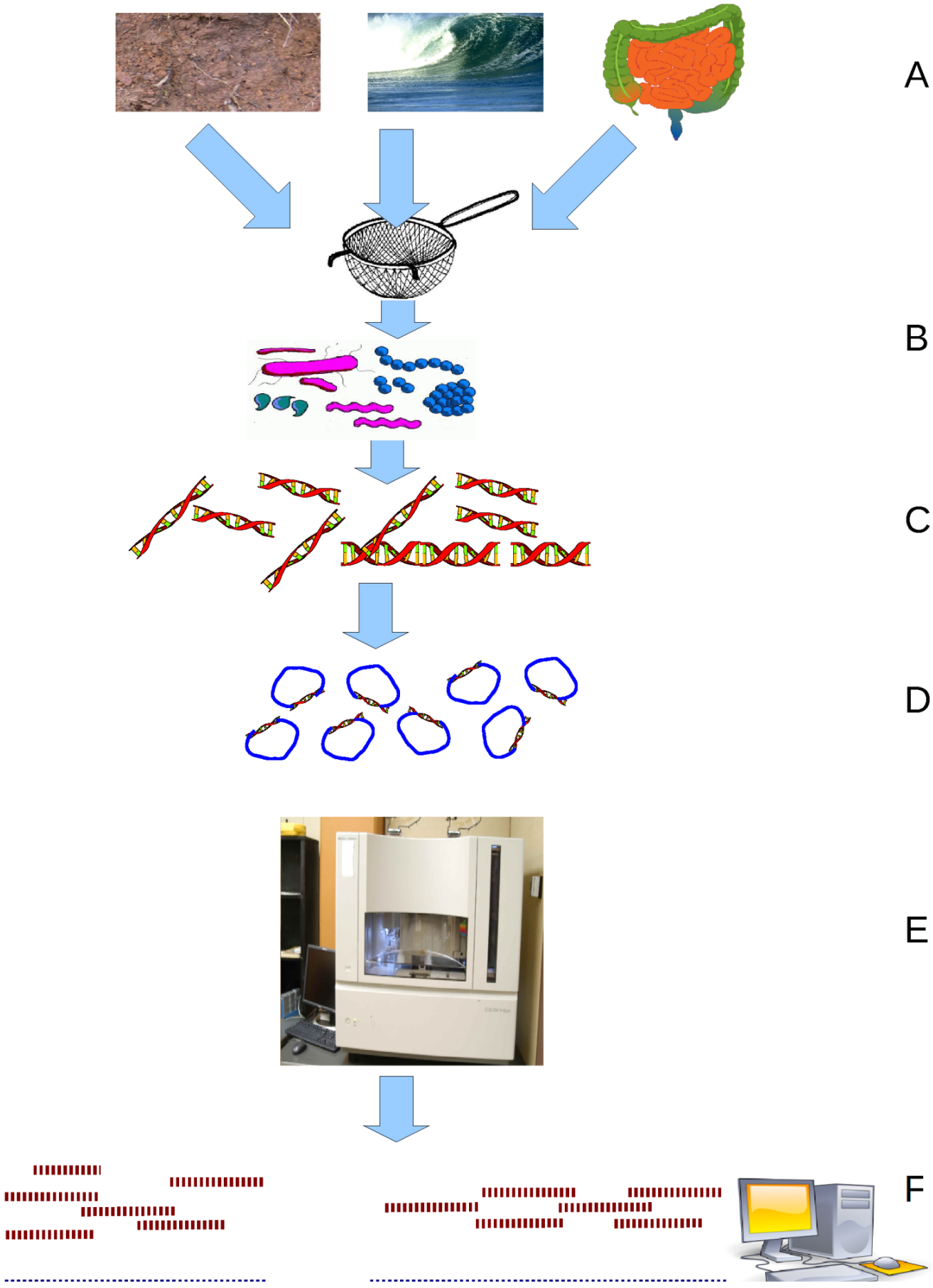
"Healthy subjects are just loaded with viruses," Wylie says. Even viruses known to cause diseases such as the common cold **were found in healthy kids.** That makes it difficult to determine **whether a particular virus is really making someone sick."**

"To figure out which viruses are friends, foes or neutral passengers on the human body, scientists first need to identify them. **Researchers still aren't very good at recognizing new viruses, says Brian Jones, a molecular biologist at the University of Brighton in England.** Hence the large pool of unknown samples in Pérez-Brocal's and other researchers' virome studies. **But even if scientists improve their identification skills, it may take a long time to figure out what the viruses are doing in the body."**

"Based on what researchers have learned so far about the virome, Jones is

convinced that viruses and other microbes “should be viewed as a part of us rather than something that lives in or on us.” They are part of the puzzle, the intricate ecosystem composed of human and microbial cells, all pushing and pulling at one another and subject to local conditions, such as diet and environment.”

https://www.google.com/amp/s/www.sciencenews.org/article/vast-virome/amp < https://www.google.com/amp/s/www.sciencenews.org/article/vast-virome/amp>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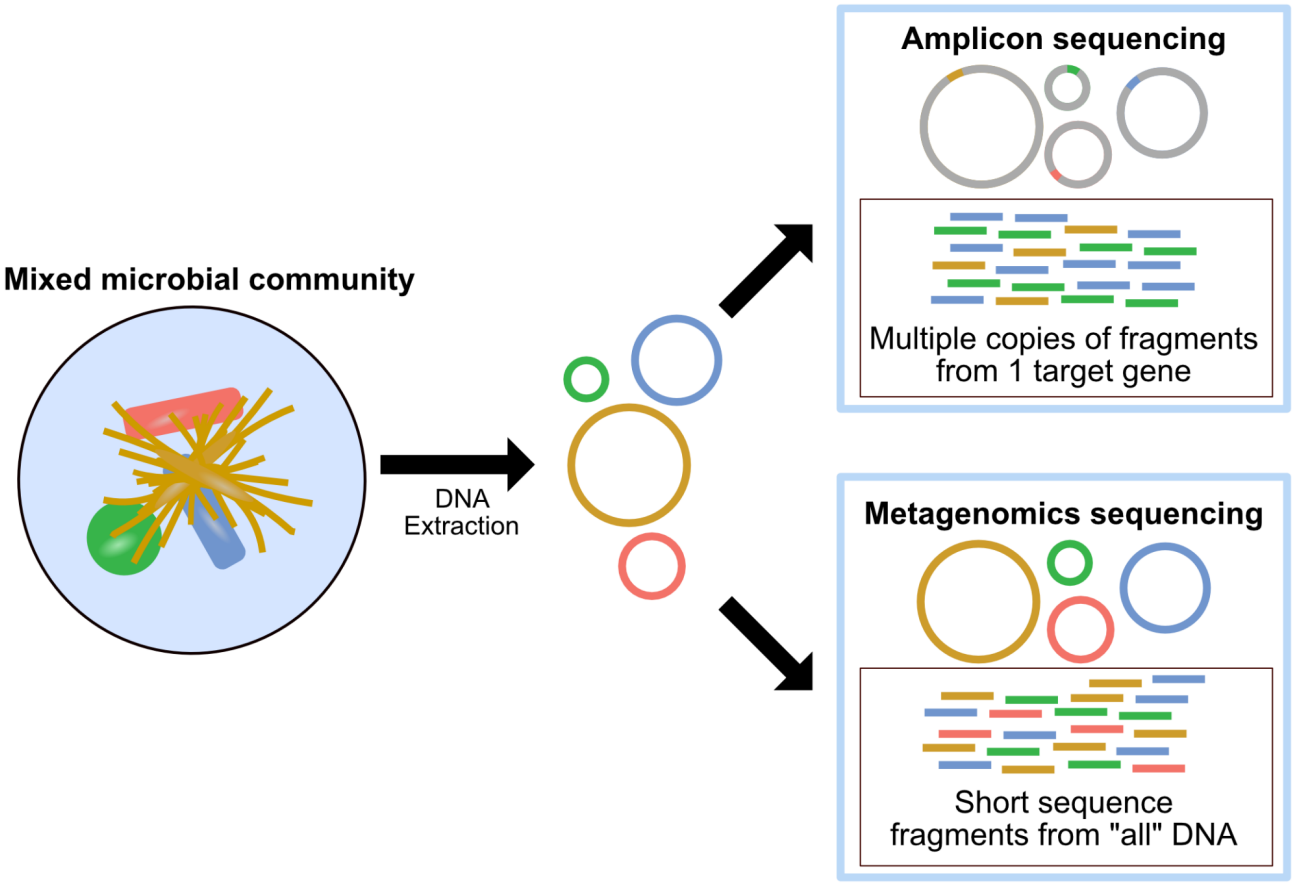
The “magic” of metagenomics.

Hopefully, after reading the above sources, it is now more clear what all the human “virome” entails. You should be able to see that, according to the latest scientific evidence, not only are we surrounded by “viruses” everywhere, we are almost more “virus” than human based on the latest sequencing technology. It’s important, however, to keep in mind that what they are calling “viruses” in the “virome” are nothing more than “repetitive strings of genetic letters” stored in a computer database. These are not particles that have been purified and isolated directly from a sample and proven pathogenic in a natural way. It is a collection of A,C,T,G’s taken from a mixed population of organisms within a sample. The particles assumed to be “viruses” are never seen nor characterized. Every organism, whether bacterial, fungal, “virus,” or whatever else could potentially be contained within the sample are broken down into free-floating RNA/DNA and sequenced by computer algorithms. This is done through a process known as metagenomics:

“Metagenomics” is the two words “meta” and “genomics”. **So genomics is obtaining the DNA sequence, but meta implies that we’re doing it of many organisms together. And metagenomics is usually used when we are studying microbial communities where we can’t separate one microbe from another.** Like there may be two bacteria that grow together, and so when you take the DNA sequence, you’re getting the DNA sequence of two bacteria together. Now, as an example of this, you can imagine that I could go in and take the DNA sequence of a person who lives in New York City. **But if I were to come in and take the DNA from everyone who lives in New York City and sequence it together, that would be the equivalent of what we’re doing when were sequencing the DNA of all of the bacteria that live in one place on your skin or your intestine together. So we’re not just looking at one organism, we’re looking at the DNA sequence of all of the organisms together.** Because we could imagine sequencing the DNA of an individual in New York, but imagine if our technology was limited and we couldn’t

separate these people in New York. **If we need to take the DNA sequence of every person in New York together, and then later we try to figure out which DNA belonged to which person, that’s often what we are doing when we’re studying bacterial and fungal communities together.”**

https://www.genome.gov/genetics-glossary/Metagenomics < https://www.genome.gov/genetics-glossary/Metagenomics>



Nothing but “random genetic strings” in a computer database.

This process of breaking down and sequencing all organisms in a sample is not without its flaws. There are challenges based on the limitations of the technologies. It is admitted that human tissue samples as well as lung mucus, **such as that used for the sequencing of “SARS-COV-2,” < https://viroliegy.com/2021/09/06/creating-the-sars-cov-2-genome/>** make it difficult to reliably obtain and interpret genomic data. It is also admitted that the use of metagenomics actually

fails **Koch’s Postulates, < https://viroliegy.com/category/kochs-postulates/>** the very criteria used to determine a pathogen exists, as there is no direct host information available. Thus, obtaining the potential etilogical agent from a diseased organism and then growing it in pure culture can not be properly fulfilled. It has been attempted to modify the Postulates for the genomic era to allow that the sequence only needs to be found more regularly in a diseased host rather than a healthy one. However, these sequences are regularly found in healthy individuals, as seen by the massive amounts of healthy “asymptomatic” people testing positive for “SARS-COV-2” and other diseases. Metagenomes are also primarily assembled and created using short reads which can often lead to erroneous, inaccurate, and incomplete genomes:

Metagenomics in Virology

“Metagenomics has quickly become a major tool for exploring viral diversity, yet several challenges need to be addressed in order to fully leverage the potential of these methods. **First, metagenomes built from limited input material are still difficult to reliably obtain and interpret, and do not yet provide a comprehensive and quantitative view of the viral community present in the sample. This includes environments with low biomass such as some human tissues, hydrothermal vents, ice cores, or ancient samples, but also samples with a thick substrate or matrix to which cells and virus particles tend to adhere such as human lung mucus or coral samples.** Improvement in the recovery of cells and virions from this type of substrates and in the generation of quantitative libraries from sub-nanogram input will help better survey these viral communities.

The second major challenge lies in the absence of direct host information for genomes assembled from metagenomes. In a clinical context, this means that one of Koch’s postulates, which requires that the candidate etiological agent be isolated from a diseased organism and grown in pure culture, cannot be fulfilled. Already, several smacoviruses which had been detected in human

samples metagenomes and suspected to represent new human viral pathogens have been found to likely infect prokaryotic cells from the human microbiome instead. In a similar way, evidence is emerging that picobirnaviruses, which are believed to be eukaryotic viruses, might actually infect bacterial cells. **These examples should thus serve as a cautionary tale when trying to detect entirely new viral pathogens from mixed samples containing both human and microbial cells. A modified Koch's postulate for the metagenomic era has been proposed in which potential new pathogens must first be present and more abundant in the diseased subject compared to matched control.** Then, experiments using either a sample from a disease subject **or an artificial virus obtained through DNA synthesis and expression in cell cultures** must be performed to demonstrate that this agent induces disease in another healthy subject. While not trivial, these additional experiments based on metagenomic results could still lead to the identification of viral pathogens much more quickly than classic culture techniques.

In an ecological context, associating uncultivated viruses to their host is also critical to understand their impact on microbial communities and to meaningfully integrate viruses into ecosystem models. **Because viral ecology studies typically include hundreds to thousands of viruses of interest, these host associations are typically derived from in silico approaches based on various types of genome sequence comparison.** While methods for in vitro confirmation of these metagenome-derived virus-host pairs are currently being developed, **they will need to improve both in terms of scale and resolution to provide meaningful host association for the vast diversity of uncultivated viruses.**

Among the expected technological improvements, two stand out as likely to benefit the field of viral metagenomics in the near future. First, long-read sequencing technologies are progressively amenable to the sequencing of environmental viral communities. **Pragmatically, this means that instead of having to assemble virus genomes from short reads, a process which can yield potentially erroneous and/or incomplete genome sequences, a complete viral**

genome could be sequenced as a single read."

https://www.ncbi.nlm.nih.gov/labs/pmc/articles/PMC7157462/ <
https://www.ncbi.nlm.nih.gov/labs/pmc/articles/PMC7157462/>

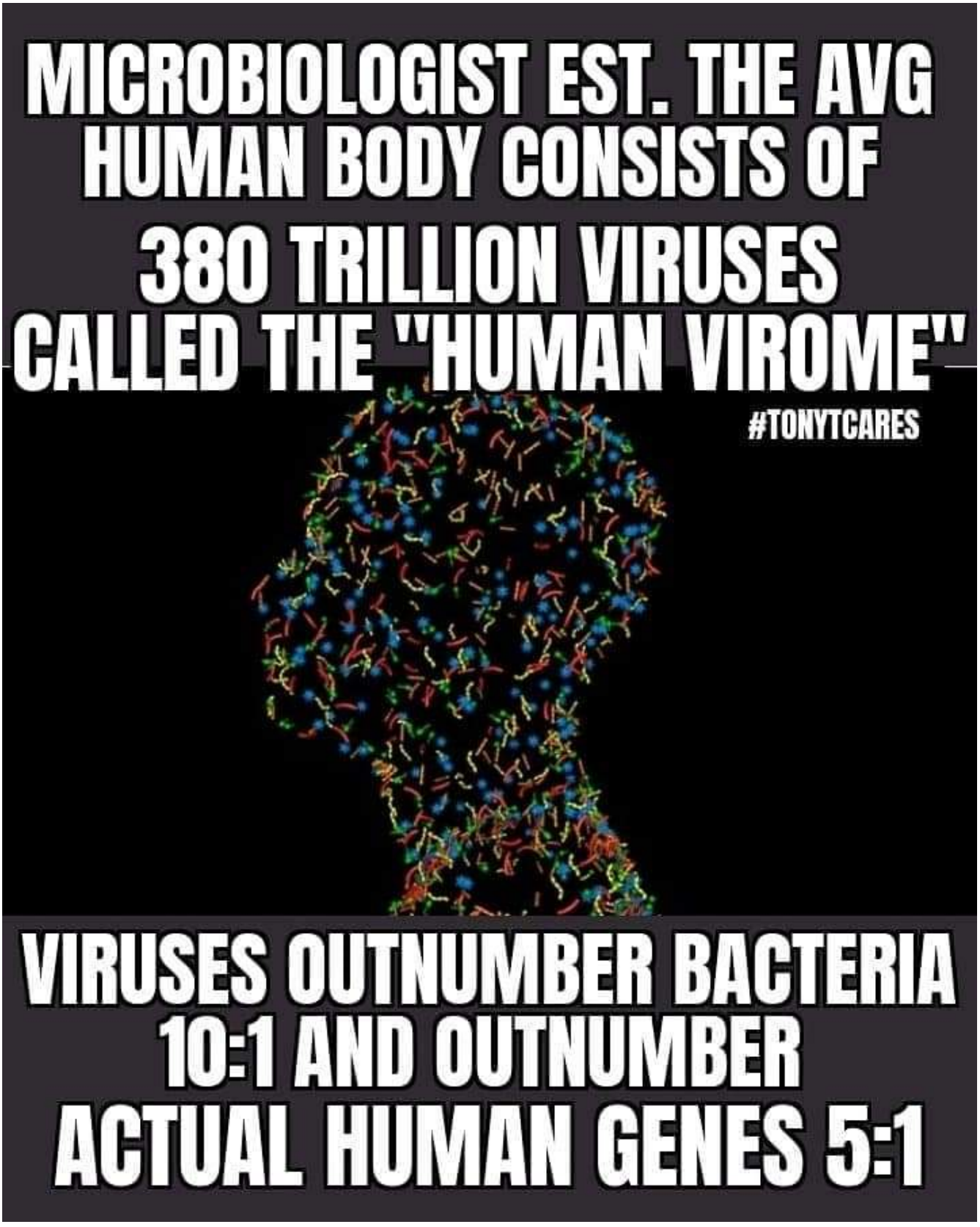
In Summary:

- It is said that **eight percent** of our DNA consists of remnants of ancient "viruses," and **another 40 percent** is made up of repetitive strings of genetic letters that is also thought to **have a "viral" origin**
- Many host districts of the human body and its mucous membranes are heavily 'colonized' **by "viruses" that are not associated with any disease**
- This has led to the concept of the "virome," **which can be considered as the set of all "viruses,"** eukaryotic and prokaryotic, present in the human body
- The "virome" includes "viruses" that infect host cells, "viruses" that infect the majority of other types of microorganisms harboured by the body, **and "virus-related" genetic elements in our chromosomes** (*in other words, these "viruses" are a part of our genetic makeup*)
- Due to the existence of commensal "viruses," it is stated that we should probably **redefine chronic "viral" infections** and **focus our attention on the host** rather than on infectious agents to dissect disease determinants
- "Viruses" **are believed to be** the most abundant and diverse biological entities on our planet **with an estimated 10^31 particles on Earth**
- The human "virome" is similarly vast and complex, **consisting of approximately 10^13 particles per human individual, with great heterogeneity** (*i.e. diversity*)
- The human "virome" comprises:
    1. Bacteriophages (phages) that infect bacteria
    2. "Viruses" that infect other cellular microorganisms such as archaea
    3. "Viruses" that infect human cells
    4. "Viruses" present as transients in food
- *In other words, the RNA claimed to be "viruses" comes from many sources*
- The nature and importance of whole "viral" populations were mostly not appreciated **until the development of advanced DNA sequencing methods** that could report the structures of whole communities
- Early metagenomic sequencing in 2002 found a large proportion of "viral dark matter" which is **sequences that looked like nothing in available databases**
- Most constituents of the human "virome" are **inferred** to be phages

- This is an inference because, in most cases, **the majority of sequences uncovered in a "virome" metagenomic sequencing experiment do not align with any information present in existing databases** so it is unknown whether they are phages or some other "virus" types
- Within a healthy adult, the "virome" is **usually relatively stable** over time
- One study found that **~80% of "viral" contigs present persisted over a span of 2.5 years** in the gut of one individual
- Another recent study tracked the gut "virome" of 10 individuals and found that >**90% of recognizable "viral" contigs persisted in each individual over 1 year**
- While it is estimated that **38 trillion bacteria** reside inside of us, they are not the most abundant microbes that live in and on our bodies **as that award goes to "viruses"**
- It's estimated that **there are over 380 trillion "viruses" inhabiting us,** a community collectively known as the human "virome"
- These "viruses" **are not the dangerous ones** you commonly hear about
- The human body is a breeding ground for phages, and despite their abundance, **we have very little insight into what all they or any of the other "viruses" in the body are doing**
- One might rightly assume that if "viruses' are the most abundant microbes in the body, they would be the target of the majority of human microbiome studies, however, **that assumption would be horribly wrong**
- The study of the human "virome" lags so far behind the study of bacteria that **we are only just now uncovering some of their most basic features**
- There is a **lack of standardized and sophisticated tools** to decipher what's actually in your "virome"
- To put it simply, when it comes to where "viruses" live in the human body, **figuring out where they don't live is a far better question than asking where they do < http://doi.org/10.1016/j.jmb.2014.07.002>**
- *Keep in mind, when they claim that 'viruses" are found everywhere within the human body, what they are referring to is "viral" RNA, not purified/isolated "viruses"*
- The race is on to find those "viruses" in our "viromes " **that have already figured out how to protect us from the bad guys**, while leaving the good bacteria intact
- **About 8% of our genome** is composed of sequences with "viral" origin, namely human Endogenous "Retroviruses" (HERVs) and they interface **between self and foreign DNA**
- Endogenous "retroviruses" are **integrated into the human genome**

- The vast majority of ERVs (particularly the ancient ERVs) **are not closely related to known exogenous "retroviruses" and are no longer capable of expressing "virus"**
- Pérez-Brocal and others are learning that "viruses," once seen only as foreign invaders that make people sick, **are an integral part of human biology**
- It is said some "viruses" **may promote health** while others may even help us gauge how well the human "immune system" works
- According to David Pride**,** an infectious disease Dr., **"we know absolutely nothing about the viruses"** that inhabit us
- Until recently there **was just no good way to identify "viruses,"** an important first step toward understanding the biology of health and disease
- As a consequence, **"virome" research is in its infancy**
- Researchers **must sequence hundreds of thousands of bits of DNA from a sampl**e — skin swabs, saliva, feces or mucus, for example, to find "virus" RNA/DNA
- Scientists have gotten really good at generating these DNA sequences; **the trick is figuring out what they are**
- Some of these DNA bits come from human cells, some from bacteria and other microbes that occupy the body, such as archaea and fungi, and **some bits may come from "viruses," but it is hard to tell for sure,** says Pérez-Brocal, because scientists **have a limited set of characterized "viruses" to use as a guide for spotting new ones**
- "Healthy subjects **are just loaded with viruses,"** Wylie says
- Even "viruses" known to cause diseases such as the common cold **were found in healthy kids**
- That makes it difficult to determine **whether a particular "virus" is really making someone sick**
- **Researchers still aren't very good at recognizing new "viruses,"** says Brian Jones, a molecular biologist at the University of Brighton in England
- But even if scientists improve their identification skills, **it may take a long time to figure out what the "viruses" are doing in the body**
- Based on what researchers have learned so far about the virome, Jones **is convinced that "viruses" and other microbes "should be viewed as a part of us rather than something that lives in or on us"**
- The process used to study the "virome" is known as **metagenomics**
- Genomics is obtaining the DNA sequence, while meta implies that the sequencing **is of many organisms together**
- Metagenomics is usually used when studying microbial communities **where one microbe can't be separated from another**

- They are not just looking at one organism but rather at **the DNA sequence of all of the organisms together**
- “If we need to take the DNA sequence of every person in New York together, **and then later we try to figure out which DNA belonged to which person,** that’s often what we are doing when we’re studying bacterial and fungal communities together.” – Julie A. Segre, Ph.D.
- Metagenomes built from limited input material **are still difficult to reliably obtain and interpret,** and do not yet provide a comprehensive and quantitative view of the “viral” community present in the sample
- This includes environments with low biomass **such as some human tissues,** hydrothermal vents, ice cores, or ancient samples, but also samples with a thick substrate or matrix to which cells and virus “particles” tend to adhere **such as human lung mucus** or coral samples
- The second major challenge lies in the **absence of direct host information for genomes** assembled from metagenomes
- In a clinical context, this means that **one of Koch’s postulates,** which requires that the candidate etiological agent be isolated from a diseased organism and grown in pure culture, **cannot be fulfilled**
- A modified Koch’s postulate for the metagenomic era has been proposed in which potential new pathogens **must first be present and more abundant in the diseased subject compared to matched control**
- Because “viral” ecology studies typically include hundreds to thousands of “viruses” of interest, these host associations **are typically derived from in silico** (*in a computer*) **approaches based on various types of genome sequence comparison**
- While methods for **in vitro** (*i.e. outside the living body and in an artificial environment*) confirmation of these metagenome-derived “virus-host” pairs **are currently being developed,** they will need to improve both in terms of scale and resolution to provide meaningful host association **for the vast diversity of uncultivated “viruses”**
- Currently, metagenomics assembles “virus” genomes from short reads, **a process which can yield potentially erroneous and/or incomplete genome sequences**



If we are to take the latest genomic science at face value, then we are as much

“virus” as we are human. It is estated that we have 380 trillion “viruses” within us and integrated into out genome. It is said that at least 48% of our genome is “viral” and that 8% of this is endogenous, meaning it comes from humans. We have within us what is now referred to as the human “virome.”

However, it is also admitted that what are claimed to be “viral” sequences are only thought to be so as the data is vastly understudied. The data is derived from metagenomics, which is the mass sequencing of multiple unknown and unrelated microorganisms within a sample using computer algorithms. No actual “viral” particles are ever found and characterized. The human “virome” is nothing but a giant collection of sequencing data assumed to be “viral” in nature. Much of the data comes from the early 2000’s when the sequencing technology was even more hampered by limitations than it is said to be now. However, even today, the technology does not exist to completely separate and characterize these genomes. They are assembled and put together using short reads which can lead to inaccurate and unreliable genomes (cough…"SARS-COV-2''…cough).

With so much of the human body composed of what virologists claim is of “viral” origin, it is clear that the idea of the exogenous pathogenic “virus” is the unproven exception to the rule and not the norm. It is also clear that they are sequencing normal human genetic material and assuming it is “viral” based on nothing but computer-generated data. There are no purified/isolated particles. There is no proof of pathogeniticity. These “scientists” have taken massive amounts of data and created a fictional narrative around it. They are trying to make us believe that there is an ocean of undiscovered “viral” genetic material out there. In this way, they can pull out any random sequence at any time from amongst this “viral dark matter” and claim a new pathogenic “virus” exists. In reality, all that they are doing is pulling out normal human fragments from our own “genome” and selling back to us the new boogeyman created from our own genetic material.