Emergence and Immergence of Viruses

Abstract

Viruses have an extremely long history and they are extremely widely spread in the planet. They are the simplest biological organisms which consist of genetic information and mechanisms to transfer this information into host for multiplication. It is therefore a natural way to comprehend a virus as a piece of information. Viruses are highly dependent on their hosts and utilize their life cycles. In viral life cycle, it is essential that new susceptible individuals need to become infectious. For this purpose, viruses have evolved to utilize different routes of transmission and survival mechanisms. In this article the mechanisms for emergence and immergence of the most significant virus types are analyzed according to Boolean logic analysis in order to provide new insights for how we perceive emergence.

Keywords

Epidemiology, complex systems, emergence and immergence.

Mechanisms for Emergence and Immergence

We believe that making sense of the mechanisms that viruses use to transfer information and to utilize different routes of transmission can serve to create new insights and analogies for understanding, and thereafter influencing, the processes of relating, interacting and evolving of individuals and organizations in higher social ecosystems.

Viruses are certainly a fine example of how the meaning of an individual agent[1] is created within relationships with its surroundings; viruses depend so heavily on their hosts that their metabolic activity and their ability to respond external stimuli are not possible without these relationships. Furthermore, viruses are a beautiful example of co-evolution, because they literally cannot reproduce themselves in isolation. Because of their multiple routes of transmission and survival mechanisms, they provide multiple views for studying connectivity and interdependence.

Robert Axelrod and Michael Cohen (2000) state that social systems exhibit patterns those are analogous to physical, biological and computational systems. This is perhaps the main reason for pursuing complexity research, and the reason for pursuing this study. There is perhaps hope that it can be of value for designing actions; give guidance to what kinds of situations may be resistant to interventions, where and when interventions may be likely to have positive outcomes.

[1] An agent processes and assimilates information, and communicates with other information processing agents based on finite, local information and relationships with a limited number of other agents.

What makes a system a system is the connections and interactions among the individual components, and the effect that these linkages have on the behavior of the components. Without these linkages we would have just a collection of components. The connections and interactions can be so strong that they influence the probabilities of later events.[2]

The target of this study is thus to assist in a difficult task of anticipation of futures. Many species, not only human species, try to anticipate success strategies of futures, because their survival depends on them. The focus of understanding the success strategies has been on understanding emergence, how new properties appear in the course of organizational development. In this article, the focus is also on immergence, how old properties disappear in the course of evolution.

In science, most theoretical breakthroughs occur when a fundamental mechanism that causes a phenomenon is discovered. For Clayton M. Christensen et al. (2004) a powerful anticipative theory needs also a good circumstance-based categorization scheme, i.e. the sense-making and conclusions based on observations and studies of a phenomena must be appropriate. Getting the categories right is vital for developing a useful theory that allows us to understand why certain actions lead to certain outcomes and others fail.

For a social scientist, theory and model building are an exhausting experience, because no theory or model can correspond to its environment. Nevertheless, we should not stop trying, because there are immense margins of improvement in our understanding concerning the mechanisms of emergence and immergence. First, models can serve as guides in exploring prospective mechanisms and constraints. Second, we can look for conditions to ensure emergence and to avoid immergence. (C.f. Holland 1998). This is something that has been taken place in management science for a quite some time, new conditions – learning (Senge 1990), knowledge (Nonaka & Takeuchi 1995) and creativity (Florida 2002), only to state some of the latest – have been continuously presented to anticipate and control the critical phases in the process of emergence.

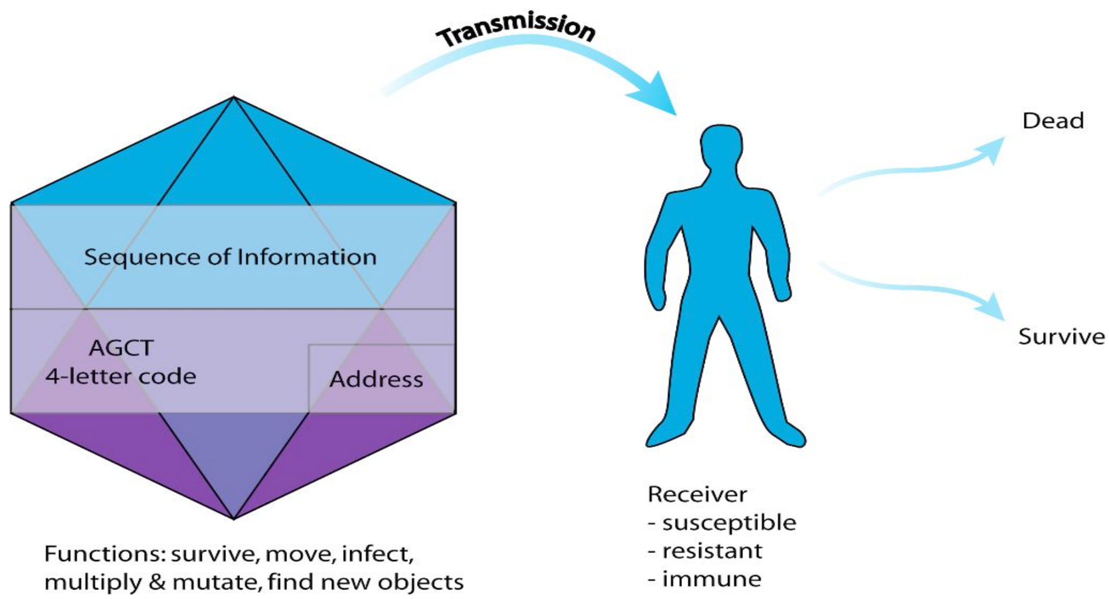
A common way of comprehending viruses is to see them as pieces of information. We take this thought one step further and comprehend information that they carry as cause and think action as informationally dependent and constrained behavior. As a consequence, independent agents are connected together by information in a way that they are no longer independent and separable from each others.

We could claim that in all human operations, whether we talk about networks of transportation, power transfer, knowledge transfer or cooperation between human beings, the dominant type of causality is not deliberate causality, but circular causality, where the role of connections and feedback loops is highlighted. We can relate the discussion about the properties of connections and feedback loops to emergence and immergence of systems and ask: How well and under which rules systems function, tolerate tosses and turns inside and from outside, grow and vanish? And search for improving our cognitive ability to observe outcomes, and infer the reasons for those outcomes.

[2] It is often pointed out that complex systems have emergent properties, e.g. consciousness arises from an interaction of single neurons that have no consciousness.

A Short Cut to the World of Viruses

Viruses consist of a genome containing information for production of next generations of similar particles. It is surrounded by a protein capsid that protects the genetic material and is essential in recognition of the host. Moreover, many viruses carry enzymes needed during their life cycle but absent from their host cells, although most of the essential functions and materials necessary for viral multiplication are of host origin. The information in the genomes of all organisms is written as a code utilizing four nucleotides, denoted letters A, C, G and T; and a three-letter code corresponds to one amino acid that are the building blocks of proteins responsible for main architecture and activities in the cells and in the body. The smallest genomes of human viruses consist of approximately 10 000 letters and a dozen genes (a sequence of information able to encode one protein molecule) whereas the largest viruses contain more than 100 000 letters and can code for more than 100 proteins. For comparison, the human genome contains $3x10^9$ letters and there are around 20 000 different proteins expressed in our cells.



Picture 1. World of viruses.

Multiplication of viruses can only take place inside living cells and outside the cells viruses are an inactive collection of macromolecules which do not have metabolic activity and do not respond to external stimuli. Because viruses do not have a machinery to move they have adapted to utilize a great variety of vehicles which allow short and long distant movement. Transfer from a continent to another can take place in infected individuals, some viruses are transmitted through vectors (e.g. birds, rodents, mosquitoes) which carry and spread the virus. In the body the viruses take advantage of the gastrointestinal route or blood stream to get into their targets. When viruses have come into contact with a potential host cell, they recognize it with a specific receptor on the cell surface which is further used in the entry of the virus particle into the cell using mechanisms borrowed from the host. This will be followed by the release of the viral genome, expression of the genes and production of a new generation of virus particles which will be able to infect new target cells and, subsequently, transmitted to new susceptible hosts.

During their evolution, viruses have adapted to the life style of their hosts using almost all the variations one can imagine for such a simple parasite. To illustrate the flow of viral genetic information to, in and from their hosts and course of the infections at the population level, we will use selected human pathogenic viruses as examples. By exploring this process and comparing it with the spread of ideas and information in the human population we will attempt to cast new light in the susceptibility, immunity, persistence as well as advantages and disadvantages shared between the systems.

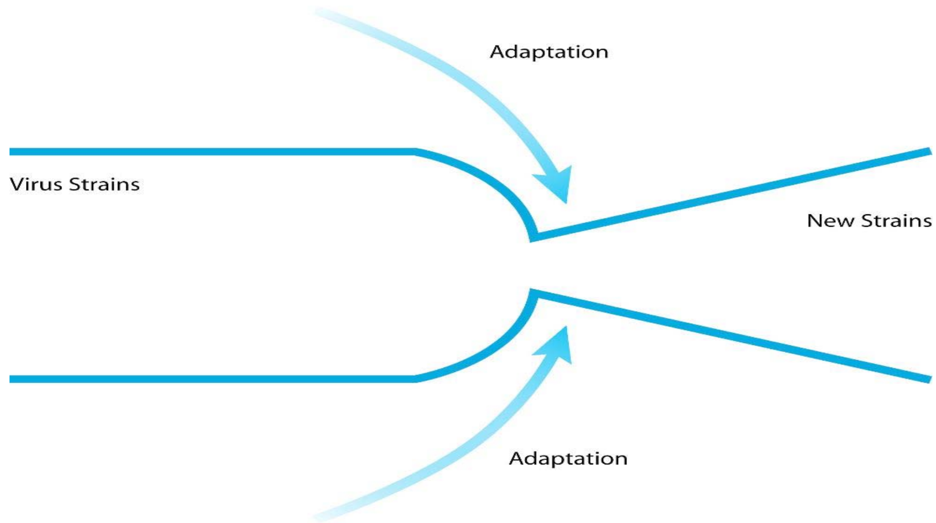
The first model will be acute viral infections. They are characterized by exposure of a susceptible individual (a person who has not experienced the infection earlier or does not for other reasons have sufficient immunity to resist the viral attack). As soon as the virus has started multiplication in the target tissues in the body (e.g. in the cells of the respiratory track) the process will lead to production of new generation of virus particles which need to find a new host soon to continue the circulation because the original host will either die or develop immunity which will eradicate the pathogen from the body. This is often followed by life-long immunity against this particular virus and therefore it may take several years before a new subpopulation, prone to the virus, is available in the community. Circulation and survival of viruses causing acute infections requires a sufficient population density and contacts between infected and susceptible individuals. Typical examples of acute viral infections are smallpox, polio, hepatitis A and influenza. As can be seen from these examples, immunization by vaccination can make the population resistant against the virus and stop its circulation. As it was seen in the case of smallpox, the whole disease can be eradicated, provided that there is no animal reservoir for the virus. For instance, this is much more difficult in the case of influenza which is found in a great variety of species.

In chronic infections there is a balance between virus replication and defense mechanisms of the body. An example of such disease is human immunodeficiency virus (HIV) infection. The virus infects leukocytes in the blood and viral genetic information is permanently incorporated into the genome of the host cells. Virus production is high (even 10^9 viral particles can be released daily to the blood stream) and the infection leads to death of a remarkable proportion of cells in leukocyte subpopulations essential in the immune response against other microbial pathogens. However, increased production of the cell population is able to maintain the balance for several years until the extensive destruction of the cells by the virus eventually leads to exhaustion of the immune system and further to the development of the acquired immune deficiency syndrome (AIDS), characterized by opportunistic infections. Currently, there are efficient antiviral strategies available that can keep virus production limited and the development of AIDS can thus be prevented. However, it seems that not even long antiviral treatment can eradicate HIV completely from the body indicating that the viral genetic information will remain a part of the host DNA in some cells and will be potentially able to initiate production of new infectious viruses.

The history of HIV infections illustrates well the association between the spread of viral genetic information and social changes. The virus was originally transmitted from monkeys to humans somewhere in Africa. First, the spread of the virus among humans was slow in the rural areas until urbanization caused extensive changes in the society that made rapid transmission further from infected individuals efficient. Subsequently, increased travel initiated the global circulation of HIV and it has caused more than 25 million deaths since AIDS was first recognized in 1981.

In latent infections the virus enters the body and either causes a symptomatic or subclinical illness. Herpesviruses typically cause latent infections where the viral genome is present in the infected cell but due to the lack or low level of expression of the viral genes the infection remains asymptomatic and the virus cannot be recognized by the immune system. Activation of viral multiplication can take place as a result of another disease (e.g. cancer) or just randomly. An example is the infection by herpes simplex virus (HSV) which may cause painful infection of the oral mucosa after the primary exposure but more often the individual does not even recognize the symptoms. During this event the viral genome enters trigeminal nerve ganglia and may remain silent for years or the rest of the life of the infected individual. However, external stress may activate viral multiplication which results in migration of HSV to the skin and causes typical vesicles, known as cold sores. Chickenpox is a common vesicular rash of children and after the recovery from the primary infection the causative agent, varicella-zoster virus (VZV), remains in the dorsal root ganglia of the spinal cord. Reactivation, known as herpes zoster or shingles, causes vesicular skin lesions in the restricted region associated with the nerves and is rather common in older age groups.

During the multiplication cycle, mutations are frequently generated in viral genomes. In addition to point mutations (errors during copying of the genetic material), larger genomic regions can be changed by recombination of different strains of the same virus or by exchange a genetic segments. A well-known example of the latter mechanism is appearance of new influenza viruses as a result of exchange of genetic material between viruses originating from different species. This can lead to development of new pathogens that have not been previously circulating in the human population and may become able to cause global epidemics due to the lack of immunity. (White et al. 2005, Hyypia 2009, Peltola et al. 2008, Ruohola et al. 2009).



Picture 2. The bottle-neck model.

The course of evolution is directed through bottle-necks. Especially RNA viruses are prone to copying errors during multiplication and a virus species is actually a quasi-species lineage of competing mutants. Viable mutants, surviving a bottle-neck of e.g. immunity or genetic make-up of the host, continue in circulation. In large, this is observed as disappearance of old and appearance of new strains of viruses.

The Method - Boolean Logic Analysis

The rationale for landscaping viruses is to improve the sense-making of their qualities and the conditions for their use as a source for analogies in organisational life. The concept of 'landscaping' is here used to define the endeavour of at once classifying viruses and representing their inter-relations in a *field* (Lewin 1996).

Landscaping, in the present understanding, creates a negotiation-space for the logic of *classification* (Ragin 1987) and the logic of *sense* (Deleuze 1969). On the one hand, viruses *vary* in respect to emergent and immergent properties. On the other hand, by virtue of being locatable on a *surface*, varieties of viruses become connectable in ways relevant to sense-making. (Aaltonen & Barth 2005).

Facilitating the classification of an item while, locating it in a topology represents a way of double-looping data. If properly framed, the act of classifying an item is transformed into an instance of double-looped learning. (Argyris & Schön 1978).

The choice of variables in Boolean models is of great significance, and partly predeterminates the possible insights of the model (C.f. Kauffman 1993, Harris & Sawhill & Wuensche & Kauffman 2002, Kauffman & Peterson & Samuelsson & Troien 2003). The focus of the study, the mechanisms for emergence and immergence, provides the vertical axis of our model, and the data, all the known viruses, the horizontal axis.

The variables defined above are placed in table 1. Though they are written in Boolean code, the values 1 and 0 should be understood as:

- 1 = the mechanism exits for the virus
- 0 = the mechanism lacks for the virus

The Data and the Analysis

The choice of the emergent and immergent mechanisms revealed the main variable types: animal-direct, animal-vector, respiratory, fecal-oral, congenital, blood, antigenic drift, antigenic shift, acute, latent, systemic, epidemic, anf endemic for emergence. And fatality, crippling, transient immunity, persistent immunity, transformation, vaccination, drugs and quarantine for immergence. Along the horizontal axis variables such as structural origin of the nucleotides, conventional Baltimore classification, number of human virus families and global incidence rates have been given. The use of Boolean logic analysis reveals simultaneously the appropriate properties of each virus, and the whole data.

Table 1. Boolean logic analysis of viruses.

Nucleic acid			DNA				RNA										
Baltimore classification			I		II	VII	III	IV					V				VI
No. of human virus families			5		1	1	1	7					7				1
Selected example viruses			Smallpox	Herpes simplex	Parvo B19	Hepatitis B	Rota	Rhino	Polio	Hepatitis A	West-Nile	Influenza	Measles	Avian influenza	Rabies	Ebola	HI
Emergence	Transmission route	Animal-direct	0	0	0	0	0	0	0	0	0	0	0	1	1	1	0
		Animal-vector	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0
		Human-human	1	1	1	1	1	1	1	1	0	1	1	0	0	1	1
		Respiratory	1	1	1	0	0	1	1	0	0	1	1	1	0	0	0
		Fecal-oral	0	0	0	0	1	0	1	1	0	0	0	0	0	0	0
		Congenital	0	1	1	1	0	0	0	0	0	0	0	0	0	0	1
		Genital	0	1	0	1	0	0	0	0	0	0	0	0	0	0	1
		Blood	0	0	0	1	0	0	0	0	1	0	0	0	0	1	1
	Spread	Contagious	1	0	1	0	1	1	1	1	0	1	1	0	0	0	0
		Variable types	0	0	0	0	1	1	0	0	0	1	0	1	0	0	1
		Prevalent	0	1	1	1	0	1	0	0	0	0	0	0	0	0	1
		Epidemic	1	0	0	0	1	1	1	1	1	1	1	0	0	0	0
		Endemic	1	0	0	1	1	0	1	1	1	0	0	1	1	1	1
	Infection	Acute	1	0	0	1	1	1	1	1	1	1	1	1	1	1	0
		Latent	0	1	0	0	0	0	0	0	0	0	0	0	0	0	1
		Chronic	0	0	1	1	0	0	0	0	0	0	0	0	0	0	1
		Systemic	1	1	1	1	0	0	1	1	1	0	1	1	1	1	1
Immergence																	
	Inherent	Fatal disease	1	0	0	0	0	0	0	0	0	0	0	1	1	1	1
		Transient immunity	0	0	0	0	1	1	0	0	0	1	0	1	0	0	0
		Persistent immunity	1	0	1	1	0	0	1	1	1	0	1	0	1	1	0
	Directed	Hygiene	0	0	0	0	0	0	1	1	0	0	0	1	0	1	0
		Vaccine	1	0	0	1	1	0	1	1	0	1	1	0	1	0	0
		Specific treatment	0	1	0	1	0	0	0	0	0	1	0	0	1	0	1

Global incidence (annual incidence rate/1000)	Eradicated	15	30	0.8	22	2000	Sporadic	0.2	0.1	75	3	Sporadic	1	Sporadic	1

The detailed analysis follows:

Emergence

Animal-direct	Human infection result in a direct contact with an infected animal (blood, bite, secretions).
Animal-vector	An insect vector transmit the infection from a natural animal host to a human.
Human-human	The infection is transmitted between humans.
Respiratory	Transmission of the infection through the respiratory tract by aerosols, droplets, saliva, or tears.
Fecal-oral	Transmission of the infection through ingestion of fecally contaminated material.
Congenital	Vertical transmission of the infection from mother to child before after birth.
Genital	Transmission of the infection via sexual interaction.
Blood	Transmission of the infection via blood through bites, needles, or transfusions.
Contagious	Most events between infected and susceptible non-infected individuals result in transmission of the infection. Less contagious viruses depend on repeated contacts (e.g. sexually transmitted viruses) or extraordinary circumstances (e.g. bite of a rapid dog).
Variable types	High variability of the virus, includes antigenic drift and shift. Antigenic drift relates to constant small mutations of the virus significantly improving the spread or maintenance of the infection. Antigenic shift relates to genomic recombination between two different types of the virus.
Prevalent	The infection is common in the population at all times.
Epidemic	The infection causes an epidemic in the susceptible population and disappears.
Endemic	The infection recurs or is commonly found among a geographically, genetically, or behaviorally limited population.
Acute	The infection is relatively brief and the virus is then eliminated.
Latent	The virus remains latently in the host.
Chronic	The virus often persists in the host for prolonged period.
Systemic	The infection spreads often from the local infection site to secondary organs.
Fatal disease	The infection frequently results in the death of an otherwise healthy host.

Immergence

Transient immunity	The infection induces an immune state that vanes by time.

Persistent immunity	The infection induces a life-long immunity, that is usually effective against re-infection or disease caused by the virus.
Hygiene	Spread of the virus can be largely limited by hygienic procedures.
Vaccination	Immunity inducing vaccine available.
Specific treatment	Infection limiting or preventing drugs or antisera available.

Discussion

Different viruses act upon varying properties and routes making them unique. Not a single virus scores at the Boolean logic mechanisms in the same manner. Although being diverse in nature, eradication of viruses has not been a prevalent property. This strongly suggests that their survival mechanisms have outstanding features. Viruses are entirely dependent on their complex hosts – the network they are connected to. Lacking of vital machineries viruses are unable to interact and intervene with outside world unless the vital connections are met. Upon intruding the host viruses orchestrate their survival, propagation and circulation. These simple vehicles utilize higher organizations human cells to raise their emergency and success without conductive managing. At failure of connection to their hosts immergence may be the dominant faith. However, adaptation to changing environment is the success of the viral survival leading to high viral emergency.

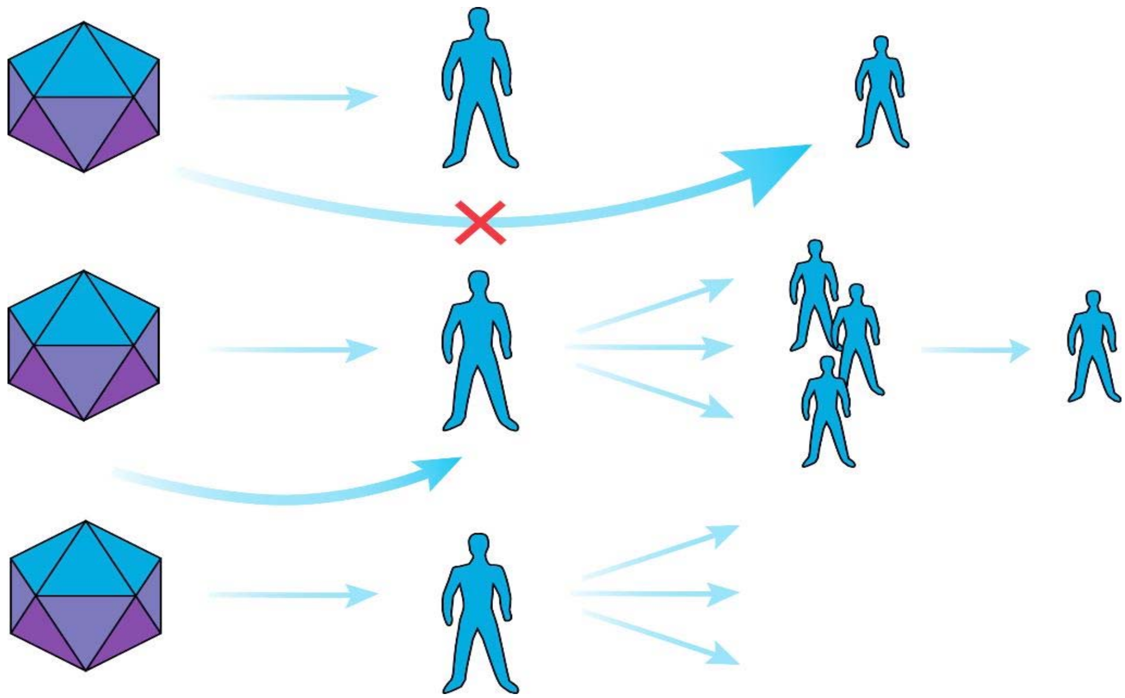
Once we have started to see our world and our actions as informationally dependent and constrained behavior, the more we see the phenomena everywhere and the more angles we use to review it. It is not only the Internet, e-mail and cell phones that are in the focus area, but also spread of rumors, epidemics and market madness as well as emergence of large systems from terrorist organizations to economies and ideologies that are seen informationally dependent. (Johnson 2001, Buchanan 2002, Barabási 2002, Watts 2003, Surowiecki 2004, Johansson 2004).

The insights that perhaps these systems are not so different after all have guided this study. That perhaps discoveries in one field can serve as a new lens in another, the results of this primary research in the world of viruses can provide us insights when thinking of our lives as human beings.

If we comprehend human life informationally and dependent and constrained activity, then perhaps the main form of causality can no longer be considered to be deliberate causality, that takes place in forms of plans and projects, but circular causality; where the emergence and immergence of futures depend more on the amount and quality of connections and networks than top-down plans; and if the world is considered predominantly non-linear and organic and not linear and mechanistic, then the significant part of organizations´ strategic work should move in this area. The less connections we find, the less we are able to benefit from them, and to influence on them to our advantage. (Hyypia 2006, Leitch et al. 2009).

The primary task of management is shifting from managing people to facilitation of emergence, and in other cases immergence, by managing relationships and contexts. The understanding of emergent and immergent properties of systems is a fundamental arena of competitive edge for organizations´ strategic work.

In contrast with linear and mechanistic world, where the emergent opportunities could be exploited by relying on symmetries, in non-linear and organic world the emergent opportunities must be exploited by relying on information asymmetries that derive from the differences in making sense of emergent and immergent properties.



Picture 3. Alternative fates of emergent viruses.

People are constantly being in contact with animal viruses, and in some instances may acquire a zoonotic infection. When the host barrier is broken, the infection often has serious consequences in the individual, who is completely naive in respect to the virus. When these infections reach epidemic proportions, the causative viruses are called emergent.

Top: In most cases, human is the dead-end host for the virus. As an example, hantaviruses are transmitted from rodents to humans through inhaled dried excreta. In humans, they cause acute disease with hemorrhagic renal or pulmonary syndrome. Different rodents carry different hantavirus species that differ in pathogenicity in humans, but human to human transmissions do not occur. Recent avian influenza A (H5N1) virus infections have had a high fatality rate in humans but not been able to spread between humans.

Middle: In some cases, a zoonotic virus can be transmitted between humans, but with a basic reproduction ratio of infection (average number of secondary infections per one infected individual) less than 1, the outbreak dies out. There have been several introductions of the deadly Ebola virus to human population, but in each known case, the outbreak affected less than 500 persons before contained. On the other hand, the number of introductions of the virus from it's mystery reservoir to humans seem to have been increasing over the last decades. In 1976, a swine influenza A (H1N1) virus circulated in Fort Dix, New Jersey for a month, and then disappeared.

Bottom: When (once) a zoonotic virus is transmitted between humans with a basic reproduction ratio higher than 1, it may adapt to human population and be maintained in it without further introductions. Humans have probably been infected with the simian immunodeficiency virus multiple times in the past. Sometimes in the last century it fully adapted to reproduction in humans and became HIV. When we learned to identify the causative agent, it was too late, and, within one generation, AIDS became a pandemic disease with devastating consequences. In 1918 an avian influenza A (H1N1) virus gained characters that made it fully transmissible in humans and caused the pandemic that was called the Spanish flu with tens of millions of fatalities. Then, the virus rapidly evolved to less disease producing and remained inhuman circulation.

In comparison with Axelrod and Cohen (2000) and Johnson (2001), where one or few viruses has been studied, this study has gone further and studies a spectrum of known viruses. In our opinion that has been vital in order to use viruses as a source of insights and analogies. The main result is that the emergent and immergent mechanisms for each virus vary and in order to be able to design appropriate and efficient interventions, they need to be planned carefully to match the relevant properties of the viruses. Following this conclusion, we claim that also the emergent and immergent mechanisms of each organization vary, and instead of trying to provide them universal answers, we should try to discover the appropriate mechanisms and let them to guide our interventions (Aaltonen 2007, Ruohola et al. 2009, Leitch et al. 2009).

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