

Abstract for ERM journal

Contemporary enterprise risk management has moved from an event based view of risk to a hierarchical, systems based approach. Risk systems that involve human interaction are classified and behave as complex adaptive systems. One of the key signatures of complex adaptive systems is that they evolve and therefore a detailed understanding of the evolution of an enterprise's risk system should reveal the nature, future likely emergence and adaptation of risks in that enterprise. In order to operationalise such an approach, a methodology is proposed in this paper that draws on phylogenetic approaches that have been successfully developed for biological evolution. The technique and process provides an insight into the lineage, pace and impact of external conditions on the evolution of risks. It also provides a unique and rational classification of risk in an enterprise which can be used to optimize risk management resources. An example of a fictitious insurance company is used to illustrate the approach.

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1. INTRODUCTION

The authors introduce a novel approach to risk analysis and management that is grounded on three interconnected principles:

1. Risks behave as complex adaptive systems, not as an aggregation of events, (Allan and Davis, 2006). This concept extends beyond the principle ‘the whole is greater than the sum of the parts’ to include Angyal’s modification that, ‘aggregation and whole formation are processes of an entirely different order’ (Angyal, 1941).
2. Evolution is a signature of complex adaptive systems (Mitleton-Kelly, 2003) and (Morel and Ramanujam, 1999); and hence risks, should by definition, evolve and follow evolutionary principles.
3. Connectivity is a fundamental property of any system. (Mason, 2005) and (Checkland and Scholes, 1990).

There is a trend, that in modern society and its organisations, risks have become more complex and interdependent (Beck, 1992, and 2004). This has been borne out by the recent systemic crisis in the financial sector, where all the banks were lending and trading with each other and the impact of their losses are felt throughout economies and society. Indeed, it is suggested that connectivity is the third dimension of risk (Allan, Yun and Cantele, 2008) to be added to the two-factor risk paradigm of probability and impact. Moreover, Mitleton-Kelly (2003) argued that the interconnected nature of the elements in a system enables both the system and its parts to evolve.

Using evolutionary theory and specifically phylogenetic techniques, developed to study the evolution of biological systems, it will be demonstrated, using a case study, that:

1. Risks can be understood to have a unique characteristic sequence, very much like a DNA to a biological entity.
2. Collective risk systems can and do evolve and co-evolve.
3. The history of the evolutionary path (path-dependency) is an important aspect of a risk; this is of course already well known to financial and insurance

professionals. The point here is to understand what the parent risk is and when a risk characteristic combines or separates to form a new lineage.

4. A risk's evolutionary progression or steps can be analysed and predictions made about how they may most likely develop.
5. Taking into account the unique evolutionary history of an organisation's risk system it is possible to determine the likely future trajectories or emergence of new or evolved risks.
6. Lastly and maybe most importantly, the paper demonstrates that the evolutionary analysis provides a unique and powerful way of classifying risks that is independent of traditional organisational boundaries and structures. This can aid effectiveness and efficiencies in managing risks and allocating risk related resources or capital.

Before embarking on the case study it is necessary to first explain the background to phylogenetics and its principles so as to appreciate how the approach has been adapted to analysing risks.

2. HISTORY AND DESCRIPTION OF PHYLOGENETIC ANALYSIS

In the eighteenth century, Linnaeus pioneered the classification practice by grouping organisms in accordance to their similarities and differences (Wheeler, 2005). Linnaeus' work, much like traditional risk management, can be described as systematic, instead of evolutionary, as the objective was to place all known organisms into a hierarchical structure. Phylogeny on the other hand, being inspired by Darwin's evolutionary approach, (Brown, 2007) not only indicates the similarities and differences between species, but also illustrates their evolutionary relationships (Pagel, 1999).

With the advances in computational capabilities and molecular knowledge, the study of classification and evolution has entered a new era. Phylogenetic analysis¹ utilising molecular information, i.e. DNA, to meet the data requirement and assigns equal weights to characters (Mishler, 2005). By doing so, the approach is less subjective – 'rather than making assumptions about which characters are important, phylogenetic analysis demands that the evolutionary relevance of individual characters be defined' (Brown, 2007).

The outputs from phylogenetic analysis are tree-like shapes, often called 'evolution trees', 'phylogenetic trees' or 'cladograms'. As illustrated in figure 1, a phylogenetic tree is essentially a connected graph that is composed of nodes and branches and does not contain any closed structures. The nodes symbolise the organisms under investigation, whereas the branches that connect all the nodes represent the relationships among different organisms, in terms of their ancestry and descent relationships. Epistemologically, a node is an entity that is homogenous and comparable to other entities being studied and its informative character states are always subject to change as knowledge of characters progresses (Albert, 2005). Therefore, the application of the phylogenetic trees, which is composed of nodes and branches that link nodes, is not restricted to organisms. Indeed all individual entities with taxonomic characters, such as species, populations, individuals, genes, or even organisations (McCarthy et al., 2000), can be analysed with this method.

¹ The terminology 'phylogenetic analysis' and 'cladistic analysis' are often interchangeable in contemporary usages and this paper does not discriminate between the two.

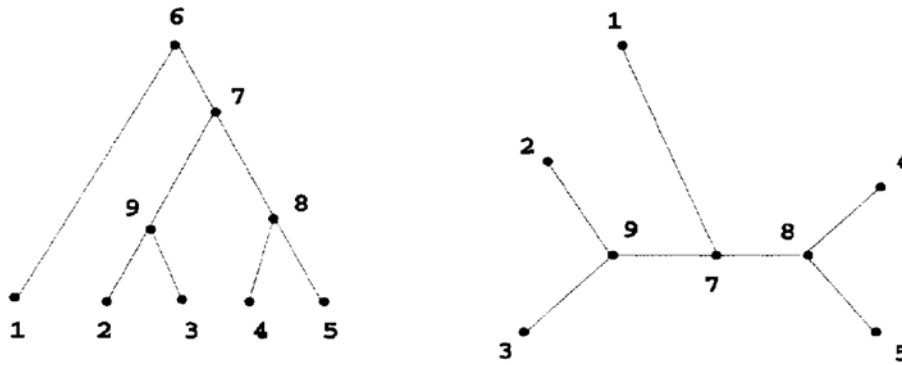


Figure 1 Example of cladograms

All phylogenetic trees can provide the same basic information, including a historical pattern of ancestry, divergence, and descent, all of which can be interpreted from their structure (Lecointre and Le Guyader, 2007). Basically, the nodes of a tree can be categorised as external or internal, according to their relevant positions. That is, nodes at the terminal tips of a tree are called the external nodes (Mishler, 2005), whilst the rest are termed the internal nodes and these are the ancestors of the former. In other words, external nodes are descendants of connected internal nodes. The links between the nodes are called the branches and the lengths of these are proportional either to the evolutionary time or the number of mutations occurring along that branch (Li et al., 2000). Evolution occurs independently along the branches emanating from each internal node and the overall structure of nodes and branches represents a given entity set's degree of diversity.

Furthermore, as can be seen in figure 1, there are two main types of trees. The one on the left hand side is referred to as a rooted tree, because of the existence of a root, at node 6, and such a tree structure determines that there is only one path from the root to each of the other nodes. In a rooted tree the directions of the branches correspond to the evolutionary times and the root is the common ancestor of all the organisms in the tree. On the right-hand side is an un-rooted tree, where a common root cannot be identified. In an un-rooted tree, only the relationships among different organisms are specified, and very limited information regarding the historical evolution process can be inferred without acquiring extra knowledge. In many circumstances, un-rooted trees occur because the characteristics or taxa of an organism diverge from the outset and thus it is not possible to determine the common ancestor, at least without additional information.

2.2 Different phylogenetic algorithms

Li et al. conducted a survey of how scientists construct phylogenetic trees and concluded that there are three major methods and algorithms employed (Li, 2000):

- distance matrix;
- maximum likelihood;
- parsimony.

In practice, these different tree constructing algorithms need to be applied with care, particularly in the context of risk analysis. For example, the distance matrix algorithm, though computational efficient, can produce inaccurate inferences under certain conditions (Pagel, 1999). The maximum likelihood method and other Bayesian methods rely more on statistical models to describe the mutation process at a molecular level (Kishino et al., 1990). This sort of model is not easy to obtain for risk analysis, and the results can be difficult to interpret.

Methods based on the principle of maximum parsimony have been by far the most widely used, because they are probably the most logical and intuitive to apply. The principle behind the parsimony approach is that *'a tree is more preferable if it involves fewer evolutionary changes'* (Lin et al., 2007). In other words, the one with the fewest evolution changes is termed a parsimonious tree, as the term 'parsimony' implies as few changes as possible (Sneath and Sokal, 1973). However, Sober notes that the parsimony algorithm does make assumptions about evolution but that those assumptions are modest and unproblematic and that the most-parsimonious tree is better supported than the others, (Sober, 2005). After considering the advantages and drawbacks of each algorithm and their experience of applying and interpreting the resulting trees in a risk context, the authors conclude that the parsimony method is the most suitable for risk analysis.

2.3 An illustrative example of parsimony algorithm

The process of phylogenetic analysis in biology is inherently composed of two phases: assembling a data matrix containing relevant information; and, inferring phylogenetic tree(s) from that matrix (Mishler, 2005). There are two further prerequisites for conducting phylogenetic analysis using the parsimony method:

1. One should ensure that the entities to be examined are comparable and the relationships between different characteristics are meaningful (Swofford and Olsen, 1990).
2. It is possible to describe the characteristics using a Boolean style measurement (1 or 0).

The phylogeny problem can then be described in a matrix such that each element (i,j), in such a matrix, corresponds to the state of character j within entity i. Figure 2 below illustrates the simple biological example, provided by (Kitching et al., 1998).

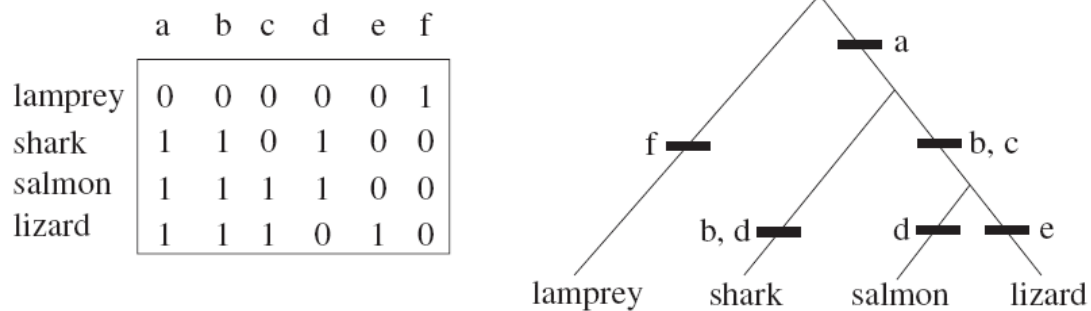


Figure 2 An application example of parsimony algorithm (after Kitching, 1998)

First, a set of six characters are described: (a) paired fins; (b) jaws; (c) large dermal bones; (d) fin rays; (e) lungs; and, (f) rasping tongue. For each of the species, their characters were measured against these six characters with 1 denoting their existence and 0 their absence. Once all species and characters were elicited in matrix, a cladogram could be obtained to represent the evolutionary relationship between the different species. Then, a V-shaped tree structure is established for placing species relative to each other. It is assumed that the characters of species evolve from none to existence and therefore one of the two branches shall be occupied by the species with the least characters, i.e. the lamprey.

The next step is to repeat the selection method to find the organism that owns the least changes to the lamprey. By calculating the least difference between each species, it

turns out that shark has the least score as shark has 3 changes to lamprey while the other candidates have 4 respectively. Thus, the other branch of the tree is devoted to the shark. Following this logic, a new tree structure can be established using the shark and salmon and finally the lizard can be added next to salmon, as the lizard evolves through the longest evolution path.

The example given above only demonstrates the logic behind the parsimony algorithm. In reality of course, there are far more than four species with six characters to analyse. Furthermore, the previous example does not guarantee to generate a tree that is optimal (Pagel, 1999). Computer-aided programs are needed for the analysis; whilst it is not within the scope of this paper to recommend software, we can say that there are packages suitable for our risk analysis approach.

3. APPLYING PHYLOGENETIC ANALYSIS TO RISKS

Scientists from biology and other fields have proposed many phylogeny tree building methodologies, such as (Coombs et al., 1981, Minelli, 1994, Tsinopoulos and McCarthy, 2000, Fernandez et al., 2001), all of which in effect follow the two-phase general process described above and share similar core steps. Taking these different phylogenetic tree building methodologies into account, the authors propose a seven step process for risk analysis applications, illustrated in figure 3.

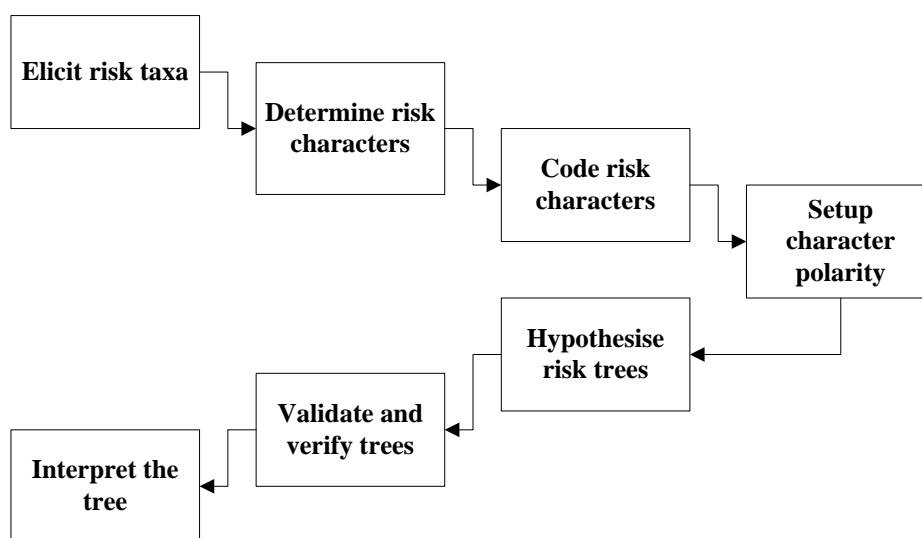


Figure 3 A flowchart of building risk cladograms

3.1 The seven-step process

3.1.1 Eliciting risk entities

Risks as entities bear considerable similarities to organisms: they exist in a particular environment; change over time; and, have uncertain outcomes. The evolution of risk is partly determined by the uncertain nature of risks and partly by the environment and human intervention. In this sense, determining the boundary of risks under investigation is similar to that in biology. In theory, one can choose any homogeneous and comparable entities to study. However, it is more meaningful to select risks that are of interest to conduct the phylogenetic analysis; usually in an organisational context this means the whole organisation or sub-divisions. It could be regional by

geography or by organisational structure and in practice the choice is usually determined by the data availability and structure.

3.1.2 Determine risk characteristics

The goal of this phase is to find as many potential characters as possible that can serve as the evidence for the existence of lineages and can expand the depth of the tree. In respect of risks it is crucial to elicit the characters that can represent risks in a comprehensive and concise way². In practice few organisations collect sufficiently rich or holistic data on risks or losses, though this does not mean that it is not achievable. Using an industry set of benchmarked risks may help broaden the risk entities representation yet remain relevant. Care is required to avoid a biased elicitation process resulting in either a single character being overly repetitive, or the inclusion of redundant characters. Both of these practices can reduce the reliability of the subsequent analysis. In biology, of course, with a rigour of the DNA identification process, this is not an issue. In this regard, we have adapted a set of criteria from Sneath and Sokal to be adopted in order to exclude any ‘*inadmissible risk characters*’, shown in table I, (Sneath and Sokal, 1973).

Criteria	Description
Meaningless characters	A character must reflect at least one property of a risk.
Logically correlated characters	If characters are in a logical sequence and one can lead to the other, they should be excluded.
Partial logically correlated characters	If characters are partially dependent, they should be adjusted so that the dependency in the characters is removed.
Invariant characters	A character that can be found in all risks makes no difference to the phylogenetic analysis. But when considering the computation efficiency issue they should probably be removed.

Table I - Criteria for Inadmissible Risk Characters (adapted from Sneath and Sokal, 1973)

² Sometimes organisations record and categorise both losses and risk in some detail, usually for audit purposes, health and safety risks for example. Risk registers provide the basic information, but a coherent classification of the entries according to clear characteristics is needed to make the phylogenetic approach workable.

3.1.3 Code characters

If the risk entities and characters have been elicited at an acceptable level of detail, they can be coded numerically into matrix form, the column of which records the risk characters and the row the risk entities. If the risk has a particular character, the corresponding cell in the matrix is assigned a 1, otherwise it is 0. After assigning values to all characters of all risks, the data matrix is assembled.

3.1.4 Setup polarity

As pointed out by (Watrous and Wheeler, 1981), setting up polarity for character evolution can reduce the possibility of experiencing a complex tree-building process. The polarity process essentially determines the direction of evolution for the entities; either they are gaining or losing characters as the norm. This can be problematic, as not all risk characters can be labelled directionally. However, if there is doubt then both versions can be reviewed and it becomes clear which version makes more evolutionary sense. Typically however, risks, like hedgerows become more diverse in its characteristics as it ages.

3.1.5 Applying the parsimony algorithm

Software toolkits use two principle approaches to build the phylogenetic trees:

- Constructing the best fit phylogenetic trees using a specific algorithm;
- Testing different phylogenetic trees with a specific algorithm to find the one with the best fit.

The first approach is more efficient, but does not present all possible suboptimal cladograms. The second can provide a more holistic view, but the computational difficulties limit its application.

3.1.6. Validate and verify

The tree output from the step 3.1.5 is only a hypothesised cladogram and validation testing is still required. Firstly, is it logical and does it have historical coherence? Can it be used effectively to explain real world scenarios and hence lead to a greater understanding of them? The caveat being of course, that the tree result can be

counterintuitive, and this may be one greatest strengths of this approach (Lapointe et al., 1994). Collective assessment of a hypothesised cladogram by multiple users can avoid individual bias, but may not help with paradigm shifting.

Secondly, adding or removing an entity is a good test of the tree stability. If a tree structure remains broadly stable when the inputs are varied slightly, the proposed structure has more robustness. Also, positioning a risk in the cladogram and linking it to its neighbouring risks can again reveal an underlying instability.

Thirdly, real world data, especially longitudinal data over time, can be utilised to test different tree structures to see whether they are phylogenetically similar.

3.1.7 Interpretation

A phylogenetic tree can reflect the evolutionary relationship between risks, why they are similar or not, how these risks might adapt, mutate and evolve in the future. It also provides a powerful classification system of the risks and the connection between the risks.

A case study will now be used to illustrate the full process and interpretation.

4. CASE STUDY

4.1 Background information for the case study

In risk management practice, many firms and organisations adopt risk registers to record and monitor their risks and such tools indeed allow for relatively easy application of the phylogenetic analysis. A risk register typically contains descriptive information of a risk and its quantitative measurements, management strategy, ownership, time span, etc., which can be directly used or converted to provide the information needed in the risk phylogenetic analysis. The authors have used modified data from a number of real world registers in this example, to create a realistic synthetic risk register. Any similarity between this register and that of any particular real organisation is entirely co-incidental and unintended.

The risk register information has been coded into the data matrix shown in figure 5. The value of 1 indicates the existence of the character in the risk whilst 0 represents the absence of the particular character.

Risks	Characteristics		Market										Credit										Operational																						
	Strategy	Asset Allocation	Asset Allocation Concentration	Other Market Risk	Investments	Reinsurance	Other Credit Risk	Insurance	low-acceptable business practices	Internal control violations	Project failures	Communication failure	Brand abuse	Violation of reporting regulations	Solvency	Accuracy of disclosure requirements	Customer due-diligence	Product compliance	Mis-selling	Misleading data	Inaccurate documentation	Systemic reporting error	Mismanagement of	Mismanagement of	Mismanagement of	Investment transactions	Liquidity needs unmet	Inaccurate design of products	Mismanagement of underwriting	Inadequate reinsurance	Inadequate claims management	IT systems failure	Low authorized access to data	Inadequate functionality	Inappropriate skills	Staff act outside authority/competence	Business interruption	Advance regulatory change	Other Operational Risk						
1. Liquidity challenge	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0				
2. Regulation changes 1	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0				
3. Violation of Privacy Protection	0	0	0	0	0	0	0	0	0	0	1	1	0	1	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0			
4. Trusted Insider Technology Risks	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0			
5. Business Continuity	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0			
6. Technology development	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0			
7. Product	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0			
8. Geographical	1	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0			
9. Regulation changes 2	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0			
10. Succession Planning	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0		
11. Model complexity	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0		
12. Convergence of Products	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0		
13. Regulation changes 3	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0		
14. Poor decision making	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0		
15. Misunderstanding of risks	0	1	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0		
16. HR policies	0	0	0	0	0	0	0	0	0	0	0	1	1	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
17. Long-term planning	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
18. Tech infrastructure	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
19. Tax rules	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
20. Regulation differences	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
21. Tax management	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
22. Infrastructure	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0

Figure 4 Character Coding

A computer assisted analysis, using the parsimony algorithm was then applied to construct the optimal phylogenetic tree, show here in Figure 6.

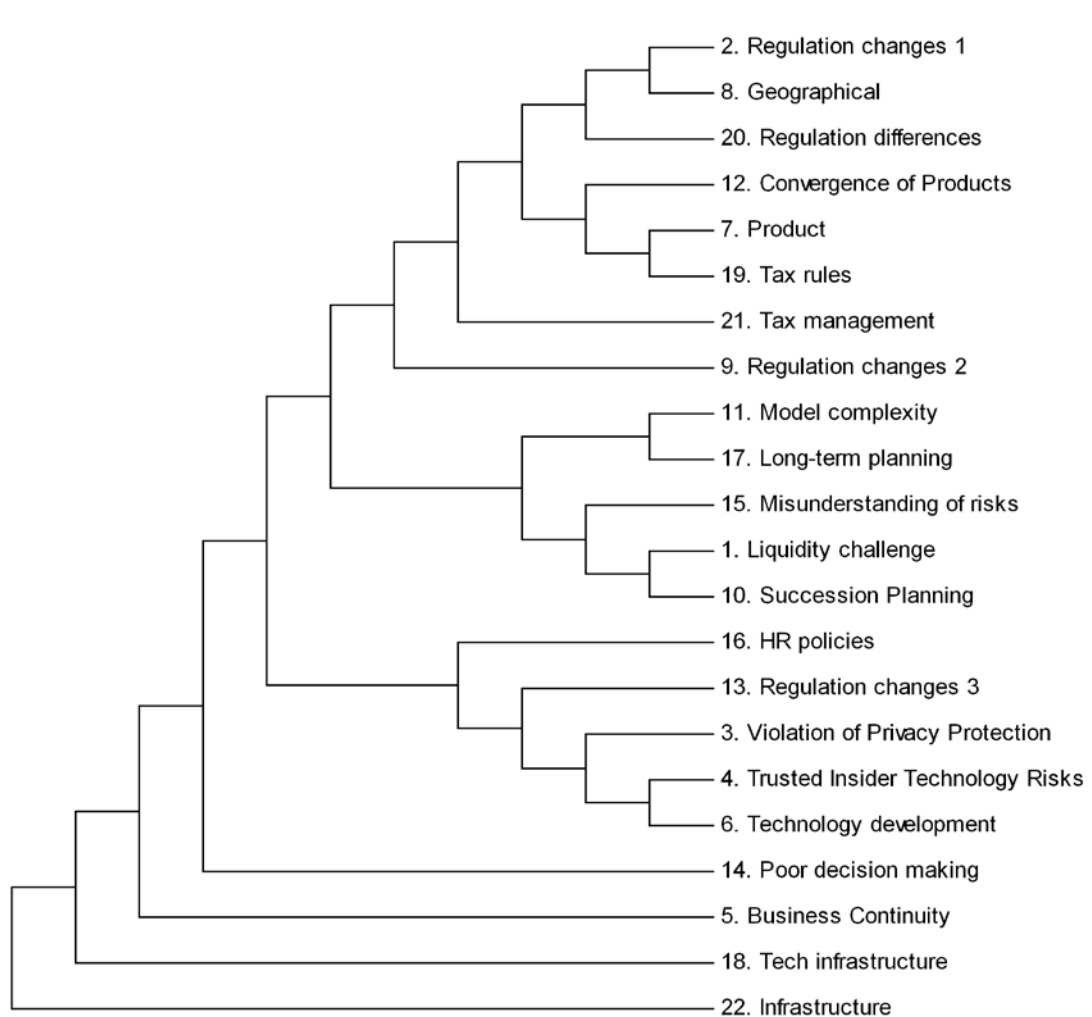


Figure 5 Result of the risk phylogenetic analysis

4.2 Implications from the case study

4.2.1 Classifying risks

The result illustrated in figure 6 exhibits a new classification for the risks in the study. For example, risks 2, 7, 8, 9, 12, 19, and 21 are likely to be in a category, which is dominated by the theme of ‘change or variance’, whereas risks 1, 10, 11, 15, and 17 are related to the products or models of the company.

4.2.2 Understanding the risk evolution process

A risk cladogram presents the evolutionary relationships between risks and illustrates where there is common ancestry. For example risks 6 and 16 share a common ancestor and have ‘*internal control*’ as a family characteristic.

4.2.3 Predicting emergent risks

The cladogram demonstrates also how new risks can emerge. Risk 11 '**model complexity**' and 17 '**long-term planning**' are close together and share some common characteristics. Due to their location we know they have evolved relatively recently. It is easier for these two risks to co-evolve and mutate, or even produce a new risk, than say risk 11 and risk 6. Also, we have insights into what might emerge next. For instance, 11 & 17 can easily mutate by sharing a character which only one of them currently possesses, for example the character 'systemic reporting errors' in risk 11. It is quite plausible that a new risk could emerge that is about long-term planning, overly complex models and now also has an additional feature which is related to deep seated reporting errors.

4.2.4 Understanding risk connectivity

The tree gives a sense of the pace of change of risks and more importantly a means for measuring how connected the risks are in an evolutionary sense. This is achieved by measuring the leg distance between different risks.

It is not the intention here to describe all the findings from the case study but to illuminate how the information might be used and interpreted. The risk cladogram allows for the visualisation of the current risk system. In nature, people cannot reverse the past, but can influence, if not manipulate, the current evolution process. It is proposed that this is true for risks as well. For instance, structuring a business to limit the ability of certain risk characteristics to propagate may successfully interfere in the evolutionary process and reduce the complexity of their management in the future, or it may unleash new challenges.

5. DISCUSSIONS

Whilst risk is considered by many to be just a social construct, it can be argued that, like money, risk is treated as though it exists, grows, interacts and has value. Risk is essentially real and alive; people act and make decisions on it, and it evolves.

One claimed merit of a phylogenetic analysis is that it provides a unique, unambiguous and objective classification solution (McCarthy et al., 2000). Ridley argued that '*Cladism is theoretically the best justified system of classification... and has a deep philosophic justification...*' (Ridley, 1993).

Our phylogenetic approach to risk analysis described here satisfies the objectivity criteria in social research, which requires that different rational people would obtain the same result under independent investigations (Bryman, 2008). There is a possibility of people obtaining diverging results if they cannot agree on the characters of risks in their original inputs for the analysis. Secondly, applying inappropriate algorithms and not testing the model's robustness can lead to the dissimilarities between entities being identified within a cladistic classification. However, we believe the approach can effectively present data, in an unbiased way that is accessible to a wider range of potential users, thereby bringing greater transparency to decision-making processes (McCarthy et al., 2000).

The structure of cladograms and the associated sub trees have significant implications for both scientific and practical risk management. Once risks are positioned in a cladogram, the comparisons of their characters are established so that people can identify the common properties and distinguish individual attributes, thereby allowing for reasonable hypotheses to be made (Andreatta and Ribeiro, 2002). Phylogenetic analysis reveals reliable evolutionary information. Without this form of analysis, evolution studies are more or less based on pure predictions (Gould, 1999). With phylogenetic risk knowledge, people can understand the order, rate, direction, and diversity of risk evolution and hence obtain greater insight into their risk system. Additionally, this type of analysis can articulate a robust roadmap of evolution. As pointed out by Mitleton-Kelly, the evolution behaviours of a complex adaptive system make the system path and history dependent (Mitleton-Kelly, 2003). In other words,

phylogenetic analysis demonstrates how individual risks have reached their current state and indicates potential ways in which risks and the risk system will evolve.

Risk management often encounters a new risk with very limited information. In this case, people are likely to use heuristic knowledge to make estimations, leading to possible biased judgements (Goodwin, 2004). With the help of phylogenetic analysis, such a problem can be relieved, to some extent, because cladograms are based on a binary description of an organism's characters and such characters can be utilised to gain a comprehension of the new risk. As a consequence, a new risk cladogram can be constructed which contains this risk. The properties of the new entry are supposed to be similar, although not necessarily identical, to its neighbours and hence this will allow for more rational predictions of how this risk behaves.

6. CONCLUSION

In the ever increasing complexity and interrelatedness of the business environment it is unhelpful and even misleading, to manage risks as a collection of isolated events. The interconnected nature of risks should be addressed holistically in risk management analysis, particularly in enterprise risk management (ERM). Management approaches should actively try to understand the whole system of risks, not the aggregated sum of the risks. The authors of this paper endeavoured to solve this problem by looking at evolutionary analysis methods from biology.

Traditional risk methods invariably require the classification of risks according to a single dominant characteristic. This immediate loss of information makes the subsequent analysis of risk behaviour problematic, and potentially worthless. By retaining the richness of multi-characteristic classification the authors have shown that phylogenetic analysis provides a more appropriate scientific basis for understanding risk development, consistent with the view of risk as the emergent property of a complex adaptive system.

Risks, like organisms, can be classified in accordance with their evolutionary relationships to obtain insight and knowledge regarding the patterns that emerge through phylogenetic analysis. A risk DNA can be achieved and as in biology it could start to unlock some of the deep interconnected secrets of complex risk behaviour, even our perceptions. The authors have reviewed relevant bioinformatics literature and recommended the parsimony algorithm. Furthermore, the authors have proposed a seven-step procedure to facilitate phylogenetic analysis. A real world case study has been carried out with the aim of explaining the process and inviting discussions. The case study demonstrates the process of classification and how emerging risks may evolve and adapt. There are issues with data quality in the risk arena and computational efficiency of large risk matrixes, validation and interpretation of complex trees. Further research is needed in these areas and close attention to developments from biological sciences may provide some partial solutions to these concerns.



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