Computational Approaches to Myths Analysis: Application to the Cosmic Hunt

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Abstract: *Different computational approaches are applied, after binary coding, to 175 versions of the Cosmic Hunt, one of the rare myths found almost worldwide. The relevance of phylogenetic networks to the analysis of myths is explained and illustrated with the Cosmic Hunt. We show how characters evolve at different rates, the fast evolving ones forming a module of characters that can be replaced almost indifferently, while slow evolving characters fit to a phylogenetic tree or network. One observes a very good correlation between the regions in which the myths were recorded and the phylogenetic representation of the data. This correlation is explained using different models of evolution taking into account different migration schemes and cultural interactions.*
Keywords: *myths, phylogenetic networks, evolution.*
Résumé: *Différentes approches de calcul sont appliquées, après codage binaire, à 175 versions de la Chasse Cosmique, l'un des rares mythes retrouvés presque partout dans le monde. La pertinence des réseaux phylogénétiques pour l'analyse des mythes est expliquée et illustrée par la Chasse cosmique. Nous montrons comment les personnages évoluent à des rythmes différents, ceux qui évoluent rapidement forment un groupe de personnages qui peuvent être remplacés presque indifféremment, tandis que les personnages évoluant lentement s'adaptent à un arbre ou à un réseau phylogénétique. On observe une très bonne corrélation entre les régions dans lesquelles les mythes ont été enregistrés et la représentation phylogénétique des données. Cette corrélation est expliquée en utilisant différents modèles d'évolution prenant en compte différents schémas de migration et interactions culturelles.*
Mots-clés: *mythes, réseaux phylogénétiques, évolution.*

Introduction

In recent years, it has become increasingly clear that a phylogenetic tree is often a much too crude representation of the evolutionary relationships between genetic sequences in evolving organisms[1]. Mutations are only one among several processes at work in living organisms. Lateral transfers, gene duplication, gene deletion or changes in gene order are just some of these other processes. For that reason, much work has

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[1] Doolittle, 2000.

been invested in the development of phylogenetic networks[2]. A phylogenetic network can be regarded as a generalization of a phylogenetic tree. Among phylogenetic networks, the so-called outer planar networks have been intensively used for their capability to describe evolutionary processes combining mutations with a number of lateral transfers or recombination[3]. Outer planar networks have been used outside of genetics, for example to describe the evolution of galaxies in astrophysics[4], language diversification in linguistics[5] or the evolution of myths[6].

The study of myths using mathematical methods has its roots in their formalization, allowing a structural analysis. After coding, typically with binary characters, the different versions of a myth can be analyzed using mathematics or computational methods. Fischer was the first who came with the idea of mathematizing myths and folktales to express the distance between types and versions. This procedure was subsequently developed by Petitot and Maranda[7].

The study of myths according to biological metaphors also has a long history[8]. Recently models and software borrowed from genetics have been used to classify versions of a same myth[9], to study the role of geography, linguistic and population boundaries in myth variations[10] as well as to reconstruct first human migrations and proto-folklore[11]. Myths are believed to evolve over space and time through transformations that may be compared to mutations and lateral transfers in genetics. A mutation corresponds to a random change of some character states. A set of characters transforming through mutation can be represented exactly by a phylogenetic tree provided a new character state appears only once[12]. One of the goals of this article is to apply computational methods to analyze a myth, the Cosmic Hunt, and to discuss the results with some simple models of evolution.

Unlike genes, cultural elements can be acquired both from other members of the same group of peoples and from outside that group, i.e. they can move from

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[2] Huson, Rupp and Scornavacca, 2010.

[3] Bryant and Moulton, 2002; Thuillard and Moulton, 2011; Thuillard and Fraix-Burnet, 2015; Gambette, Berry and Paul, 2012.

[4] Fraix-Burnet, Thuillard and Chattopadhyay, 2015.

[5] Forster, Toth and Bandelt, 1998; Atkinson and Gray, 2005; McMahon and McMahon, 2005.

[6] d'Huy, 2012a, 2013a, 2013b.

[7] Lévi-Strauss, 1955; Fischer, 1959; Petitot, 2001; Maranda, 1971, 2001.

[8] Sydow. 1934; Hafstein, 2001.

[9] Abler, 1987; Oda, 2001.

[10] Ross, Greenhill and Atkinson, 2013.

[11] d'Huy,2012a, b, 2013a, b, 2016.

[12] Semple and Steel, 2003.

people to people without the need for those peoples to be genetically related. Thus, the distribution of cultural elements and genetic markers will not necessarily co-occur across different populations. Transmission may occur within a population or through cultural interaction between different populations. Myth elements can be transmitted with possibly some changes (like inversions, removal of some parts or creation of new elements) or combine versions of several myths. The differences and similarities between the evolution of genes, languages and cultures have been also thoroughly studied[13]. The conclusions are that despite the important differences between genes, languages and cultural traits, similar theories and methods (such as NeighborNet or statistical tests on the influence of an insulation factor versus geographical proximity) can be applied to all of them separately. In this paper, we will often use genetic terms or refer to processes known in biology. A whole discipline in computational science, called soft computing, includes bio-inspired computational methods, such as neural networks or genetic algorithms, that have found many applications in engineering[14]. It is in this spirit that analogies with genetic terms have to be understood.

What is essential to know about phylogenetic trees and networks (Outer planar networks)?

A phylogenetic tree represents under the form of a tree the relationships between one or more populations that are believed to form a unit. This unit is generally called a **taxon**. The taxa are characterized by a number of characters that can take several states. A **binary character** has two states (yes/no, present/absent, …, or translated in binary form 0/1) while a **multistate** character may have several states (blue, green, brown). A **phylogenetic tree** represents in a coded form the relationships between taxa based on their states. A phylogenetic tree on multistate characters can be transformed into a phylogeny on binary characters[15]. For that reason, we restrict the discussion to phylogenies on binary characters. A phylogenetic reconstruction method is generally used to search for the best tree representation of the data. The best tree may be a perfect representation of the characters (in this case, it is called a **perfect tree**) but may also sometimes be a very bad representation of the data; therefore, any result must be carefully validated.

In order to explain the similarities and differences between phylogenetic trees and **phylogenetic networks**, one has to understand what is a **split** and what is a

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[13] Ross, Greenhill and Atkinson, 2013; Korotayev and Khaltourina, 2011.

[14] Thuillard, 2001.

[15] Stevens and Gusfield, 2010; Thuillard and Fraix-Burnet, 2015.

circular order of the taxa. Cutting an edge of a tree "splits" the taxa into two subsets A and B. For each split, there is a character on which each taxon in A has the same state (for instance 1), while all the taxa in B have the complementary state (0 in the example). A **circular order** on a phylogenetic tree corresponds to an indexing of the end nodes according to a circular (clockwise or anti-clockwise) scanning of the end nodes. One observes in Figure 1 that along a circular order all ones as well as all zeros are consecutive. This property is called the **circular consecutive-ones' property**, a property shared by both perfect trees and phylogenetic networks (or more precisely a special type of phylogenetic networks called outer planar networks). Let us note that the idea of ordering taxa defined by binary characters, so that the consecutive-ones' property are fulfilled, finds its root in the work by Flinders Petrie's work on seriation[16].

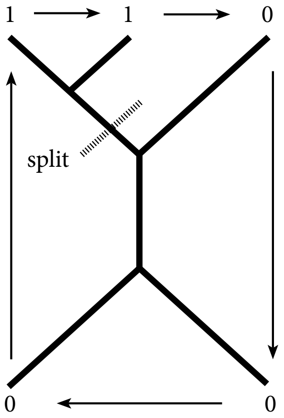

Figure 1.
A split on a tree is defined by two complementary subsets of taxa, the first subset with all taxa having state 1 on a given character and the complementary subset with all taxa with state 0 on the same character. A planar representation of the tree is shown with a clockwise (arrows) circular order of the taxa.

Outer planar networks[17] permit the simultaneous representation of alternative trees and are thus generalizations of trees. An outer planar network reduces to a phylogenetic tree if the so-called 4-gamete rules are fulfilled by each pair of binary characters. The **4-gamete rule** states that for each pair of binary characters at least one of the 4 possible gametes (one gamete among (1,0), (0,1), (1,1) or (0,0)) is

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[16] Petrie, 1899.

[17] Bryant and Moulton, 2002; Dress and Steel, 1992; Huson and Bryant, 2006.

missing (The cladistics formulation is not used in this article and therefore terms like homoplasy are not employed). We are now ready to explain the differences between a tree and an outer planar network with the examples of Figure 2 (Below we will use indifferently the term phylogenetic networks or outer planar network despite that outer planar networks are one among many types of phylogenetic networks).

	Bacteria	**Eagle**	**Platypus**	**Lion**
Mammal glands	0	0	1	1
Lay eggs	0	1	1	0

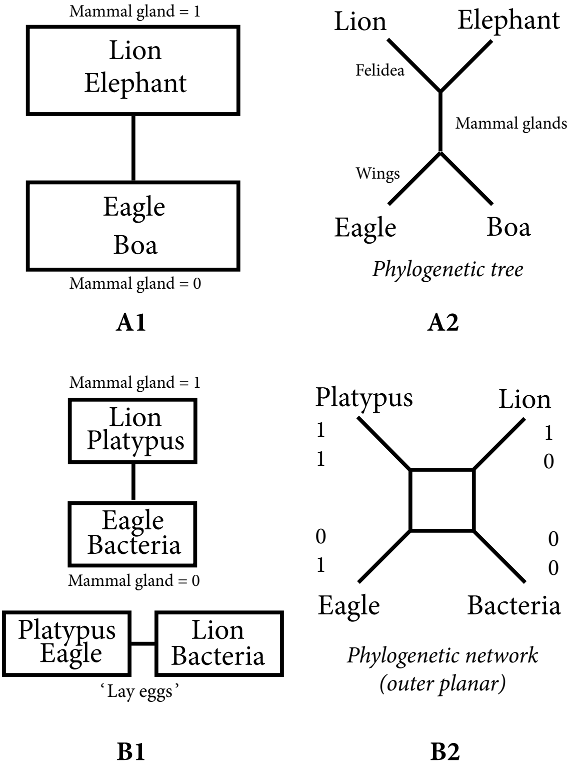

Figure 2.

A1) The character 'Mammal Glands' splits the taxa into two complementary subsets; A2) Phylogenetic tree obtained on a set of 3 binary characters;
B1) Two splits that are incompatible with a perfect tree description;
B2) Outer planar network representing exactly the 2 splits. The 2 characters fulfill the circular consecutive-ones' property (but not the 4-gamete rules) and can therefore be represented by a phylogenetic network.

Figure 2A represents graphically a split between two complementary subsets consisting on the one side of the taxa, “Lion” and “Elephant”, two mammals and on the other side of the taxa, “Eagle” and “Boa”, two non-mammalian animals. The split is represented by an edge connecting the two complementary subsets. Adding two other characters, the 4 taxa can be described by a perfect phylogenetic tree. The circular order of the planar tree representation is so that each character fulfills the circular consecutive-ones’ property on the circular order (Fig 2A). Figure 2B describes another example using the two characters “Mammal Glands” and “Lay eggs”. There is no phylogenetic tree that describes exactly those relationships. No two splits are compatible with a phylogenetic tree, but there is nonetheless a circular order of the 4 taxa with the circular consecutive-ones’ property fulfilled by all characters[18]. An important result on phylogenetic networks states that if the circular consecutive-ones’ property is fulfilled by all characters on some circular order then the data can be exactly described by an outer planar network as represented in Fig 2B. In summary, the 2 splits in Fig.2B can be exactly described by a phylogenetic network but not by a phylogenetic tree.

In genetics, a lateral gene transfer corresponds to the transmission of genetic material between different genomes. Translated into the language of binary characters a lateral transfer between taxa corresponds to the replacement of the state of some characters by the corresponding states from another taxon. If a **lateral transfer** takes place between 2 taxa that are adjacent on a phylogenetic tree (i.e. the two taxa are consecutive in a circular order), then the lateral transfer preserves the circular consecutive-ones’ property and therefore[19] can be described exactly by an outer planar network. A phylogenetic tree is defined by its nodes and edges with possibly some weight on the edge. They are multiple planar representations of a phylogenetic tree that are completely equivalent. So, by using the degrees of liberty on the planar representation of a phylogenetic tree, one understands that a tree can accommodate many lateral transfer and still preserves the circular consecutive-ones’ property on some circular order of the tree. Figure 3 shows such an example. Using the degrees of freedom on the planar representation of a tree, the tree representation on the left is transformed into the tree representation on the right. All lateral transfers (arrows) are between adjacent taxa on the circular order and the phylogenetic tree can exactly be described after lateral transfer by an outer planar network on the same circular order.

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[18] Bandelt and Dress, 1992

[19] Thuillard and Fraix-Burnet, 2015.

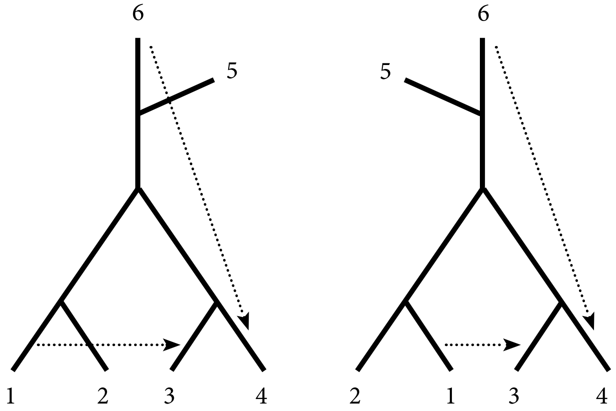

Figure 3.
Two different planar representations of the same tree. The tree representation on the right is so that lateral transfers (represented by arrows) are only between taxa that are adjacent on the circular order. The tree with the lateral transfers can be represented exactly by an outer planar network.

SplitsTree4[20] is used in this study to reconstruct an outer planar network. In real world applications, it is quite rare that all characters fulfill perfectly the circular consecutive-ones' property. Quite often a subset of characters fulfills well the consecutive-one's property while some other character states seem quite random. In order to find out which characters carry most information, one may compute to what extent all 1 are consecutive. A measure of the deviation to a perfect outer planar network is given by the so-called contradiction[21] taking a value between 0 and 1 (for a perfect outer planar network the contradiction is zero). Computed on a single binary character, the contradiction is zero if the circular consecutive-ones' property is fulfilled on the circular order. This study uses a contradiction C of the form

$$C_i = (|S(n) - S(1)| - 2 + \sum_{j=1}^{n-1} |S(j+1) - S(j)|) / \sum_{j=1}^{n} S(j))$$

with C_i the contradiction taking values between zero (perfect outer planar network and one) on the ith character and *S(j)* the taxon state at position j on the circular order.

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[20] Huson and Bryant, 2006.
[21] Thuillard, 2007; Thuillard and Fraix-Burnet, 2009, 2015.

Analysis of the Correlations between Characters

The Cosmic Hunt is described as motif F59.2. 'Pursuit of game leads to upper world' in the Motif-index of folk-literature[22]. More specifically, this is a tale where « certain stars and constellations are interpreted as hunters, their dogs, and game animals, killed or pursued.[23]]» An illustrative example is this very short version recorded among the Smith Sound's Inuit:

> «A number of dogs were pursuing a bear on the ice. The bear gradually rose up into the air, as did the dogs, until they reached the sky. Then they were turned into stars. The bear became a larger star in the center of a group. The constellation (the Pleiades) is called nanuq, 'bear'»[24].

The different versions of this motif are mainly located in Eurasia and North America, where it was linked with, but by no means limited to the bear.

The association between the Cosmic Hunt and the bear both in Europe and North America has been puzzling for a long time. G. Bancroft already wrote in 1888 that «It is a curious coincidence, that among the Algonquins of the Atlantic and of the Mississippi, alike among the Narragansetts and the Illinois, the North Star was called the Bear.[25]» Stansbury Hagar wrote: «this legend of the celestial bear, whose seasonal position eternally corresponds with the features of the legend (...) was general from the Point Barrow Eskimo on the north, to the Pueblo on the south, and, singular as it is that these stars should have been associated with the same animal in the Old World and the New before the time of the first-known inter-communication…there seems little doubt of the fact that this interpretation was common to both continents.[26]» He was not the only one to remark this coincidence. And in 1929, William Tyler Olcott noted that, in the context of North American mythology, «by no stretch of the imagination can the figure of a bear be traced out of the stars in this region, and it is one of the great mysteries as to how the constellation came to be so named.[27]» The presence of the Cosmic Hunt on both sides of the Bering Strait and the parallel between certain Eurasian and Amerindian versions to the tiniest detail suggest a deep historical connection, that could be Paleolithic in origin[28].

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22. Thompson, 1989.
23. Berezkin, 2005a.
24. Kroeber, 1899.
25. Bancroft, 1888.
26. Hagar, 1900.
27. Olcott, 1929.
28. Berezkin 2005a, 2012.

The widespread diffusion of the Cosmic Hunt makes its study very interesting. Specific details among the Cosmic Hunt versions, such as the association of the hunter's arrow (or its point) with one of the celestial objects above the Orion's Belt, or the association of Alcor, a weak star in the handle of the Big Dipper, with a dog or a cooking pot, is too specific to have emerged independently in Asia and in America and points toward historic links between the versions. The motif was first examined by Yuri Berezkin by using an areological approach[29]: the diffusion of each variant allowed conclusions to be drawn concerning the past evolution of the motif. The Russian scholar concluded that the motif emerged in Central Asia; the Orion Belt was seen as three ungulate animals. This variant may have been brought into America more or less at the same time as the motif of Ursa Major identified with seven men (according to Berezkin, the primacy of this variant would be proved by its deeper implantation into inner Asia and inner America). Then a new variant of the Cosmic Hunt interpreting Ursa Major as a bear or an ungulate would have emerged first in Eurasia and then brought into America. Around the end of the Pleistocene times, this version could have been mainly widespread in Western Eurasia, only reaching Northeast Asia shortly before 5000–6000 B.P. borrowed and brought into America by the ancestors of the Eskaleut-speaking peoples.

More recently, one of us had the idea of using phylogenetic tools to analyze the same motif[30]. The results of the statistical analysis of three different databases suggested an East Asian origin of the tale, in which the Big Dipper could have been first considered as an ungulate pursued by a hunter, such a variant having been disseminated, more or less altered, in North America at the end of the Paleolithic period. The results also suggested that a variant connecting the Cosmic Hunt, Orion and the Pleiades probably began to spread later from Asia; and also, that these new variants were brought from Beringia into America spreading as far as South America and reaching the northern extremes of North America.

Berezkin's and d'Huy's models are necessarily based on simplifying assumptions. They require further refinements and tests to improve their effectiveness or to be refuted. It is why we reactivate these researches on a new foundation.

In the current paper, mythologies from 1347 populations from all over the world were examined in order to build a database with the largest possible number of Cosmic Hunt versions: 176 versions were found, from Africa (27),

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[29] Berezkin 2005a, b, 2012.

[30] d'Huy 2012b, 2013b, 2016.

North-America (67), South and Meso-America (36), Eurasia (40), Oceania (6). Each version was analyzed by using the concepts of “motifemes” and “allomotifs” introduced by A. Dundes in order to identify “empirically observable structural or emic units”[31]. For example, “All members of the hunt were transformed into stars” is a “motifeme” where different “motifs” may be used: the game could be a bird or a big mammal, and then an herbivore or a carnivore, etc. Then there can be one prey, or two, or three… and one hunter or more, the latter being a human or an animal. By comparing the different versions, one can identify a number of such “allomotifs” (All ‘allomotifs’ were treated as binary characters.). In our database, 206 allomotifs were identified by this method, and coded on a presence/absence/uncertainty basis (i.e.: 1/0/0.5).

The distribution of allomotifs (considered here as “characters”) in the Cosmic Hunt provides already many clues on how myths may evolve. Figure 4 shows a heat map representing the simultaneous occurrence of two characters after ordering the different characters.

One observes in Fig.4-6 three main types of characters:

- Characters, such as Orion or Carnivore or Ungulate, that have a high co-occurrence with a large number of other characters. Most characters defining the main splits in the tree (or outer planar network) belong to this category
- Clusters of characters in which almost all possible pairs of characters appear within the cluster. These characters define modules of interchangeable characters. Upon further examination, these characters are generally grouped in the same region of an outer planar network. From the evolutionary perspective, evolution seems to operate on the module. Within a module, characters seem to evolve so rapidly that the phylogenetical signal is lost. A notable exception are the European myth versions that can be described as a tree with 3 branches when the different clusters of characters are treated as single characters (Fig. 5).
- Characters that are quite rare. These characters are often associated to a small number of versions in a similar cultural environment.
- Characters that are not correlated in any particular manner to other characters. Such characters are mainly not informative in the context of a phylogenetical analysis and can safely be removed.

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[31] Dundes, 1962.

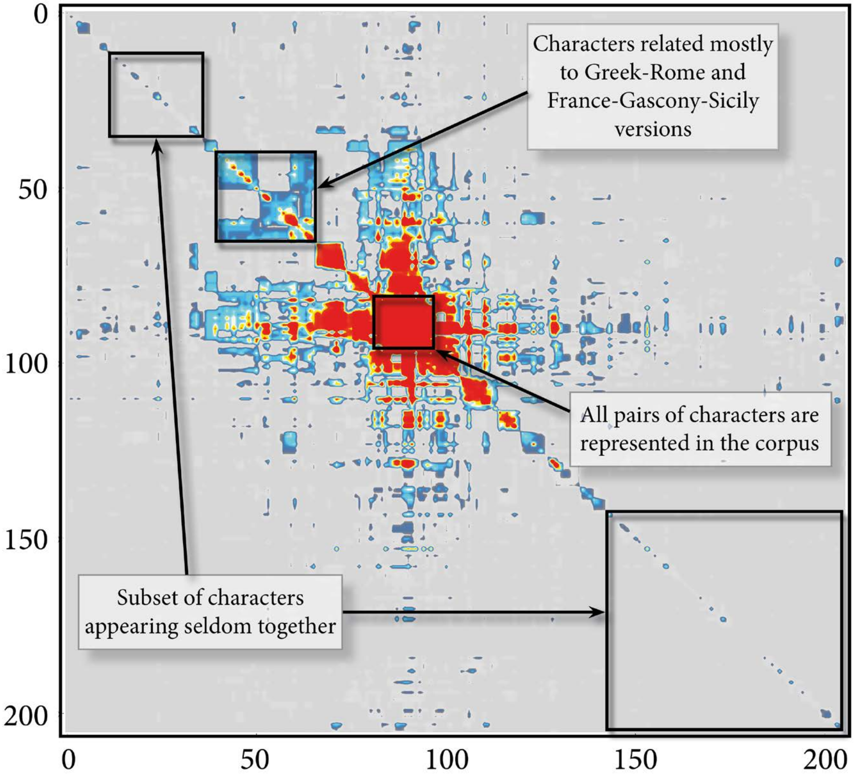

Figure 4.

Heat map representing the number of simultaneous occurrences of two characters (red: high number; grey: low number). The number represent the 206 characters after ordering with NeighborNet. The algorithm used to generate the heat map has 3 different steps. In step 1, a distance $D_{i,j}$ *is computed for each pair of characters (i , j). The distance is obtained by computing first the number of co-occurrences of state 1. In step 2, the characters are ordered by applying a NeighborNet approach*[32] *on the 206 x 206 distance matrix (-D) with each entry corresponding to one of the 206 characters. In step 3, the number of occurrences of pairs of characters with both state '1' is computed and represented using a heat map based on the order of the characters found in step 2.*

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[32] Bryant and Moulton, 2002; Thuillard, 2007.

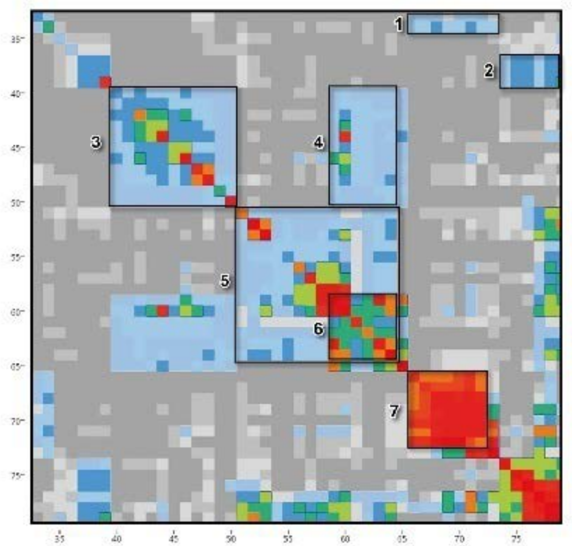

Figure 5.

Enlargement of part of Fig.4, focused on characters specific to ancient Greece-Rome and France-Gascony, Basque, Sicily. The situation is typical of a 3 branches tree relating the two clusters (Ancient Rome, -Greece) and (France-Gascony, Basque, Sicily).

1. Pursuer=Sirius is related to Orion (7).

2. Circumpolar regions: 'Game has six legs' and 'Milky way = pursuer' track'

3-5. Characters specifics to versions found in France-Gascony, Basque, Sicily and in ancient Greece, Rome, share a number of characters (6) but have also two subsets of specifics characters (3: France-Gascony, Basque, Sicily; 5 without 6: Ancient Greece, Rome).

3. Populations having domestic animals and possibly involved in cattle raids

4. Populations having domestic animals (3) and 'pursuer wants revenge' (8)

5. Divinity and sexual taboo

Some characters are correlated for obvious reasons, as for instance the characters Game=Herbivore and Game=Ungulate. Some correlations are quite informative. The hunt of a carnivore is always associated to at least 3 hunters (Fig. 6), while the number of hunters varies when the game is an herbivore!

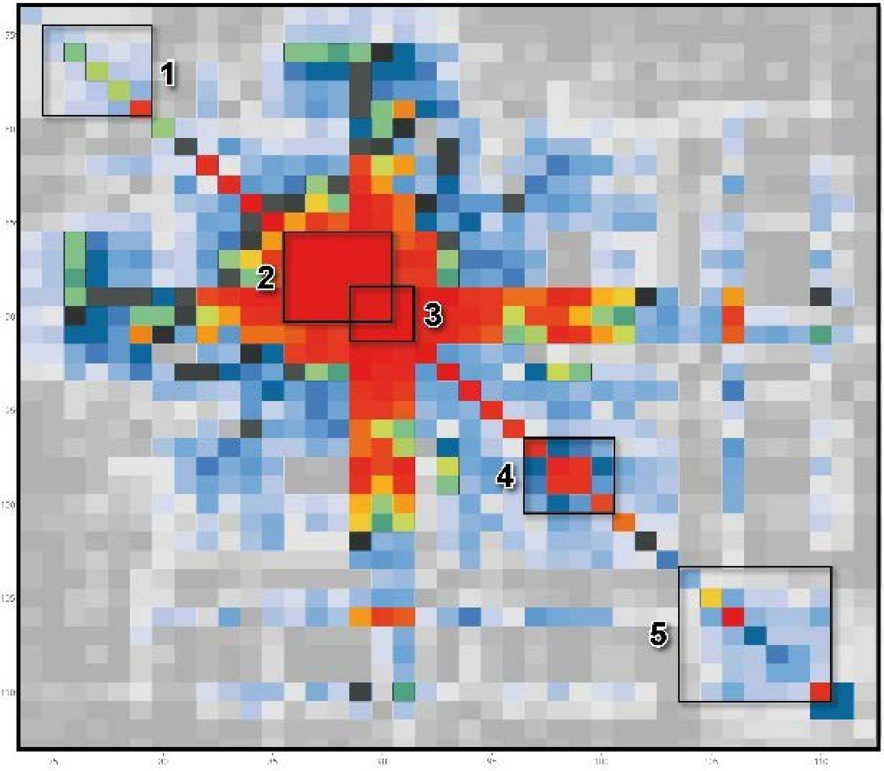

Figure 6.
Enlargement of part of Fig.4 that shows some interesting correlations.
1. Circumpolar regions. Correlation between 'Milky way = pursuer' track' and (2), (3).
2. 'Game = ungulate'. 'Persuer(s) = man or men'
3. 'Nb of prey = 1'

Phylogenetic Classification of Myth Versions

Figure 7 shows the outer planar network obtained after iterative application of NeighborNet[33]. The distance between 2 taxa is obtained by summing over all characters the differences in state value. The algorithm starts with all characters. At each iteration, the characters with a relative contradiction value[34] below a given

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[33] Bryant and Moulton, 2002.

[34] Thuillard, 2007; Thuillard and Fraix-Burnet, 2009

threshold are selected. The threshold is lowered at each iteration thus eliminating more characters at each iteration. With this approach, one selects characters that are well described by an outer planar network or a tree and eliminates non-informative characters.

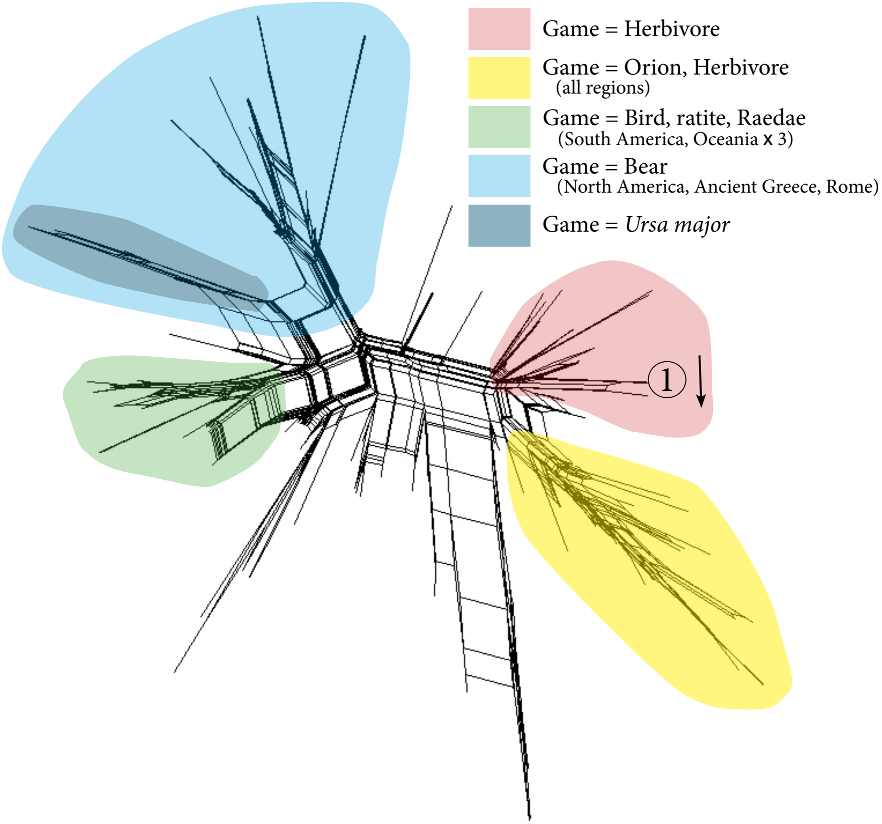

Figure 7.

Figure 7 shows the character states on all taxa and characters using the circular order of the taxa on the x-axis and the different characters on the y-axis after clustering the characters using NeighborNet in the character space. The position of the first taxa is indicated by a '1' and the one uses a clockwise (arrow) circular order (Taxa list in annex).

One observes that the resulting outer planar network can be approximated as a phylogenetic tree with 4 main branches. One branch groups North

American versions of the myth with the main defining character Game=Ursa Major often together with Game=Bear while a second branch contains mostly South American versions in connection to a ratite or another bird and/or Game=Southern Cross. A third cluster contains myths versions involving mostly Orion and the character Game=Herbivore. The last cluster is characterized by Game=Herbivore. In summary, one observes 4 main clusters together with some clusters in the intermediary region between the main splits, that are more difficult to precisely characterize. The main splits define a tree to a good level of approximation (The 4-gamete rules are fulfilled by the characters defining the main splits).

One finds out that actually a small number of characters defines alone the main splits in the tree. Restricted to the character Game=Ursa Major, one observes a very good correlation between the different continents and the order of the taxa on the outer planar network. The correlation is less marked for Game=Orion.

The interpretation of the results is not quite straightforward. Let us give some examples showing the difficulties. One observes 2 clusters within North America in relation to the presence or absence of Ursa Major=Game. In the absence of a model, one cannot interpret the split between the two subsets of characters as it may as well be the result of a single appearance of a character or the result of stochastic events leading to the loss of a character. More information is necessary to decide between the two interpretations. Similarly, one would like to find out how the transformation between the Game=Ursa Major and the Game=Orion versions of the myths did happen. The connection between the two versions is done by the character Game=Herbivore. From the point of view of a phylogenetical description, having a split described by a single character is perfectly fine. Nevertheless, one would be interested in finding elements indicating how the transition did took place. Let us discuss 2 possible mechanisms of transition (known in genetics) that would also favor a complete transformation of the myth keeping only a few of its characters.

- Following the thought of Eldredge and Gould[35], evolution may proceed rapidly during short periods following a dramatic destruction of a large part of the taxa leaving possibilities for species surviving the extension and adapted to the new eco-system to strive. Such evolution may be transferred to the study of myths[36]. For instance, let us imagine some populations, possibly on some strong evolutionary pressure, in which simplified versions of a myth do survive. At this stage the myth may revitalize for some reasons and becomes

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[35] Gould, 1972.

[36] Sydow, 1934; Lévi-Strauss, 1974; d'Huy, 2013b, c.

what C. von Sydow calls an ecotype[37]. The hypothesis is plausible to explain the transition from the main characters Ursa Major and Herbivore to Ursa Major and Carnivore during the passage to America of a small migrating population.

- In biology, the creation of a new gene may occur through gene duplication. After gene doubling, the main biological function is often fulfilled by one copy of the gene, while the second gene is free to evolve. If at one point the new gene brings an evolutionary benefit compared to having both active genes, then the first gene may get lost. The creation of different versions of (co-evolving) myths may be viewed as the non-biological equivalent of gene duplication. Evolution through the co-evolution of several myths may be a strong hint for cultural interaction. Such instances are possibly found among Saami versions (Game= Bear and Game= Deer). In the case of a single remaining version, the remaining myth may combine elements of both versions. According to von Sydow[38], one observes a certain unification of the variants within one and the same linguistic or cultural area on account of isolation from other areas. There are 2 versions having both Orion and Ursa Major simultaneously as characters (Evenk-Tungus and Tlingit). Could the myth have its origin in the region extending from Eastern Siberia to Alaska? Or is it simply a region in which interactions between myth versions took place?

Figure 8 shows the character states on all taxa and characters using the circular order of the taxa of the phylogenetic network (Fig.7) on the x-axis. The different characters on the y-axis are obtained after applying NeighborNet in the character space. One observes that 10 clusters explain most of the classification, each cluster of characters forming a module. Let us mention that taxa in one cluster may not have all characters realized (i.e. state 1).

<u>Cluster 1</u> contains among others the characters: Game= ox or cow, Game= domestic animal, stolen animal, Game=Human beings, Number of prey=2. One may infer that this group is related to populations having domestic animals and possibly involved in cattle raids, an important motif in Indo-European mythology.

<u>Cluster 2</u> contains among others the characters: Game = Deer, Bighorn, Antelope, Nb. of prey=3 and characters related to Orion: 'Game= Orion', 'Three animals form Orion belt', 'visible bow/arrow/spear'. One may infer that the second group of characters corresponds to hunting of animals with horns in relation with Orion.

<u>Cluster 3</u> contains a significant number of taxa with the characters Game has 6 legs and/or Game=Elk, moose and/or Pursuers on Skis

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[37] Sydow, 1934.

[38] Sydow, 1934.

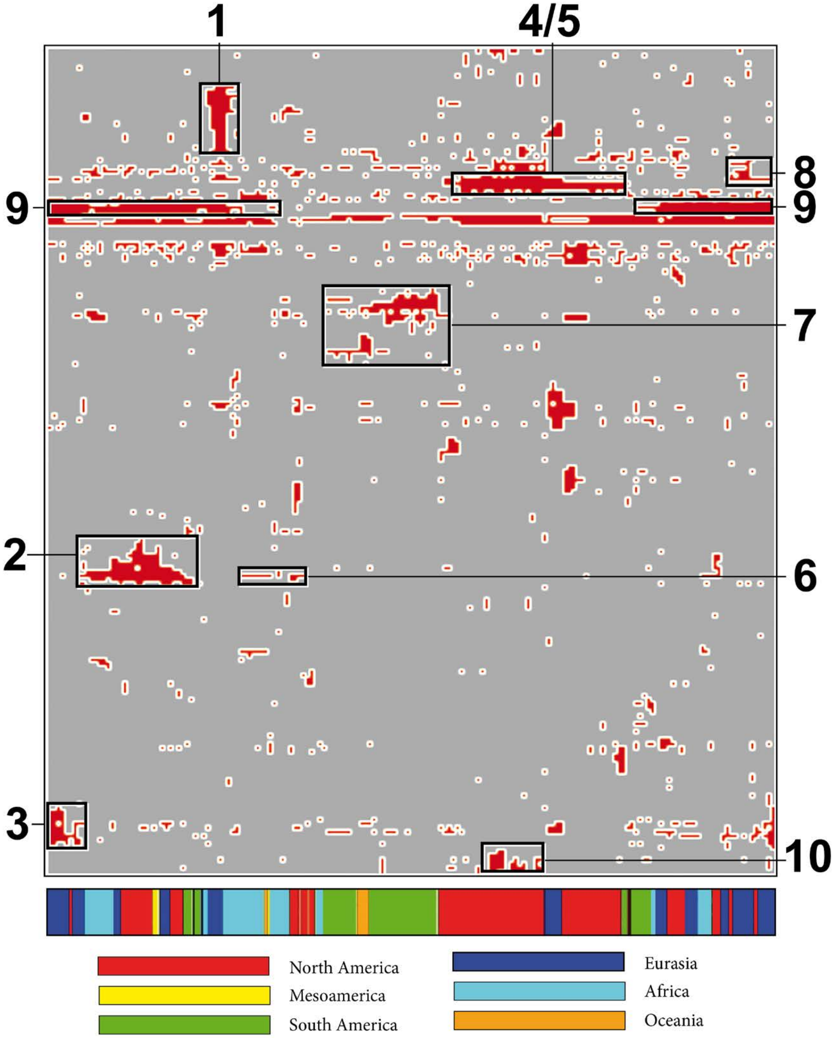
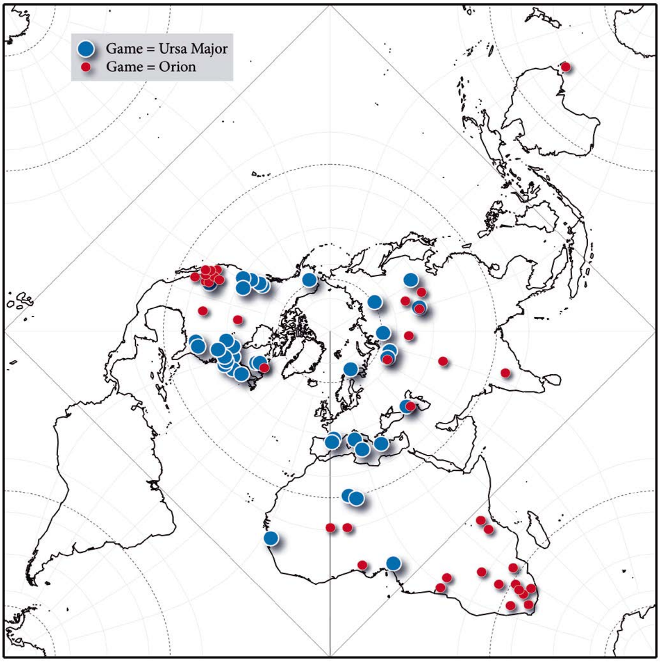


Figure 8.
Plots of all character states on the 206 characters after ordering on both the x and y-axis with NeighborNet. The main clusters of characters are described in the text. (Red=state 1, grey: state 0). The color coding at the bottom indicates the continents.

<ins>Cluster 4</ins> corresponds to Game=Ursa Major
<ins>Cluster 5</ins> corresponds to Game=Bear


● Game = Ursa Major
● Game = Orion

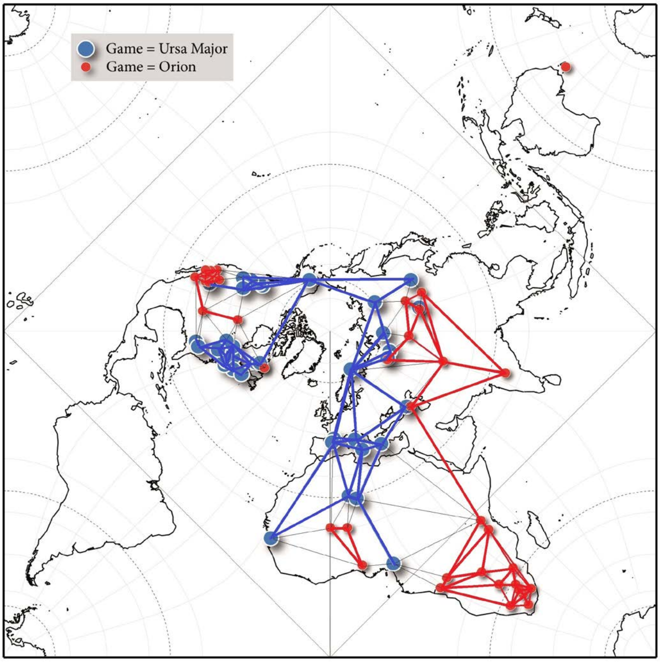

● Game = Ursa Major
● Game = Orion

Figure 9.

a) Locations of the occurrences of the Game=Orion and Game=Ursa Major versions of the Cosmic Hunt. For visibility at a worldwide level, some geographically close versions are sharing the same coordinates. b) Same map after triangulation between the different locations followed by the removal of the single edges (thin lines) connecting two points of different colors.

Cluster 6 contains Game=Orion in connection to Game=Herbivore

Cluster 7 is related to populations at lower latitudes, Game = Southern Cross and animals, encountered in South America and Oceania. Game = Rhea, Game = Ratite

Cluster 8 is a second cluster related to Game=Ursa Major in connection to Game=Herbivore

Cluster 9 contains Game=Herbivore, Game= Ungulate

Cluster 10 contains characters related to the Northern hemisphere, Corona Borealis, hunt and the changing seasons: Animal alternatively alive and dead in sky, Hunt has cosmic consequences (seasons, etc.).

Finding Greek, Roman and North American myths in the same cluster is a surprising result. Examining the character states appearing at least 10 times in the North American myths, one finds out that Greek, Roman and North American myths have in common the characters: 'Game=Bear, big mammal, Ursa Major', 'Number of prey=1' that are over-proportionally represented in North America compared to the rest of the taxa. Removing these characters shifts the Greek-Roman myths outside of North America. Accordingly, in previous databases, Greek and West European versions did not cluster systematically with North Amerindian versions[39]. Also, one observes in Fig. 5 that a number of quite rare characters is shared by the taxa Sicily, France-Gascony, Basque and the Classical Greek and Roman versions. Some characters are quite specific to the Sicily, France-Gascony, Basque cluster while some other characters are more specific to the Classical Greek and Roman versions.

The geographic repartition of the main versions of several myths have often been shown to furnish important hints on their possible chronology[40]. In the cosmic hunt, the version with Game=Orion has a very broad repartition including Oceania, Africa, Eurasia, North America, while the version with Game=Ursa Major is not well represented in Africa, nor in the south of Eurasia. Figure 9a shows the worldwide repartition of the different versions. One observes an overlap of the Orion and Ursa Major version in several regions. Curiously, no Game=Orion

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[39] d'Huy 2012b, 2016.

[40] Berezkin, 2005a, 2013; Witzel, 2012; Le Quellec, 2014, 2015.

version is found in Europe despite the fact that Orion the Hunter is well known in Greek mythology. From the repartition of the two versions, it is quite difficult to deduce a chronology. Quite surprisingly, Orion always appears in conjunction to an ungulate also in North America despite the fact that Game=Ursa Major is in a large majority of cases associated to Game=Bear.

Fig. 9b shows the results of a point triangulation on all points corresponding to the different locations, followed by the removal of the single edges connecting two points of different colors. The red triangulation corresponds to Game=Orion versions. The blue triangulation corresponds to Game=Ursa Major versions. One observes that there is an uninterrupted triangulation of the Game=Ursa Major versions between Africa and North America, which is not the case for the Game=Orion version. The continuity of the Game=Ursa Major version on both sides of the Bering's strait suggests that the passage into America of the Game=Ursa Major version of the Cosmic Hunt myth may be posterior to the Game=Orion version, the Game=Ursa Major versions replacing locally some of the prior versions but let us note that more complex alternative models may explain the observations in the scenario of the prior passage into America of the Game= Ursa Major version.

Discussion: correlation between location of myths and phylogenies

Figure 5 shows a good correlation between the location (continents) and the circular order of the taxa in the phylogenetic network. In this section, simple migration models are introduced to understand the relations between phylogenetic representations and migratory paths. The first model assumes that any migration path is followed only once and that a new character appears only once. In other words, the model assumes that the different myth's versions can be represented by a phylogenetic tree.

Figure 10A gives an example in which migratory paths do not cross. If the evolution of myths is only through mutations, then the perfect tree representing the different myths versions has a planar representation with a circular order that is compatible to the circular order of the migration tree. The line, connecting adjacent taxa on the circular order, forms a single loop. This result is quite general and not limited to the details in Fig.10. Let us mention here that if a migration path splits at some node without any change in the myth or if on a path several mutations occur then the result still holds. Figure 10B shows an example in which the migration paths do cross. In such a situation, there is a perfect tree describing the different versions, but the circular order of the taxa may not be consistent with the migratory tree.

Figure 10 models a situation with 2 migration waves. Let us recall that Fig. 5 shows a good correlation between the circular order and the geographic position in the two subsets of taxa associated with either the character Game=Orion or Game=Big Dipper.

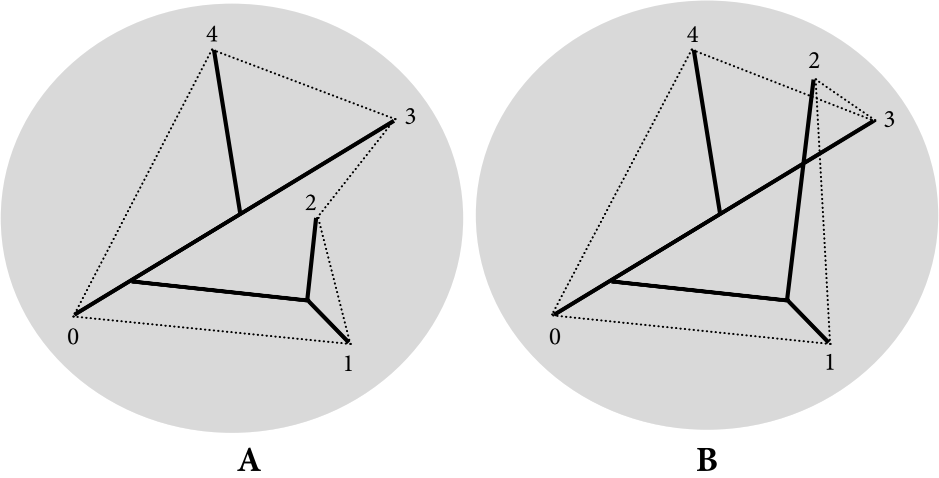

Figure 10.

A) Migration paths are not crossing. The phylogenetic tree describing the different myth's versions has the same circular order as the migration tree. The line connecting adjacent taxa in a circular order forms a single loop; B) The migratory paths intersect at some point. If one assumes no interaction at the intersection, then the evolution of the myth is described by a tree. Geographically far-away regions may be adjacent on a circular order corresponding to the phylogenetic tree.

The model in Figure 11 may explain the long evolutionary distance between some Orion and Ursa Major versions despite the geographic closeness of these versions (Fig.9). The regions (Eurasia, North America) associated to the taxa adjacent to the Orion cluster are the most probable regions in which the split took place (The procedure in Fig.7-8 was repeated on the taxa containing states related to Orion and Ursa Major. The root of the Orion branch is within Eurasia and North America).

Let us repeat the discussion to the case in which cultural interactions generate new versions of a myth. Figure 12 presents a simple model of an interaction described by a lateral transfer between 2 myth's versions (section 2).

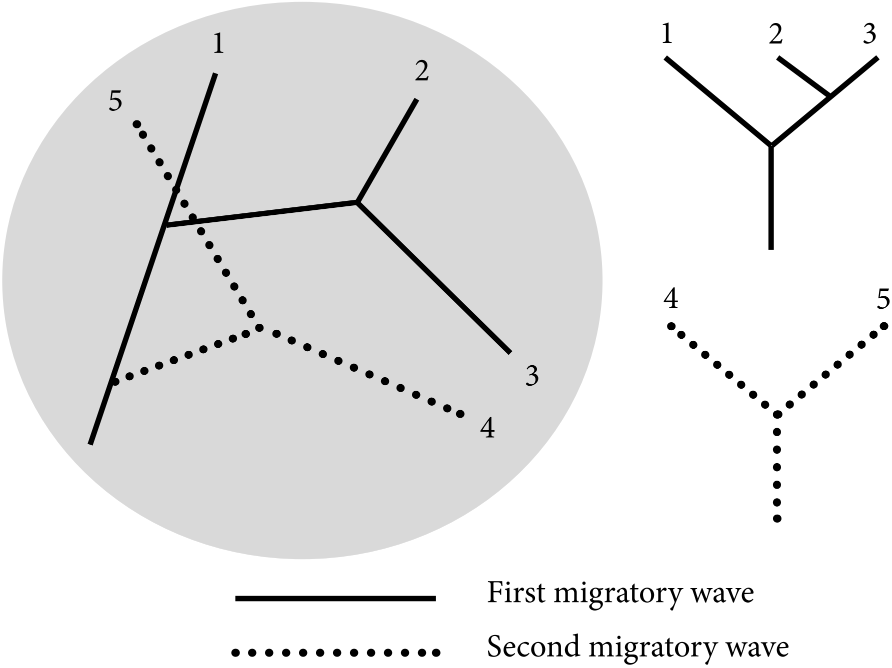

Figure 11.
Model of Fig.9A in case of two migratory waves.

The character states of the new version (labelled as 3 in Fig.12) have the character state of one of the two taxa involved in the lateral transfer (labelled as 2 and 4). With this definition of lateral transfer, the mathematics behind the treatment of a lateral transfer is the same as in classical phylogenetic studies (section 2). Fig. 12 illustrates the result that if the migratory paths do not intersect and lateral transfers are between adjacent nodes then the different (coded) versions are exactly described by an outer planar order.

The above models represent well the evolution of myths through migration, but what about evolution through diffusion[41]? Obviously, diffusion and complex transformations may play an important role, but the goal of the simple models is to discuss the relationships between geographical proximity, phylogenetic trees and outer planar networks. The question of diffusion versus migration has been extensively discussed in the context of gene evolution for instance by Cavalli-

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[41] Propp, 2009.

Sforza[42]. The interaction in Fig.12 could also be the outcome of diffusion of the myth versions from the locations labelled as 2 and 4 followed by the interaction through a mechanism that can be described as a lateral transfer in the space of coded myths at location 3.

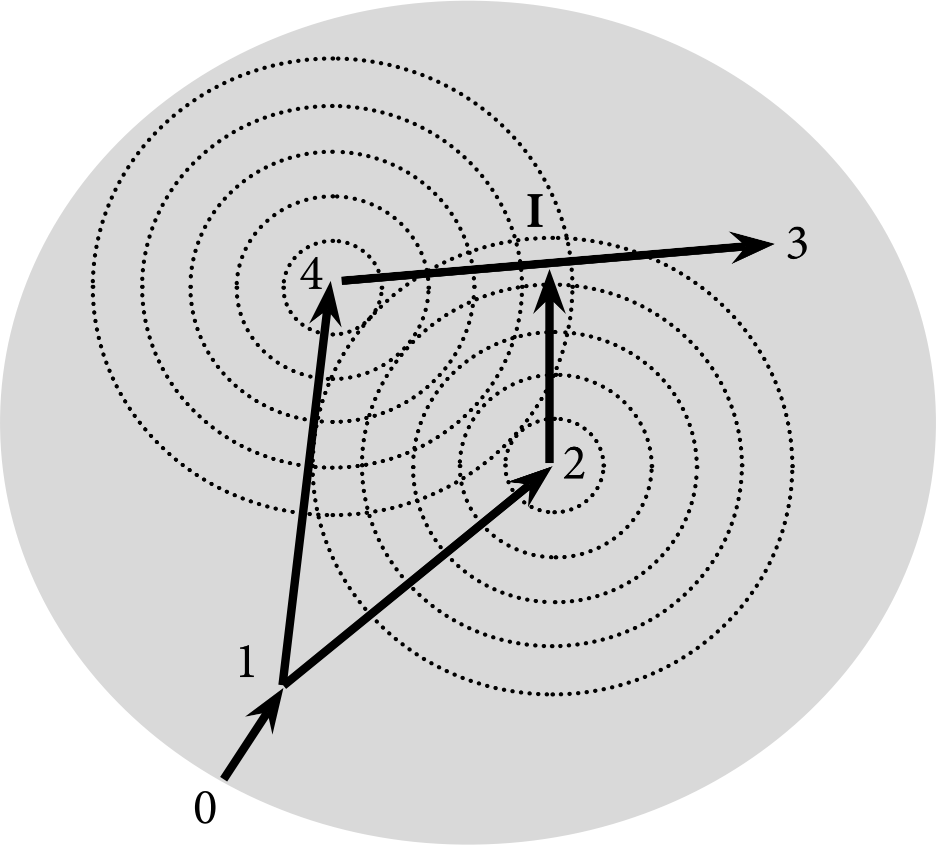

Figure 12.
Migration paths are not crossing. The phylogenetic network describing the different myth's versions has the same circular order as the migration tree. The arrows show the direction of migration. Let us note that this figure may describe evolution through migration and/or diffusion. (The graph may describe the diffusion, symbolized with circles, of two versions from the geographic position of the taxa 2 and 4 followed by an interaction at the node I, in the form of a lateral transfer, resulting into the taxon 3).

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[42] Cavalli-Sforza, Menozzi and Piazza, 1994.

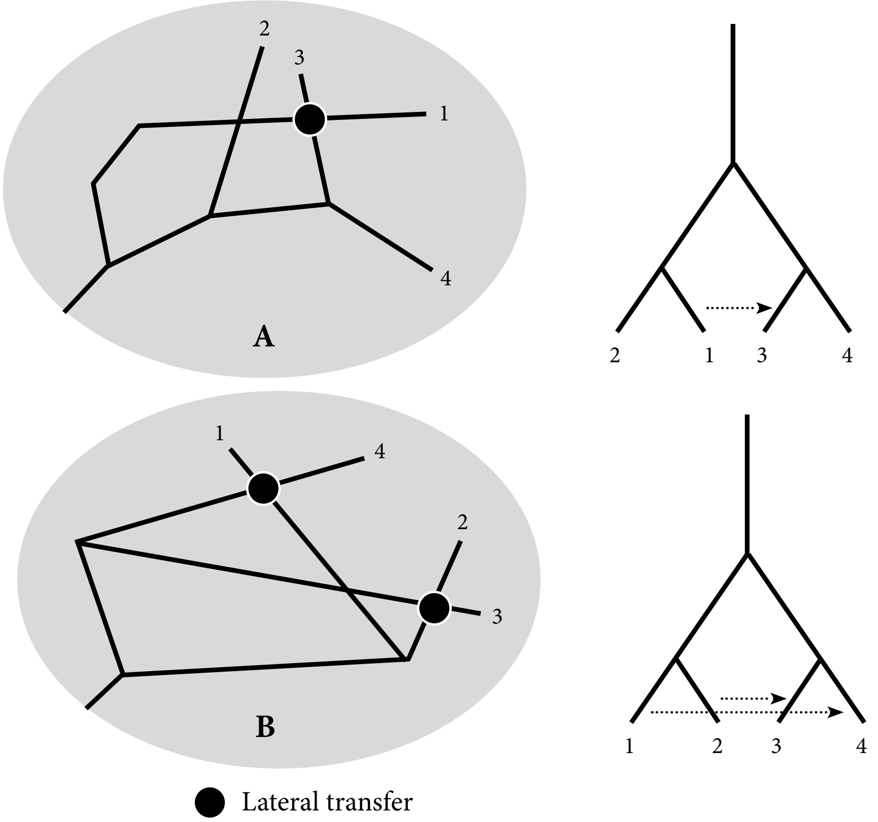

Figure 13.
Examples of evolution following migration paths together with some local interaction in the form of lateral transfers leading to A) an outer planar network structure; B) an outer planar network with some contradictions. Solid points indicate the geographical position of a lateral transfer event and the arrow shows the lateral transfer in the tree representation.

Figure 13 sketches the situation in which two versions interact locally. Let us assume that the interaction can be described as a lateral transfer meaning so that after coding the character states of the new version have the character state of one of the two taxa involved in the lateral transfer. As observed by many researchers[43] and explained by one of us, phylogenetic trees are quite robust against lateral transfers[44].

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[43] Doolittle, 2000; Greenhill, Curie and Gray, 2009.

[44] Thuillard, 2009; Thuillard and Fraix-Burnet, 2015.

Figure 13A shows an interaction along a migratory path. The interaction can be described after coding as a lateral transfer between consecutive taxa on a circular order. The different versions can be described by a perfect phylogenetic network. The geographic proximity is not preserved on the circular order of the taxa except in some special cases that we will not discuss here. The model may explain an instance in which the relation between taxa is perfectly represented by an outer planar network while geographic proximity is not fulfilled.

In the situation of Fig 13B, no phylogenetic tree or network does generally describe exactly the data.

A probable lateral transfer can be observed in a Snohomish version of the Cosmic Hunt. The cosmic hunt version includes the motif pushing the sky (i.e.: people decide to push the sky up because it is too low and they are always hitting their head against it). One observes that this Snohomish myth is classified within Eurasian myths. Is it a consequence of the lateral transfer event (or some other interaction) or a numerical artefact? Does it correspond to an independent migration in North America from Eurasia? Is it the remain of the first diffusion of the myth in the New World, placing this version in an intermediate point between Eurasia and America? Using the methods in[45] (adapted to the special case of binary characters) one finds that the lateral transfer event is most probably between the taxon 'Snohomish' and the cluster 'France-Gascony', 'Basque' and 'Sicily'. Considering the large Basque community on the west coast of North America, it suggests a recent interaction between the Snohomish and the Basque version (A large Basque population lives on the west coast of the US).

Figure 14 can be used to discuss the different hypotheses on the correlation between ancient migratory paths and the phylogenetic representation of the different characters. Recalling the discussion of Fig.10, there are obvious deviations to the perfect situation with a single loop (or two loops if one considers Orion and Ursa Major separately). Nevertheless, a quite good correlation is observed between the mains groups of lines and accepted migration paths over the Bering Strait and also between some hypothesized ones. New results suggest that there has been recent gene flow between some Native Americans from both North and mainly South America and groups related to East Asians and Australo-Melanesian[46]. The main support to this hypothesis given by the analysis of the Cosmic Hunt is the presence of the characters Game=bird, Game=ratite and Pursuer=Centaurus in both South America and Oceania, but the presence of both characters might also be the result of convergence caused by similar

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[45] . Thuillard and Moulton, 2011.

[46] Raghavan *et al.*, 2015.

environmental and latitudinal situations (Pursuer=Centaurus is also a character found in Africa).

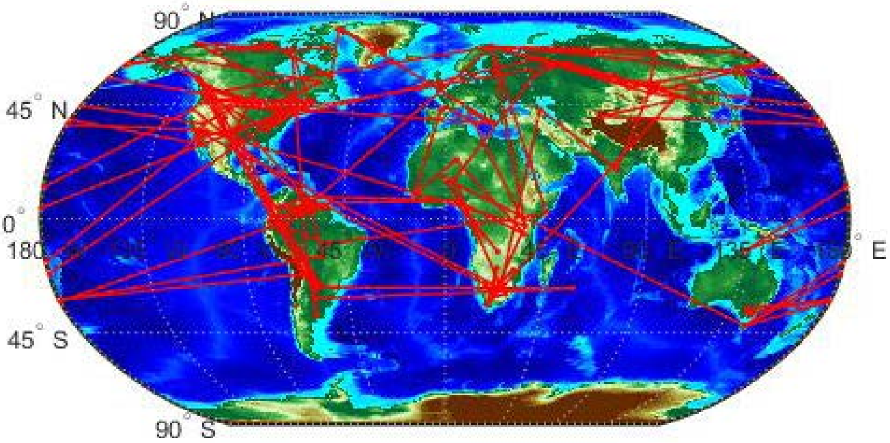

Figure 14.
Using the circular order in Fig.7, the different geographic regions associated to the people in the different versions are represented on the world map with a line relating 2 taxa adjacent in the circular order.

Let us discuss the case of co-evolution between a myth and its geographic position. It's possible to assume that below a given latitude a character changes states (for example because the fauna may be different or a constellation may not be visible at some latitude). Figure 15 sketches such a situation.

Provided the circular consecutive-ones' property is preserved, then a perfect phylogenetic network can describe exactly the evolution. One can show that if the migration tree in Fig.15 is so that the convex hull of the tree crosses only twice the latitude corresponding to the switching of the state, then the circular consecutive-ones' property is preserved[47].

Astronomy is a source of information to discuss whether a possible migratory path is connected to the propagation of the Orion version. Orion is a winter constellation in the northern hemisphere. Precession of the Earth's axis around the north ecliptical pole has a great impact on the visibility of Orion in different epochs, due to its close location to the ecliptic. At the location of the Bering Strait, Orion was invisible for many millennia from around 17 000BC. This precludes an early passage into America of the Orion version through migration after a stop of possibly

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[47] Thuillard and Fraix-Burnet, 2009.

several millennia in Beringia. We can therefore postulate that the simultaneous presence of the Orion versions in both Eurasia and North America is relatively recent. Accordingly, in Africa, Orion is also involved in three quarters of the known versions, and more than half of them include one or several dogs as pursuer(s). As the dog was domesticated in Eurasia around 35.000 YBP and introduced into Africa much later, these versions must be much posterior to the migration of Homo sapiens out of Africa[48]. As Ursa Major has been visible through the ages at those latitudes, it is not possible with the same approach to set bounds to a possible passage of the Ursa Major version to America, which could have happened a long time ago, and possibly during the first settlement of North America.

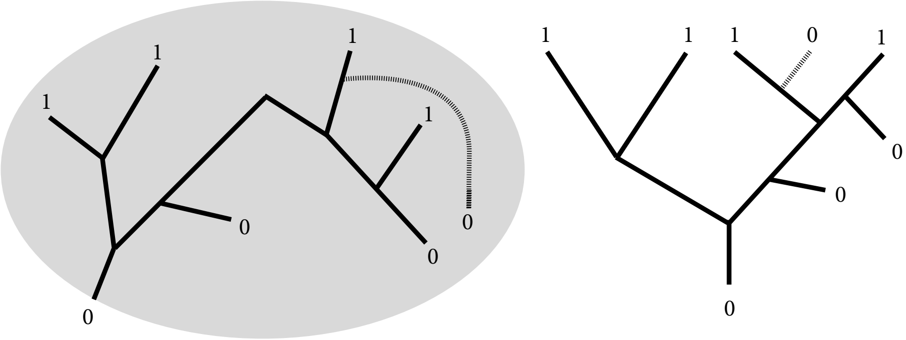

Figure 15.
Example showing a co-evolution between latitude and the state of a character. The tree defined by the solid line fulfills the circular consecutive-ones' property and may be described by an outer planar network while the addition of one edge leads (dashed line) to data that cannot be described exactly neither by a perfect tree nor a perfect outer planar network.

A very difficult question is to determine how and when the Cosmic Hunt first appeared in America. Orion's visibility in Beringia furnishes a limit to the earliest date the Orion's version reached America. A number of versions of the Cosmic Hunt are related to the Pleiades. The 'Game=Pleiades' versions are found in the American continents, associated to 'Game=Carnivore' (a bear pursued by a dog) or 'Game=Herbivore' (a tapir or a caribou pursued by a man/men). A majority of versions are connected to a revenge after an animal is stolen or after a woman has left with a bear. The 'Game=Pleiades' versions in North America have been mostly collected among people (Inuits and Tlingit) believed to have migrated relatively recently. It follows that the 'Game=Ursa Major' version is probably

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[48] Berezkin, 2012.

the only remaining candidate for having reached America at the time of the migration into America. The observation that the Ursa Major and the Pleiades versions contain herbivores and bears as game in both Europa and in America, contrarily to the Orion versions in which the game is very predominantly an herbivore, seems to contradict this last hypothesis. The character 'Game=bear' in both Europa and America may also be a coincidence – the bear being symbolically very important in both areas.

Conclusions

An outer planar network is an appropriate representation of the different versions of a myth in case of cultural interaction. A proper coding of each myth with binary characters is central to this approach. For binary characters, distance-based approaches and character-based approaches are closely related and it is therefore quite legitimate to use NeighborNet to search for the best representation of the data. In this study, a NeighborNet algorithm was used to iteratively select characters well correlated to splits in the outer planar networks. Phylogenetic analyses combined with a detailed study of the most informative characters furnish much more information than the outer planar network alone. The detailed examination of correlations between outer planar networks and characters often significantly restricts the number of plausible explanations on the evolution of the different versions. This study shows the utility to integrate all available information as exemplified with the analysis of Orion visibility at the latitude of the Bering Strait. The precession of the Earth's axis gives ground to refute the hypothesis of an early passage of the Orion versions of the Cosmic Hunt through Beringia.

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