

# Tracing Taxonomic Arcs: A tool for palaeoecologists and environmental educators

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## ABSTRACT

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Palaeobotanical knowledge can, and should, be harnessed for use in environmental education. Environmental education seeks to both share knowledge and promote a sense of ethical responsibility to the landscape. A conceptual tool, the trace arc, is presented here to aid palaeoecologists in illustration of the biological relationship between any two organisms. Linking taxonomy, genealogy, and anatomy, it allows the scientist to illustrate these complex studies in a visual or verbal fashion. It can be used by palaeobotanists and other ecologists to demonstrate the relevance of their researches to the general public, and by environmental educators to define a path of kinship between their students and any other living organism, thereby fostering stewardship and empathy with other organisms.

**Key-words:** Biosphere, education technique, science education, scientific illustration, environmental stewardship

## INTRODUCTION

“Ultimately, there would be only a single tree, incorporating all living things without exception...” (E. C. Pielou 1979).

What do the following pairs have in common? A student and a green praying mantis; A leaf of the world’s largest teak tree, Kannimara, and a schoolteacher; A pet dog, and the coconut bought on the street; and the English Crown Prince Charles and his ancestor Leopold, the deceased Duke of Albany?

The answer is that all are directly, biologically related to each other. In this article, a tool for teaching the links of kinship between any two living things is presented. This tool draws directly on palaeoecological knowledge to trace that connection.

The world is experiencing environmental stresses that are threatening ancient lineages of life as well as the landscapes and ecosystems they inhabit. Environmental education is a cornerstone to all conservation science efforts, not only to encourage

people to protect our natural world, but also to foster a sense of purpose and motivation. However, even faster growth of a land ethic of sustainable coexistence with nature is required (Leopold 1949). Humans are naturally biophilic, attracted to life (Wilson 1984). Furthermore, humans have a strong sense of family responsibility, investing tremendous care in their children and other kin. A tool to foster kinship with other organisms in the Earth’s biosphere would therefore be of use to environmental educators in encouraging people to care about the fate of Earth’s biota.

In this article, one such tool is introduced, the trace arc. Trace arcs are an education concept that combines the scientific disciplines of taxonomy, genealogy, and plant anatomy so as to relate any two living things. These time-linked relationships are understood by, and used regularly by, palaeoecologists. All that is required is a basic starting knowledge of some of the major groupings in biology. The goal of this article is to provide a tool for placement in the “kit” of both palaeoscientists and environmental educators and scientists that is versatile



enough to be used for a wide range of audiences. A secondary goal is to strengthen the fundamental analogy of taxonomy- the relationships of living and extinct organisms- as a branching, tree-like pattern, by linking actual branches and leaves from living trees to the taxonomic tree of life (Pielou 1979).

For educators, taxonomic trace arcs can not only add depth and linkages to lessons, but also to validate the kinship between any organism and the students attending. For the scientist, traces offer a simple tool so as to explain and share the relevance of the ecological sciences to the general public. Finally, the trace serves to graft together the disciplines of taxonomy and forest structural measurement in such a way as to generate a useful conceptual tool.

The purpose of understanding these arcs is to educate students about the interrelation of all life, and their kinship with other organisms. It provides a way to document that relationship, and to connect a seemingly irrelevant organism directly to their own lives.

First, the concept of tracing an arc is introduced. Second, the three levels of taxonomic, genealogic, and anatomic are described with special reference to the transitions between them. Finally, detailed examples are given for the educator to use as a starting point for their own arc tracing. In the text of this article, *italics* are used for taxonomic groupings, individual organisms, or anatomical units.

## CONCEPT

Taxonomic arcs are simply the lineages of biological ancestry and descent that connect two organisms. An arc upward, like a rainbow, has an uppermost point, known as the zenith. Similarly, following evolutionary theory, every two organisms, living or extinct, have a once-existing common ancestor (or ancestral parents). In the “up” portion of the arc, one lists the preceding ancestors of the first organism until the common ancestor is reached. In the “down” portion of the arc, the subsequent descendants are listed until the second organism is reached. It is not necessary that every known stage in taxonomy is addressed. Levels can be skipped: not only would the sequence become cumbersome to recount, but it also unlikely that one will know every

point upon the arc. Common or Latin names can be used, depending on the context and audience.

For example, a student is a *human*, and *green praying mantis* is an insect in the order Mantodea. Going upwards on the arc, a *human* is a *primate*, a *mammal*, a *vertebrate* and an *animal*. Both the praying mantis and the student are *animals*. This is the peak of the arc. Going downwards, the mantis is an *animal*, an *arthropod*, and a member of the *mantid family*. In this arc of kinship between these two animals, several levels were skipped, including, for example, the *placental mammals* in the upwards section and the *insects* in the downwards.

An upward taxonomic trace from humans to the biosphere is described at length as an educational tool by Dawkins (2004) in the book, *The Ancestor's Tale*. In this book, each level of taxonomy above *Homo sapiens* is studied, with an effort to describe the individual ancestor shared by members of that taxonomic grouping, and to explain which other organisms also share this ancestor.

In Hindu, Buddhist, and Jain religious beliefs, all living things are sacred because they are the reincarnations of the soul, and are therefore related to each other. This promotes care and respect for nature- for example, Jain monks will sweep the ground before them and wear screens over their mouths so as to not accidentally kill the insects which may be in their path.

The mechanics of social altruism, or sociobiology, in animals is studied by Wright (1995), Wilson (1975), and Dawkins (1990). These scientists describe the mechanism by which kinship dynamics cause cooperation. The closer that any two social organisms are related, the more they will cooperate. A logical extension of kinship-caused cooperation is that a sense of kinship with all living things will promote cooperation and, hopefully, altruistic preservation of nature.

Several exceptional situations exist in which this tool is not easily usable. In the biological realm, not all reproduction is done by direct descent between individuals. Some bacteria, for example, transfer gene segments laterally, thereby reproducing a portion of themselves without creating a new organism. Inbreeding can confuse the definition of ancestor and descendant.



Clonal reproduction, whether by vegetative growth or by clonal propagation, can create new individuals that are not genetically dissimilar to their direct ancestor. Some organisms, such as slime molds or fungal networks, defy standard definitions of what an organism actually is.

Three phase of arc traces can be defined, from the most general to the most specific: tracing by taxonomic groups, tracing by individual ancestors, and anatomical subunits.

### HIGHEST PHASE- TRACING BY TAXONOMIC GROUPS

The science of studying the relationships of living organisms is called taxonomy. The word taxon comes from the Greek word meaning “a branch.” Linnaeus codified and integrated previous knowledge of taxonomy into one connected “Tree of Life”, and later Darwin and Wallace (1858) described the mechanism by which this diversification of life was formed. A taxon is a group of organisms which share a common ancestor. At its most resolute, a taxon is a *species*, a group of interbreeding or indistinguishable individuals. At broader groupings, a taxon is a grouping of organisms descended from a common ancestor, such as a *genus* or *kingdom*, comprised of multiple species.

Each taxonomic step on the arc refers not to a relationship of direct parental descent, but rather to a series of nested groups of organisms. For example, a *genus* does not give rise to a *species*, but rather conceptually encompasses it.

An upwards taxonomic trace will loosely follow the Linnaean classification system upwards through the steps, finally including the biosphere of all living things:

Species → Genus → Family → Order → Class → Phylum → Kingdom → Biosphere

There are some additional groupings not listed here, such as *infraorders*, *suborders*, *subfamilies*, *botanical tribes*, and *subspecies*. When *humans* are being described, clans, tribes, races and nationalities are roughly equivalent to the *subspecies* grouping. This is often best avoided, as it is both complicated and controversial.

*Homo sapiens* is our *species*. The *genus Homo* is another taxon, encompassing us and our now extinct relatives. The *family Hominidae* includes us and the other great apes. The *order Primates* further includes monkeys and lemurs. *Class Mammalia* also includes all other mammals- dogs, pigs, elephants, mice, and kangaroos. *Phylum Chordata* brings in the other vertebrates- fish, reptiles, and amphibians. *Kingdom Animalia* includes all of the animals- insects, starfish, mollusks, and jellyfish. Finally, the *Biosphere* includes all living things, including the other eukaryotic organisms such as plants and fungi, and even more distantly related protozoa and chemosynthetic bacteria.

Returning to the previous example relating the *human student* to the *green praying mantis*, one can begin tracing up from the student- *Homo sapiens* → *Homo* → *Hominidae* → *Mammalia* → *Chordata* → *Animalia*. At the level of the Kingdom, *Animalia*, a taxonomic grouping has been reached which includes both the human student and the mantis in questions. Tracing downward to the mantis yields *Kingdom Animalia* → *Phylum Arthropoda* (spiders, insects, crabs, centipedes, shrimp) → *Class Insecta* (six-legged insects) → *Order Mantodea* (mantises). In the absence of taxonomic detail in the field setting about the *family*, *genus*, or *species* of the *green praying mantis*, the arc goes up from *species* to *kingdom*, and then back down to *order*.

The levels of taxonomic grouping for any species are available in an organized fashion on the internet via the Tree of Life project (Maddison & Schulz 2007), or Wikipedia (2010).

### MIDDLE PHASE- TRACING BY INDIVIDUAL ANCESTORS

A genealogical arc traces kinship by referring to a sequence of individual ancestors. Genealogical traces are below the phase of the taxonomic trace. When one refers to an individual ancestor, they are describing a single organism that was or is alive for a discreet period of time. Unlike the taxon steps described above, each step on an arc that refers to an individual ancestor implies a direct parent to child (downward) or child to parent (upward) relationship. The step does not describe a relationship of nested groups.



The vast majority of individual ancestors are deceased and unknown. The taxonomic trace at an individual phase is very difficult to track completely, as it requires a detailed knowledge of lineage that is simply not available. This type of work is the study of genealogy, and is only very rarely applied to non-human organisms. One example in the animal kingdom is the pedigree of stud horses or dogs.

Individual relationships for human ancestries are often recorded as genealogical family trees. It's important to remember that these trees are merely a small twig on an extensive human family tree stretching back to the common ancestors of humanity. The largest documented branch is probably that of *Confucius*' descendants; 2,560 years after the birth of the Chinese philosopher, 2 million people trace their family tree back 80 generations to him (Confucius: Descendants 2010). The use of computer software for managing genealogical trees has made the available information more accessible and organized.

One prominent example is the tracing of relations between the Royal House of England (British Royal Family 2010). For example *Prince Charles*, the current Crown Prince of Britain, is related to *Leopold, the Duke of Albany*, born 1853. How were they related? Following this arc of individual ancestors upwards, *Charles*, born in 1948 is the son of *Queen Elizabeth II*, daughter of *George VI*, son of *George V*, son of *Edward VII*, and the son of *Queen Victoria*, at the zenith of the arc. Following the arc downward, her son *Leopold*, born in 1853, is related to *Charles* even though they were born one hundred years apart.

Note that the listing of a generational grouping, i.e. parents, grandparents, or great-grandparents, is not the same as the naming an individual ancestor, i.e. *Mum*, *Grandmum*, or *Great Grandmum*. In the first instance, a trace upward is more like a taxonomic grouping, in that it encompasses more and more individuals (two parents, four grandparents, eight great-grandparents) as it progresses upwards. In the second, a trace upward is a series of single individuals.

Not all individual traces are possible to complete. It can be claimed that any two individuals of the same species are undoubtedly related, by some ancestor. Two

individual *spruce trees* in a forest must certainly be related. But how can these lineages be traced back to their common ancestor? It may only be a few generations back, but it may also be back thousands or millions of years. Even if this zenith organism could be somehow identified, it would not be feasible to provide individual names for all of the *spruce trees* in between. In this case, one must content one's self with merely acknowledging that they are somehow related through many steps of individual ancestors, as are *all living things*.

### COMBINING TAXONOMIC GROUPS AND INDIVIDUAL GENEALOGY

There is a challenge in connecting these two phases: the sequence of genealogical ancestors to the nested groups of the taxonomic trace. Difficulties will be encountered because of the difference in concept, and the lack of information.

First, the conceptual differences between the linear sequence of individual ancestors and the nested groupings of taxonomy must be considered. Following an individual organism's genealogical lineage back into the distant past will eventually come to an ancestor that could no longer be referred to as a member of the same species. The ancestor encountered immediately before is actually the common ancestor to all of that species-level taxon. At this point, the upward trace can shift from a following series of individuals to following the increasing taxonomic groupings.

Second, there is inevitably a lack of information, and a lack of naming ability, in any genealogical trace. As with the spruce trees mentioned earlier, one will not be able to follow one's student's ancestry back through their *Mum-Grandmum-Great Grandmum* to a point where the individual ancestor is the ancestor of all *Homo sapiens*. This level of detail is simply not available.

While the *human student* and the *green praying mantis* are both individuals, it is impossible to completely bridge the gap between individual ancestry and taxonomic groupings. Furthermore, it will be utterly impossible to name or conceive of the lineage of individual ancestor *mantises* leading back to the first *green praying mantis*.



A mention of the countless individual ancestors of the student in question leading back to the first *human* will allow the switch from describing a genealogical trace to a taxonomic trace.

### LOWEST PHASE-ANATOMICAL SUBUNITS

At an even more resolute phase, below genealogical ancestors, are traces based on anatomical branching. This conceptual phase is most useful when describing the anatomy of the higher plants. Anatomical traces consist not of nested groupings, or lineages of organism descent, but lineages of anatomical subunits. This is perfectly illustrated by the classic above-ground branching structure of living tree. Anatomical traces are useful in that they allow the extension of a taxonomic trace to individual branches and flowers.

In essence, though, different cell subunits organisms are related in a lineage of genetic material stretching back to their first identity as an *individual organism*. Every red blood cell in a *human's* body is a descendant of the *original blastula cells*. For sexual *eukaryotes*, like *humans* and *plants*, this generally means all cell division after our parent's gamete cells (sperm and egg), formed via meiosis, met and their union started the process of mitosis.

In a *eukaryotic* organism, this is a lineage of *cell nuclei*. It is impossible to directly identify the sequence of ancestral cells within most organisms, but in higher *plants*, this can be directly observed of as a branching lineage of *buds*. In a complex, non-modular animal like a *human*, these traces are impossible to track back. Generally, anatomic traces at a sub-organism level are only feasible for branching organisms such as plants.

The perfect illustration is found in the branching structure of a *tree*. Assume that in the center of the bottom of the tree trunk are the original cells from the tree *seed*. Every *bud*- whether it sprouts a leaf or flower- is a direct descendant, through several generations of buds branching several times, of those *seed cells*. Furthermore, there is also an unseen branching structure underground in the *roots*.

One can literally, physically, trace back from a *leaf* or *flower bud* to the *trunk* of the *tree*. From that *leaf*,

conceptually follow the physical path inwards to the *trunk* and the *base*. In some plants, many branching points are invisible, as they represent a point within the plant, in a past time. Some are also lost to predation or competition. For educational purposes, though, each branching node can be treated as a new generation.

### COMBINING ANATOMICAL SUBUNIT WITH INDIVIDUAL GENEALOGY

The anatomical subunit, below the individual genealogy on the arc, is equal to the individual at the point of the seed cells. For sexual eukaryotes like us, this is the distinction between meiosis, the combining of parent's DNA to form a new individual, and mitosis, the division of cells within an individual. When referring to a plant, this is known as the seed or a spore, and when referring to a human, this is known as the blastula (fusion of sperm and egg).

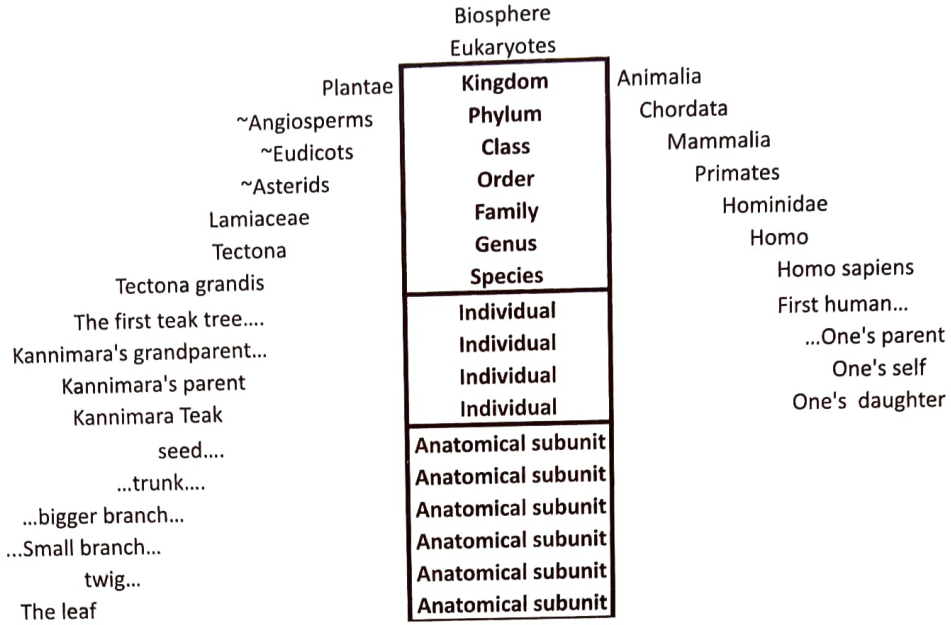
In a plant, to describe the kinship between a leaf and an ancestor, a mention of the original seed is required to bridge the two phases.

### EXAMPLES

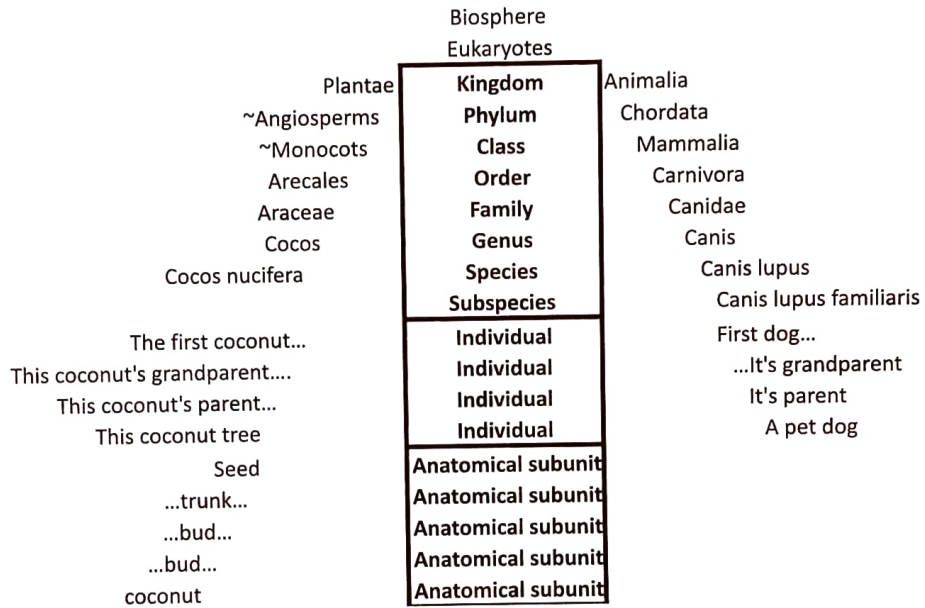
Three examples are presented here, using living organisms. The taxonomic traces for the following pairs are illustrated: *A leaf of the Kanimara Teak* and *a one's daughter*, *a coconut fruit* and *a pet dog*, and between *one's self* and *penguins* (Text-figures 1-2)

Each arc begins in the lower left, and moves up and rightwards to the zenith, then down and rightwards to the end. Note the transitions on the arc between anatomical subunits and individuals, and between individuals and taxonomic groups. Above the topmost point of the arc, *Biosphere* is included as a reminder that all life on Earth is related, and therefore all trace arcs will be reach their zenith at this level. A tilde, “~”, is used to denote a taxonomic level that is not an official Linnaean classification, and ellipses, “...” are used to denote a series of steps that is not listed (in other words, equivalent to “etcetera”). All taxonomic groupings were taken from the on-line encyclopedia Wikipedia (2010). More formal situations can demand more technical resources such as the internet project The Tree of Life (Maddison & Schulz 2007).

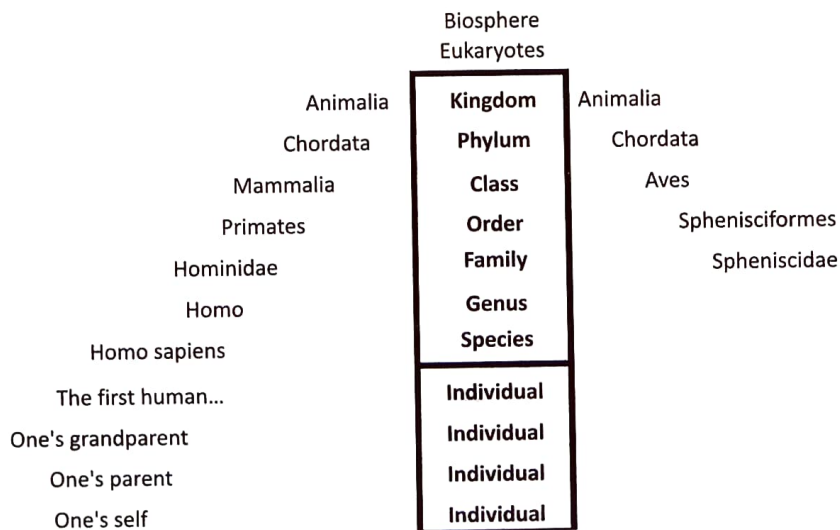
GEOPHYTOLOGY



**Text-figure 1.** A leaf of the Kannimara Teak and one's daughter



**Text-figure 2.** A coconut fruit and a pet dog.



**Text-figure 3.** One's self and penguins.



## ADDITIONAL ELEMENTS

Two additional elements can be added to the trace arcs to add information to the illustration: time, and characteristics.

For each level of a trace arc, the timeframe of its existence can be presented. This is often seen in palaeotaxonomic illustrations. The time can be enumerated either as time elapsed (e.g. millions of years ago) or by calendar timeframes (e.g. 1886-1950 A.D.). Knowing the time frames associated with the divergence, or reproduction, of each taxonomic, genealogic, or anatomic level can add a new dimension to the arc, and can further aid the educator in linking the organisms to astronomical, geological or climatic time scales.

The characteristics that define each taxonomic level can be added to the trace arc. For example, extinct lineages of animals, such as dinosaurs, are formally described by physical characteristics, such as bird-hipped or lizard-hipped. The presence of a new physical characteristic is often what defines the existence Linnean taxonomic level. At a genealogical level, any aspect of the physical shape or life history of the individual can be added. At the anatomic level, the position and eventual fate of an anatomical subunit (such as a branch) can be added to the trace.

These two elements can aid the educator in sharing knowledge about the organisms, but care must be taken not to make the arcs too information-dense and overly unwieldy.

## APPLICATIONS

Using the concept of taxonomic traces, palaeobotanists can demonstrate actual linkages with their study organisms, and thereby use their knowledge of taxonomy to not just show the relevance of palaeoscience, but to also promote enthusiasm and feelings of kinship with the natural world. The arc can be very simple or impossibly complex. For a *student*, merely mentioning that *humans* are related to the *insects* because both are *animals* is making a very simple, yet profoundly true, trace. For more technical disciplines, such as formal taxonomy, attaining enough information to create a complete lineage is the directly pursued goal.

Taxonomic traces can be used for teaching purposes in several situations. A field trip to the forest becomes an intricately complex meeting with relatives of all varieties. Visits to the zoo can become richer by relating each animal to each other, and to the *students* themselves. The fascinating lives of the *Archaea* chemosynthetic bacteria can be linked to the more familiar *plants* and *animals*. Ethical issues, such as medical testing on *primates*, can be gauged in regards to our levels of kinship with these animals. At a genealogical level, the current issues of immigration and disputed ancestral homelands can be assessed with a biological angle. Issues of land management and forest clearance can be made more relevant to the decision-makers by clarifying the levels of kinship involved. Historical and newsworthy events can be directly linked to the lives of the *students* and their *family*. At the junction of taxonomy and genealogy, findings of the earliest human and hominid skeletons can be made more directly relevant to the lives of the students.

## CONCLUSION

The concept of the trace arc is a framework for listing and teaching the direct linkages of kinship between any two living things. It can be utilized at the three phases of the species, individual, or anatomical subunit. It can be made very complicated, or very simple. For biological scientists, trace arcs provide a structure for making their work on other species or other individuals accessible to the general public. For environmental educators, it offers a conceptually robust and flexible tool for promoting biophilia, illustrating kinship, and, hopefully, instilling a sense of responsibility for all other organisms and individuals on Earth.

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