So what is phylogenetics good for?
Phylogenetics is a tool of basic science:
- Identity - where does an odd organism fit on the tree of life? Who are its closest relatives? (Classification)
- Identity - is this group of organisms a natural group? Are they defined by homologous traits? (Classification)
- Identity - is this one, two, or three (etc.) species? (Classification)
- Character evolution - has this trait evolved convergently or only appeared once?
- Anthropology, parasitology, biogeography...

So what is phylogenetics good for?
Phylogenetics can be applied to:
- Conservation: test wood, ivory, meat products for poaching
- Agriculture: find ancestral “source” cultivars
- Forensics: rapid virus evolution can help identify source
- Medicine: determine closest relatives of organism that has anti-cancer compounds
- Epidemiology: Where is the most likely geographic origin of a virus outbreak, like Ebola?

Can answer basic questions
Like... *What is this thing?*
**Tongue worms**
**Pentastomida**
- parasites of vertebrates
- in lungs or nasal passages
- 95 species
- 4 legs + mouth
- annelid-like, odd
Can answer basic questions
Like...Where did humans come from?

Can answer basic questions
Like...Is this one species or three?

Can answer complex questions
Like...Did our domestic animals infect us with tapeworms?

Or these Palaeoanthropological questions:
What prey species did our ancestors feed on?
When did our ancestors start eating animal flesh regularly?
Did our ancestors scavenge food shared by other carnivores?


Parasites can be used as independent markers of human evolution
Phylum Platyhelminthes: Class Cestoda - Tapeworms

- Endoparasites of vertebrates (in gut)
- ~ 3,500 species
- Absence (loss) of digestive tract and mouth
- Absorb nutrients across body wall

Class Cestoda - Tapeworms & people

~ 135 million people with tapeworms
Handful of species infect humans; 4 + genera

3 species of *Taenia* mature only in humans
we are the only definitive (final) host:

- *Taenia saginata* - intermediate host: cattle
- *Taenia solium* - intermediate host: pigs
- *Taenia asiatica* - intermediate host: pigs

Class Cestoda - Tapeworms & people

Dr. Hoberg, curator of the US National Parasite Collection in Beltsville, Maryland,

- studied evolution of these three species.

“How did they become our parasites? Where did they come from?”

Class Cestoda - Tapeworms & people

Traditional hypothesis: *Taenia* spp. “jumped” into humans from cows, pigs etc, ~ 10,000 years ago

Predictions
1. If true, the phylogeny would show the closest relatives of our *Taenia* species to be species that infect cows, pigs, dogs, cats... etc
2. Phylogenetic estimate of divergence dates would be ~ 10,000 years ago

The phylogeny

Hoberg’s results:

Closest relatives of the *Taenia* in humans are *Taenia* in wild African carnivores. **Not domestic spp.**

“Our” tapeworm species 0.78- 1.7 million years old. **Not 10,000 years old.**
(started in *Homo* sp. prior to leaving Africa)

“In short, phylogenetic, geographical, ecological, and molecular-divergence evidence... suggest that *Taenia* became associated with hominids and the genus *Homo* prior to the origin of modern humans in Africa.”

If correct, then we infected our domesticated species!
Can answer complex questions

Like...Did early Homo sapiens interact with other species of Homo?

Phylogeny of human head/body louse

Deep (old) split within the louse phylogeny

1.18 million years ago

How is this possible if modern Homo sapiens is less than 0.2 million years old?

H. neanderthensis [0.6 mya]
H. erectus [1.8 mya]

Sister-group comparisons

Power (& strength of argument) increases with increasing # of sister-group comparisons

e.g. 500 species with trait “X” spread among 30 different lineages - each with small sister groups.

= when “X” evolves, species richness increases

Genetic Analysis of Lice Supports Direct Contact between Modern and Archaic Humans

Phylogeny of human head/body louse

Mapped onto phylogeny of genus Homo

H. neanderthensis is too recent

Deep split is consistent with split between H. erectus and our lineage

Sister-group comparisons

Beetle coevolution with plants

Beetle coevolution with plants

**Plant hosts:**
- Green = Coniferous (184 beetle spp)
- Red & blue = Angiosperms (104,096 beetle spp)


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**HIV Example 1:** Florida dentist case

1990 case: Did a patient’s HIV infection result from an invasive dental procedure performed by an HIV+ dentist?

CDC used phylogenetics to test this

HIV is a rapidly evolving virus so in a short time span mutations appear and are fixed into descendent lineages (HIV genes evolve about 1 million times faster than human genes)

Prediction: if the dentist is the source of the infection then the patient’s HIV strains will be evolutionary descendents of the dentist’s strain

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**HIV example 2:** Forensic evidence

**Phylogenetic tree of HIV sequences from the DENTIST, his Patients, & Local HIV-infected People:**

![Phylogenetic tree diagram]

**Part of the envelope (env) gene**

Legal case: branch support really matters

**Yes:**

The HIV sequences from these patients (f1 within the shade of HIV sequences found in the dentist.

**No**

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**Very rigorous analyses**

- MrBayes - 5 million steps, 50% burnin
- MP - 100,000 Bootstrap reps
- ML - 10,000 to 1,000 reps


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**So what is phylogenetics good for?**

Any field that studies organisms or their products (e.g. molecules)

All life evolves and phylogenetics provides us with surprisingly powerful tools to understand the patterns and implications of this evolution
Study Questions

Describe, with details, two examples of phylogenetic methods being used outside the field of taxonomy (e.g. to answer a question of macroevolution, anthropology, parasitology, forensic science, etc.)