Key ideas from Hadfield et al. 2014

Many traits may not really be readily identifiable as belonging to one partner in an ecological interaction (e.g., virulence).

In our context, then, we are asking whether host range should be considered as solely the property of the parasite, or whether it also depends on the hosts. E.g., the main effect of parasite history is that related parasites have similar host ranges, whereas the main effect of host history is that related hosts may be infected by parasites with similar ranges. Does that make sense? That is essentially the virulence example posed by Hadfield et al, recast replacing virulence with range. It’s unclear to me whether that makes much sense, though.

If it does make sense, then you can also spin it the other way, and ask by the diversity of parasites that infect a host (the “parasite range,” I suppose?). Related hosts may be infected by a similar set of parasites, and related parasites may infect a similar set of hosts. Somehow that one seems to make more sense to me than the other.

They develop a GLMM approach that allows them to “separate patterns of interest into three sources of phylogenetic signal: host/parasite specialism-generalism; host/parasite evolutionary interactions; and the coevolutionary interaction. Their method can deal with non-Gaussian data, spatial replication, and sampling bias.

They apply it to a dataset of 206 parasitic flea species infected 121 mammals in 51 regions of the Arctic.

How the model works: they extend a model of Tony Ives, defining a phylogenetic covariance structure with 5 components:

1. “The first term [] is the contribution of the main effect of host phylogeny to the covariance…we refer to as **the variation in parasite species richness (PSR) explained by the phylogeny**.” In other words, we look for phylogenetic signal in the parasite species richness across hosts, ignoring any effects of the parasite phylogeny.
2. “The second term [] is the contribution of the main effect of the parasite phylogeny to the covariance, and is **the variation in host-range (HR) explained by the phylogeny.** In other words, we look for phylogenetic signal in the host range across parasites, ignoring any effects of the host phylogeny.
3. “The third term is the contribution of the host evolutionary interaction to the covariance, and captures **the degree to which related hosts have similar parasite assemblages** irrespective of parasite phylogeny.” From this I take this term to be referring to the interaction between the hosts, only. In other words (based on Fig. 1), this term looks at each parasite in turn, and asks to what extent host relatedness explains variation in which hosts the parasite is found. It’s a bit unclear to me how this is different from (1), but I think what it means is that it’s looking very specifically for interactions between hosts that are missed by (1), which is essentially “blind” to the identity of the parasites. This term says, if parasite 3 is found in host 8, does that make parasite 3 more or less likely to be found in the close relatives of host 8? (I think.)
4. The fourth term [] is the contribution of the parasite evolutionary interaction to the covariance, and captures **the degree to which related parasites have similar host assemblages** irrespective of host phylogeny.” I take this term then to be referring only to the interaction between parasite species; with the difference between (1) and (3), this term does not ignore the identities of the host, but rather says, if parasite 3 is found in host 8, does that make host 8 more or less likely to be infected by close relatives of parasite 3?
5. The fifth term [ “is the contribution of the coevolutionary interaction to the covariance, and captures **the degree to which related parasite live on related hosts.**

The also define a non-phylogenetic covariance structure with three terms:

1. “ captures interspecific variation in parasite species richness that is not due to phylogeny.”
2. “ captures interspecific variation in host range that is not due to phylogeny.”
3. “ captures associations between specific host and parasite species not due to phylogeny.” They point out that this term will not be identifiable unless replicate incidence matrices have been sampled in time and space. (Otherwise, there is just a single number (0 or 1) for each host-parasite pair.)