Aim 3: **X-Net : Interface to cross species networks inference.**

**Rationale:** We propose to build an intuitive web interface that will give biologists access to all the data, tools, and analysis pipelines available in the public domain. The interface will allow biologists to store Networks so they can save, create, query, and refine their network using the tools such as the ones mentioned in Aims 1 and 2. This will lead the experimental biologists to identify candidate networks of genes which they can experimentally validate.

**Novelty:** Other web-based tools allow researchers to query and browse gene networks, such as PlaNet (REF) and Atted-II (REF), offering large networks of pre-calculated networks, which may get updated periodically. X-net allows biologists to select subsets of experiments or even to load their own experiments. X-net also gives reserchers the ability to change parameters such as orthology thresholds for multispecies networks.

**[Dennis thinks we don’t have room for this paragraph] Significance:** In AIM1 we developed a strategy to infer a co-expression network by training on closely related species. In AIM2, we developed a method to merge co-expression information from several different species into one using a voting method. In addition to our novel methods of creating inferred correlation networks, there are several other researchers who have published interesting methods in peer-reviewed journals. Even though these methods and networks are available for everyone to download one needs to have some knowledge in computer programming in order to use the data for their own work. X-net will empower the biologists to use their scientific intuition while browsing a network looking for candidate genes or candidate network of genes responsible for a specific phenotype.

**X-net’s interface**:

There are two main Network Analysis functionalities we propose to create in X-net 1) the ability to create a species-specific multinetwork for any given species, and 2) the ability to create a multispecies elected network.

1. **Species-specific multinetwork**: Network interactions can be divided into two types: those that are determined experimentally and those that are inferred. A species-specific multinework is simply the union of all different types of interactions. The interface for a species-specific interface would allow the researcher to choose: edge types, thresholds (e.g. correlation above 0.6), and sources of data. The species-specific network might come from inference. For example, a biologist working on Glycine max may want to use protein-protein information from Arabidopsis would simply
	* 1. Choose Arabidopsis as the source,
		2. Choose Glycine max as the target,
		3. Choose an orthology definition and threshold
		4. Click on the “Run Interolog” button
		5. Wait for the link to a network.
2. **Multispecies voted network:** The multispecies elected network will allow researchers to combine any type of networks and from any number of species into one multi-species network where the edges and nodes have confidence values based on votes (in the style of Aim 2). See figure 6?
	1. To provide this feature to the community, we will create a Network Cart in VirtualPlant ([www.virtualplant.org](http://www.virtualplant.org)) (Katari et al 2010) where biologists will be able to store, manage, and refine their networks. Because our user community of biologists find the existing “gene cart” idea very intuitive, we believe that they will perform some very sophisticated queries with their network carts as well.