Visualizing Ecosystem Energy Flow in Complex Food Web Networks

Kelly A. Kearney\textsuperscript{1,2} and Kerim Aydin\textsuperscript{2}

\textsuperscript{1}University of Washington, JISAO, \textsuperscript{2}NOAA Alaska Fisheries Science Center

**Objective**

When applied to ecosystems with hundreds of nodes and thousands of edges, most standard graphing tools produce network graphs that are cluttered at best and illegible at worst. To be useful, a graph should include the following features:

- Node properties indicate the size of the biomass pools, in a visually perceivable and comparable way.
- Nodes do not overlap each other.
- Node labels are legible and do not overlap each other.
- Label word length does not influence visual perception of node size.
- Node position can be related to trophic level.
- Edge direction is clear.
- Edge properties indicate magnitude of flows between groups.
- Edges are resolved such that the major pathways can be seen, and edges do not blend into a single blob of ink.

Here we demonstrate a set of algorithms to produce such a graph.

**Node positioning: Trophic level and trophic groups**

Trophic groups refer to species that share similar prey and predator groups. Gauzens et al. (2014, JR Soc Interface 12:1–29) presented an algorithm to detect these groups within a food web. We couple that grouping with the D3 visualization library (Bostock et al., 2011, IEEE Trans Vis Comput Graph 17:2392–2399) as follows:

1. Use D3 circle pack layout with Gauzens et al. grouping; this scales area of nodes to biomass.
2. Connect nodes to their trophic group members. Use D3 force layout with collision detection to position them.
3. Create vertical axis corresponding to trophic level. Nudge nodes towards their trophic level values as the force layout runs.

**Edge routing: Divided edge bundling**

An example of divided edge bundling. Color indicates direction: red = source, blue = target. Edge width is scaled to the cube root of biomass (t km\textsuperscript{-1} yr\textsuperscript{-1}).

To reduce visual clutter in dense network graphs, edge bundling algorithms draw edges that are close to each other, in either graph structure or geometric space, as bundled curves. The divided edge bundling algorithm (Selassie et al. 2011, IEEE Trans Vis Comput Graph 17:2354–2363) does this via a physical simulation of spring and Coulombic forces between control points on neighboring curves. It is particularly applicable to food web visualization because it preserves both direction and magnitude of edges.

For further details on these algorithms, as well as examples and code, see: http://tinyurl.com/kearneyOS2016

**An example: Three Alaskan ecosystems**

The network diagrams above, based on Ecopath models (Aydin et al., 2007, NMFS–AFSC-229), highlight both the similarities and differences in community composition between the Eastern Bering Sea, Gulf of Alaska, and Aleutian Islands fisheries management regions. Ecological network indices (right and below), based on 1000-member Monte Carlo parameterizations of each model, further quantify structural differences.

---

**Figure Legends**

- **Eastern Bering Sea**
- **Aleutian Islands**
- **Gulf of Alaska**

**Tables**

- **Number of groups**
- **Number of links**
- **Number of internal links**
- **Link density**
- **Connectance**
- **Compartmentalization**

**Graphs**

- **Cumulative biomass vs. Trophic level**
- **Biomass (t km\textsuperscript{-1})**
- **Trophic level**

**Charts**

- **Total system throughput**
- **Total system throughput**
- **Total production**
- **Catch mean trophic level**
- **Gross efficiency**
- **Assemblage**
- **Extent of development**