The Gaggle

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The practice of biology often requires the simultaneous exploration of many kinds of data. No single software tool, web site, or combination of Bioconductor packages, can do justice to these data. Furthermore – and despite significant effort having been devoted to integrating many kinds of data within single programs and web sites in recent years– the challenge presented by heterogeneity of biological data is only likely to increase, as are the the number of useful programs and web sites for exploring that data.

The Gaggle (Shannon et al. 2006) tackles this heterogeneity by providing a simple mechanism for broadcasting data among properly *gaggled* programs. And, contrary to expectation, careful semantic mapping is *not* required for these broadcasts to be useful.

In the Gaggle, the data types are distilled versions of data types commonly used in bioinformatics (and, indeed, in many other scientific fields). They are essentially free of biological semantics, but they take on rich semantics when they are interpreted by the receiving program. For instance: a simple list of (gene) names may be used to select rows of a matrix in R, nodes in a Cytoscape network, metabolic pathways in KEGG, and protein-protein associations in EMBL's STRING. This works equally well for the other data types – matrices, networks, and associative arrays (about which more below).

The Gaggle is open source and written in Java. We rely upon (and are grateful for) the R package *rJava* for Java/R integration. Further information about the Gaggle may be found at **http://gaggle.systemsbiology.net** and in the references.

The current vignette illustrates the Gaggle with a very simple example. We create a random edge graph in R, broadcast it to Cytoscape for display, followed by broadcasting selected node names back and forth.

The four Gaggle **data types** are translated into R as follws:

- name list (mapped to an R character list)
- matrices (R matrix)
- networks (GraphNEL object)
- associative arrays (R environment)

'***Geese***' are programs or web resources adapted to run the Gaggle. They are typically written independent of the Gaggle (as with R), and then adapted to the Gaggle with a modest amount of programming. (See the paper and website for more details.) Some current geese are:

- Cytoscape (see http://www.cytoscape.org)
- TIGR Mev (see http://www.tm4.org/mev.html)
- STRING goose (see http://string.embl.de)
- a variety of name translators

A companion website for this vignette may be found at which we encourage you to visit. It presents more background, several demos beyond the one presented here, and Java Web Start links from which you can (with one click) download and run all of the necessary geese, including the **Gaggle Boss** which must always be started first in any Gaggle session you run.

`http://gaggle.systemsbiology.net/R/vignettes/1`

1 Technical Background and Notes

The **Gaggle** is a simple, open-ended collection of RMI-linked Java programs, which broadcast selected data to each other at the user's behest. These broadcasts are managed by a simple RMI server, the **Gaggle Boss**. Though it is not stricly necessary, we find it very convenient to launch most geese via Java Web Start links in a web page. For the **R goose**, simply install the gaggle package as you would any other R or Bioconductor package. Please see the companion website for a generally useful set of Java Web Start links.

You **must** always start a Gaggle Boss on your computer before you start any geese. Every goose registers with this boss as it starts up; if it isn't running, you get no gaggle capabilities.

Upon receiving a broadcast, each goose interprets the data according to its own, local semantics. (This strategy of **semantic flexibility** is discussed at length in the Gaggle paper.) The **KEGG** goose, for example, responds to a list of gene names by displaying the metabolic pathways to which they have been annotated; having no sensible interpretation of matrices or networks, the KEGG goose simply ignores those broadcasts. The **STRING** goose will present a web page for the discovery of protein associations; the network which results may be broadcast back to the Gaggle.

As of this writing (June 2006) web resources – bioinformatics websites like KEGG and EMBL's STRING – are included in the Gaggle by way of naive, home-grown web browsers, written by us in Java, and tailored to the details of these sites. These browsers

work reliably, but they leave a *lot* to be desired. In recognition of this, we have been experimenting with Mozilla (Firefox) extensions, which allow us to use a full-fledged, popular browser in the Gaggle. Expect more on this front soon, and please be patient with our initial attempts at gaggling websites, until we improve them!

2 Demo: Broadcast a randomEGraph to Cytoscape for viewing; broadcast selected nodes back to R

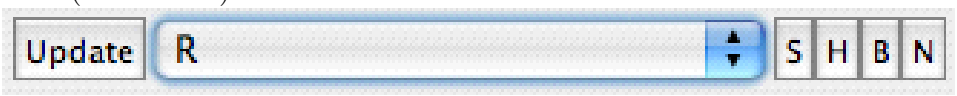
In this first demonstration, we

- Start the Gaggle Boss (browse to `http://gaggle.systemsbiology.net/R/vignettes/1`, Part 1, for web start links)
- Start Cytoscape
- Start R, and load the gaggle package
- Create a randomEGraph, broadcast it, and see it displayed in Cytoscape
- Select a few nodes of the graph in Cytoscape, and broadcast them back to R
- Broadcast these selected nodes back to R again, but this time, not as a list of node names, but as a connected subgraph (that is, with edges included)

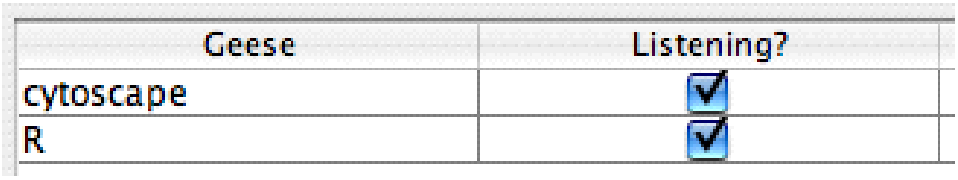
```
> library(gaggle)
> gaggleInit()
> set.seed(123)
> g = randomEGraph(LETTERS[1:8], edges = 10)
> broadcast(g)
```

You should see an 8-node, 10-edge network appear in cytoscape.

Switch your focus to Cytoscape, and select a few nodes by drag-selecting with your left mouse button. Then look near the top of the Cytoscape window for the broadcast buttons (**S H B N**):



These stand for **S**how, **H**ide, **B**roadcast names, and broadcast **N**etwork, respectively. The *target* of these actions is picked by manipulating the 'goose selection menu' which shows **R** in the illustration. (See below for how to broadcast and select target geese using R function calls.) If the **Boss** is the target, then your broadcasts are sent to *all* of the geese who are registered with the Boss – though one can manipulate the user interface of the Boss so that it only forwards messages to selected geese).



Click the 'Update' button to ensure that your goose has a fresh list of all currently running geese for you to choose from.

Inasmuch as the R goose does not have a full-fledged graphical user interface, function calls must be used instead of buttons and menus to interact with the Gaggle. Here are the relevant commands:

- **geese ()** names of the current geese
- **setTargetGoose (someGooseName)** one of the names returned by 'geese ()'
- **getTargetGoose ()** find out the current setting
- **broadcast (someVariable)** this generic function suffices for name lists, graphs, matrices, environments the broadcast goes to the current targetGoose, or to the Boss by default.
- **showGoose ()** raise the window of the current target goose
- **hideGoose ()** hide the window of the current target goose

When using a new goose with which you are unfamiliar, you can often learn your way around from the tooltips associated with buttons in most GUI geese. These 'flyover' explanations of otherwise tersely named buttons should help you to use the various geese.

Returning, now, to the Cytoscape goose, with at least a few selected nodes, broadcast this selection back to R. There are two kinds of broadcasts available to you: of just the names, or of the selected subgraph. Whichever you choose, your R console will display a message indicating the type and size of the broadcast it has just received. (These messages, unfortunately, are not displayed by the Windows Rgui application.) You must then call one of the following methods in order to assign this data to an R variable:

```
> selectedNodes = getNameList()
> subgraph = getNetwork()
```

You may also select nodes in the Cytoscape goose from R. (You may wish to clear the current selection, if any, in Cytoscape first, using the **Cl** button near the top center of the Cytoscape window). Then, in R:

```
> broadcast(c("B", "E"))
```

3 For More Information

For more information, and for more extensive demonstrations, please visit
`http://gaggle.systemsbiology.net/R/vignettes/1`
and the Gaggle website:
`http://gaggle.systemsbiology.net`

4 Issues with the gaggle package on Windows

The gaggle package depends has a couple of issues running under Windows. Both can be worked around as follows.

- Because of an issue with the rJava package, on which the gaggle package depends, your CLASSPATH must be set in a certain way. Make sure your Windows CLASSPATH does *NOT* contain the following entries, or the gaggle package will not work:
  - . (representing the current entry)
  - Any entry with a space in it (e.g. C:\Program Files\Example)
  - The path to the R bin directory
- It is recommended to use the command-line version of R (R.exe) with the gaggle package. You may use the graphical version (RGui.exe), however if you do so, you will not see any informative messages from the R goose (for example, notifying you that a broadcast has been received). This is due to an issue with the graphical version of R on Windows.

5 References

- Shannon P, Reiss DJ, Bonneau R, Baliga NS. The Gaggle: A system for integrating bioinformatics and computational biology software and data sources, *BMC Bioinformatics* 2006, 7:176.