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# Supplementary Information for “PAFway: Pairwise Associations of Functional annotations in biological networks and pathways”

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## 1 Supplementary Methods

### 1.1 P-value of sum of edge weights

The recursive functions referred to in the main text are:

$$P(x \geq z_{a,b} | c_{a,b} = i) = cdf_i(z_{a,b} | c_{a,b} = i) = \int_{-\infty}^{\infty} pdf_{i-1}(y) cdf_1(z_{a,b} - y) dy \quad (1)$$

and

$$pdf_k(x) = \int_{-\infty}^{\infty} pdf_{k-1}(y) pdf_1(x - y) dy \quad (2)$$

, where  $cdf_1(x)$  and  $pdf_1(x)$  are the cumulative density function and probability density function, respectively, for the distribution of edge weights, which we estimate with kernel density estimates (density function in R).

Equation (1) and (2) come from standard formulas for calculating pdfs and cdfs for sums of pairs of continuous random variables. In particular, for two probability distributions  $A$  and  $B$ :

$$cdf_{A+B}(x) = \int_{-\infty}^{\infty} pdf_A(y) cdf_B(x - y) dy \quad (3)$$

and

$$pdf_{A+B}(x) = \int_{-\infty}^{\infty} pdf_A(y) pdf_B(x - y) dy \quad (4)$$

In our case, we say that if  $c_{a,b} = i$ , then  $z_{a,b}$  is constructed by sampling  $i$  values from the probability distribution of edge weights and summing these values together. This will give the same final outcome as would the following procedure:

1. Sample  $i - 1$  values from the distribution of edge weights and find the sum
2. Sample one more value from this distribution of edge weights
3. Find the sum of (1) and (2).

This means that when we calculate Equation 2, we can calculate  $P(x \geq z_{a,b} | c_{a,b} = i)$  from  $P(x \geq z_{a,b} | c_{a,b} = (i - 1))$ .

## 1.2 Implementation with Fast Fourier Transform (FFT)

Note that both the functions for  $\text{pdf}_k(x)$  and  $\text{cdf}_i(x)$  are convolutions of two functions; recall the definition of convolution:

$$\text{convolution}(f, g)(y) = \int_{-\infty}^{\infty} f(x)g(y - x)dx \quad (5)$$

This can be expressed in terms of Fourier transforms:

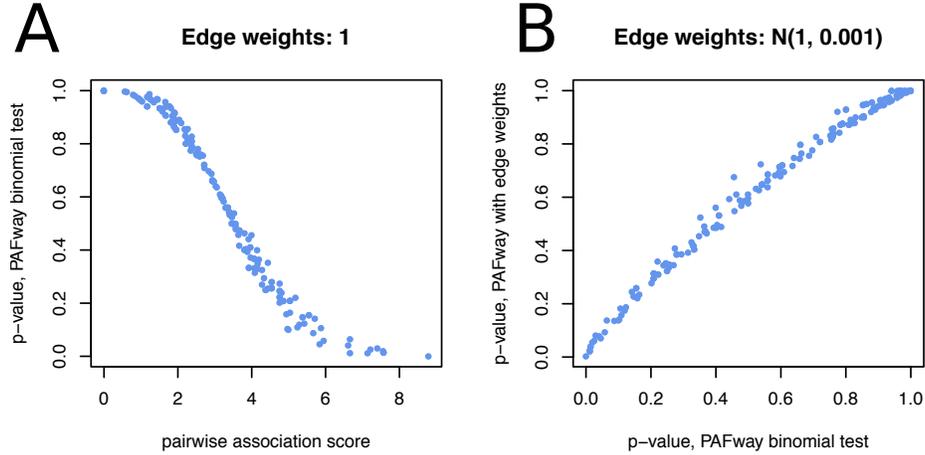
$$\int_{-\infty}^{\infty} f(x)g(y - x)dx = \text{Fourier}^{-1}(\text{Fourier}(f(x))\text{Fourier}(g(x))) \quad (6)$$

We estimate this with a discrete Fourier transform via the Fast Fourier Transform (FFT). This means that instead of calculating an integral, we sample  $f(x)$  and  $g(x)$  at  $m$  discrete points, forming the vectors  $f[x]$  and  $g[x]$  of length  $m$ . The discrete form of the convolution can be calculated by the following summation:  $h[k] = \sum f[x]g[k - m - x]$  for all valid  $x$ , leading to a vector of  $h[x]$  of length  $2m$ . In order to prevent the vector from expanding in size too much as we estimate  $\text{pdf}_k(x)$ , we drop the elements in the beginning and end of the vector that have values that are very close to zero (by default  $f[x] < e - 05$ ).

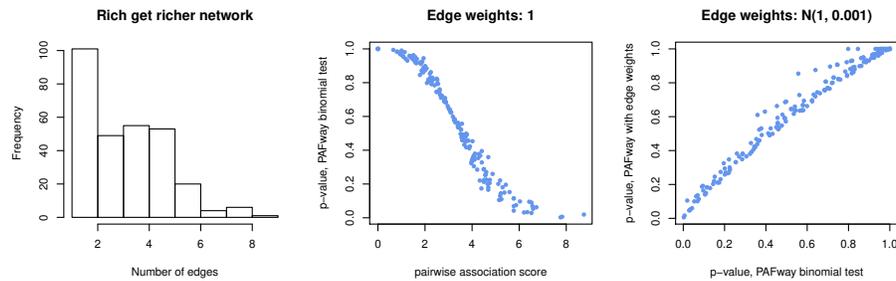
## 2 Supplementary Results

### 2.1 Biological evidence that the PAFway network in *Arabidopsis thaliana* is reasonable

The main output of PAFway is a network of functional annotations, which is shown in Fig. 1 in the main text for an *Arabidopsis thaliana* network. These results are consistent with what we would expect: for instance, cold acclimation is known to be related to response to salt stress [5], response to salt stress is known to be related to water homeostasis [1], and response to cold is related to developmental growth [7]. Also, by definition, heat acclimation will impact the plant's response to heat. Some edges are more surprising and warrant further investigation, such as whether cell growth impacts cold acclimation.



**Fig. 1.** Verification that PAFway produces reasonable outputs. (A) PAFway produces results that are consistent with a pairwise association score. (Note that a higher pairwise association suggests a lower p-value) (B) The FFT-based approach for estimating p-values with edge weights produces results that are consistent with a binomial test, when the edge weights do not vary substantially from 1.



**Fig. 2.** Verification that PAFway produces reasonable outputs for a Rich-Get-Richer (RGR) network. (A) A random RGR network was made, by making the probability of generating a new edge associated with a node be proportional to the current number of edges associated with that node. This is the distribution of edge weights that were produced. (B) This is the equivalent figure to Fig. 1(A) for this RGR network. (C) This is the equivalent figure to Fig. 1(B) for this RGR network.

## 2.2 Verification that method performs accurately

First, we compare the results of PAFway to a pairwise association score that is similar to the one proposed by [3, 14], where  $S(a, b)$  is the association score between GO term  $a$  and  $b$ ,  $p_{a,b}$  is the proportion of edges in the network that go from GO term  $a$  and  $b$ , and  $p_a$  and  $p_b$  are the proportion of genes in the network that have GO terms  $a$  and  $b$ , respectively.

$$S(a, b) = \frac{p_{a,b}}{p_a p_b}$$

Values greater than 1 indicate that the edge type is enriched in the network, while values less than 1 indicate that the edge type is under-represented in the network. However, this metric does not indicate whether the over- or under-representation in the network is significant. Additionally, this method does not enable us to incorporate information about edge weights.

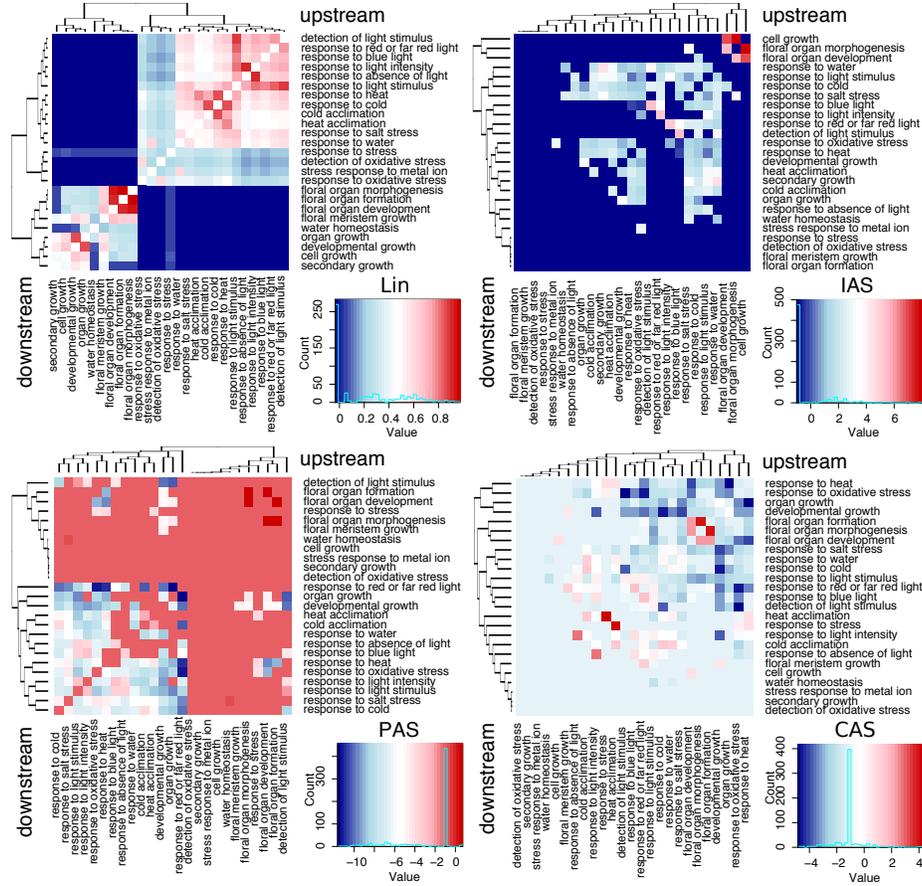
We find that the results are highly correlated to one another when the edge weights are one (Fig 1(A)) or close to one (Fig 1(B), edge weights sampled from a Gaussian with a mean of 1 and standard deviation of 0.001), in a random network with 300 genes, 1000 edges and 14 functional annotations and scale-free (Fig 2) networks.

## 2.3 Comparison to NaviGO

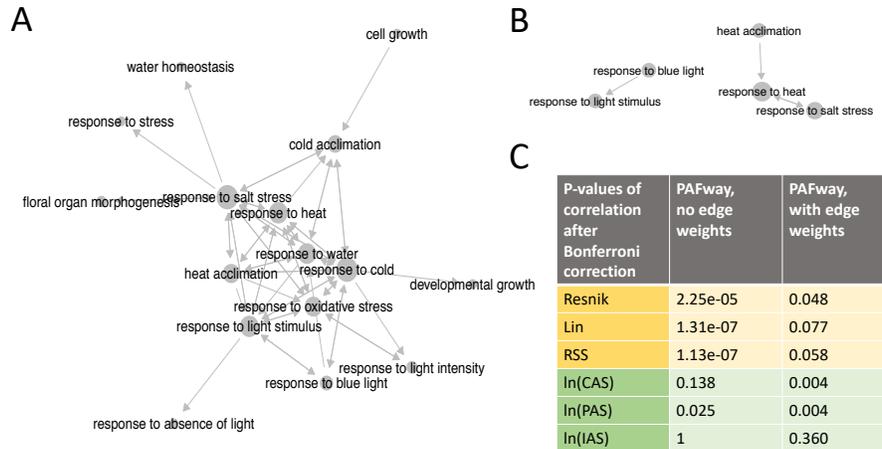
NaviGO [13] is a tool that allows the user to calculate the similarity between pairs of GO terms, based on either semantic similarity [11, 12, 6] or how often they appear together in gene annotations [3], the scientific literature [3], and in physically interacting proteins [14].

The GO consortium have organised all GO terms into three non-overlapping directed acyclic graphs (DAG) that describe their relationships [4]; for instance, there are many different GO terms describing specific responses to many kinds of stress, but these all fall under the GO term ‘response to stress’ and so are connected to this GO term in the DAG. Semantic similarity scores reference the structural relationships between GO terms within this DAG. For instance, the Resnik score is calculated by first finding the lowest common ancestor of the two GO terms and taking  $-\log$  of the proportion of genes that have that annotation [11]. The Lin score [6] is the information content of the lowest common ancestor and the relevance semantic similarity (RSS) score [12] weighs the information content by the probability of observing a common ancestor by chance. On the other hand, the Co-occurrence Association Score (CAS), Pubmed Association Score (PAS), and Interaction Association Score (IAS) measure the relative enrichment of two terms co-occurring in gene annotations (CAS), the literature (PAS), and in protein interaction networks (IAS) [3, 14]. These three metrics use a similar ratio as the pairwise association score  $S(a, b)$  described in the previous section.

To evaluate how our results using PAFway are correlated to these other metrics, we began by selecting a number of GO terms that are relevant to the



**Fig. 3.** Comparison of selected GO terms under semantic similarity (Lin) and other pairwise-association scores (PAS, CAS, IAS). Resnik and RSS are not shown because they produce results that are extremely similar to Lin.



**Fig. 4.** Comparison of PAFway to other metrics that compare pairs of GO terms. (A) PAFway summary network of AraNet, when edge counts are considered. (B) PAFway summary network of AraNet, when edge weights are considered. (C) Comparison between PAFway p-values and other metrics in NaviGO.

main research interests of our lab group. These included GO terms associated with sensing and acclimating to light, temperature and water, stress response, growth, and flower development. Then, we calculated the following values for the AraNet gene network: (i) various pairwise GO comparison metrics using NaviGO (Fig 3) and (ii) the PAFway p-values, with and without edge weights.

For all GO term pairs where there was at least one connection in AraNet, we compared their PAFway associated p-values with the scores produced by the three semantic similarity metrics (Resnik, Lin, and RSS) and the three pairwise association scores (CAS, PAS, and IAS). Interestingly, there was more of a correlation between semantic similarity measures and the results from PAFway when edge counts (not edge weights) were considered. On the other hand, when edge weights were considered, the results were more significantly associated with the CAS and PAS scores, which measure co-occurrence of GO terms in gene annotations and in the literature. This suggests that while PAFway provides results that are somewhat consistent with other metrics of pairwise GO term similarities, it also provides new insights that cannot be directly gleaned by these metrics.

## 2.4 Comparison to BiNGO

BiNGO [8] is a popular cytoscape plugin that is similar to PAFway, in that it depicts the GO terms as a network. More specifically, it identifies GO terms that are enriched in clusters (or communities) within a network, and then depicts these enriched GO terms as a network, where edges represent the underlying

network structure of the GO DAG. For instance, *phosphate metabolic process* points to *dephosphorylation* because dephosphorylation is a type of phosphate metabolic process. Non-enriched GO terms are also included in the BiNGO network if they are required to make it fully-connected. The BiNGO GO term network differs from the PAFway network, because PAFway edges relate to GO term associations within the original biological network, rather simply reflecting the GO term definitions. In this section, we demonstrate the differences between these networks and illustrate how they can work together to improve our ability to interpret large biological network.

First, we find communities within the AraNet network, using spinglass community detection[10] (5 runs), followed by consensus clustering with K-means. We found 131 unique communities, but 20 of these communities were substantially larger than the others, so we focus on these. Fig 5(A) shows some of the key words found among the GO terms in a random selection of the largest communities.

Fig 5(A) shows the BiNGO network that results from the analysis of the first of these communities (the word cloud in the top left). The full networks output of BiNGO is shown in the upper right panel of Fig. 5(B), but this is too large to be easily visualised, so we include a zoomed-in version of an interesting sub-network related to amino acid biosynthesis.

For our PAFway analysis, we decided to focus on GO terms that were highly enriched in each community ( $p\text{-value} < 1e - 10$ ) and that were not commonly found to be enriched among the top 20 largest communities (were found to be enriched in less than four of the 20 other communities). The results of PAFway (with no edge weights) are shown in Fig. 5(C-D) as for the BiNGO network in Fig. 5(B) and for a sample of other sub-networks in Fig. 6. These can be expressed as either a network (Fig. 5(C)) or a heatmap (Fig. 5(D)). From this, we learn additional information that we cannot see from the BiNGO network. For instance, the close relationships between the biosynthesis pathways of the hydrophobic amino acids leucine, isoleucine and valine is much clearer from the PAFway output.

However, since BiNGO and PAFway provide different information, they can be used hand-in-hand to analyse a network. In particular, BiNGO can be used as an initial tool to identify GO terms of interest, which can be investigated in the context of the network structure using PAFway.

### 3 Discussion

This manuscript introduces a method for condensing a large hairball network into a network that links functional annotations or GO terms. We show that it provides complementary biological insights to other methods for comparing pairs of GO terms [13, 3, 14, 11, 12, 6]. It also provides complementary information to BiNGO, a popular way of visualising GO terms in a network format [8].

PAFway produces very different outputs depending on whether edge weights are considered. This is because in the AraNet network, the distribution of edge

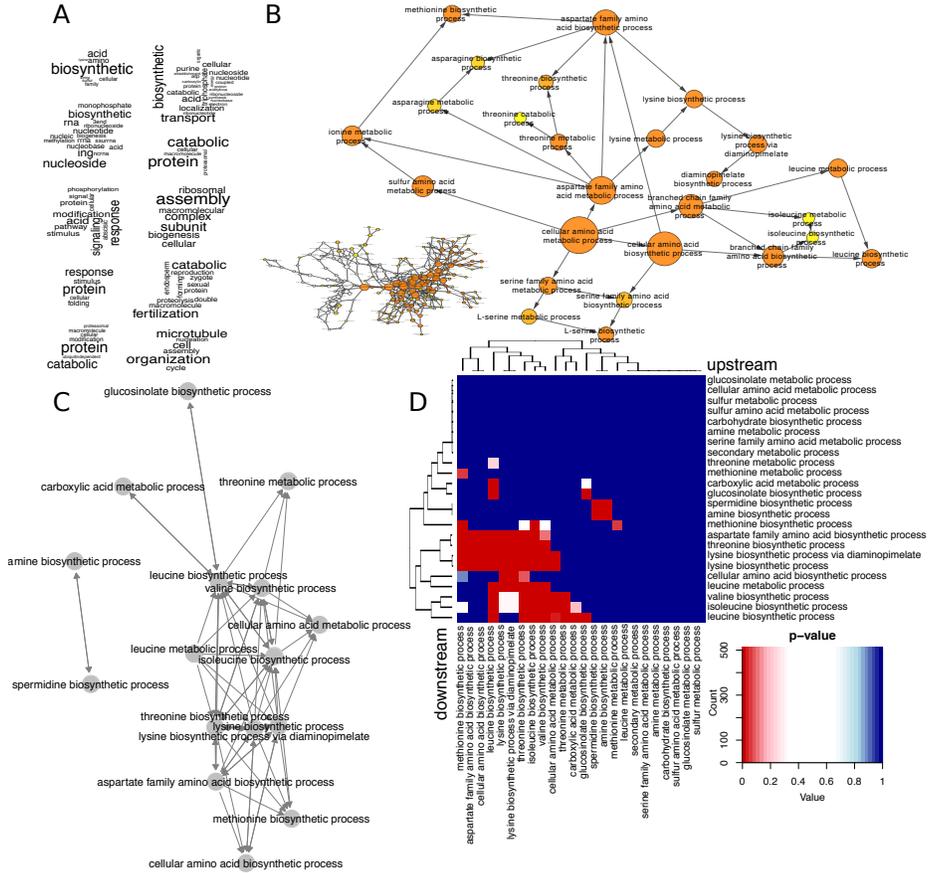
weights has a long-tail, so a small number of edges that have a very high weight play a more important role in the resulting network. On one hand, this is a good thing because these edges are much more likely to be biologically meaningful, so they should be weighed more heavily. On the other hand, the results may be less robust, because they depend on the values of a few edges. We recommend using both techniques and comparing the results.

Another consideration is whether to display the results of PAFway as a network or heatmap. The heatmap allows us to visualise the distribution of p-values that do not make the cut-off, so it can provide complementary information. For instance, it is often easier to see ‘cluster’-like behaviours from the heatmap visualisation. However, it may be tempting to add *meaning* to spurious relationships between GO terms that are not significantly linked when observing the heatmap visualisation, so in many ways the network representation is preferable.

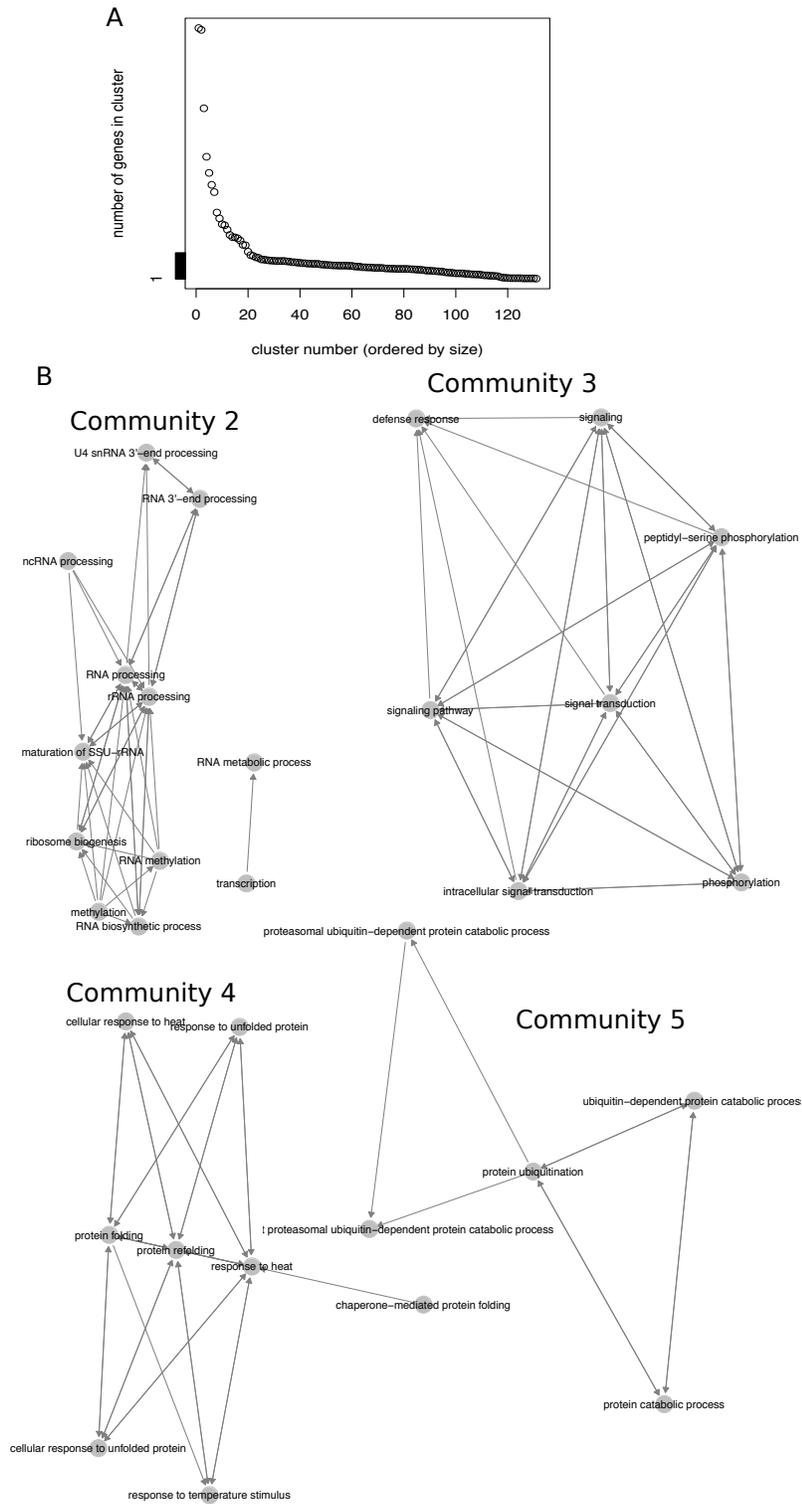
Another issue is that most edges in these large hairball networks are likely to be false positives. Indeed, many validation studies find that at most half of the edges are direct targets [2, 9]. While having many false positives will decrease the sensitivity of our method to detect relationships between functional annotations, this should not effect the specificity of the method if the false positive edges have randomly distributed gene function annotations.

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**Fig. 5.** Comparison of BiNGO and PAFway outputs. (A) Word clouds of key words among GO terms that are significantly enriched in a random selection of 10 of the 20 largest communities in AraNet. (B) BiNGO network of one community (the one represented by the top-left word cloud in (A)). The full network is shown in the bottom left portion of this panel, but a zoomed-in sub-network that is related to amino acid biosynthesis and metabolism is also shown. (C) This is the network output of PAFway for the community shown in (B). A heatmap representation of this PAFway network is shown in (D).



**Fig. 6.** Data from more communities (A) The size distribution of the communities (B) The PAFway network for a few additional communities, ignoring edge weights, and correcting for multiple hypothesis testing with Bonferonni. The other 15 networks are available on the Github.

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