Network Models in the Evaluation of Software Clustering Algorithms

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***Abstract*—Software modularization recovery algorithms help to understand how software systems decompose into modules, but they**

Software modularization recovery algorithms... bla bla

***Keywords*-reverse engineering; software modularization; empirical evaluation; complex networks;**

In the context of our research, we consider classes as the components

I. Abstract

Software modularization recovery algorithms automatically recognize a system's modular structure by analyzing its implementation. Due to the lack of well document software systems, though, the issue of testing these algorithms is still underexplored, limiting both their adoption in the industry and the development of better algorithms. We propose to rely on software models to produce arbitrarily large test sets. In this paper we consider three such models and analyze how similar the artifacts they produce are from artifacts from real software systems. [1]

II. Introduction

Development of large-scale software systems is a challenge.

A key to success is the ability to decompose a system into weakly-coupled modules, so each module can be developed by a distinct team. Failing to do so results in duplicated code, non-parallelism, one's work impacting another's work etc.

The ability do modularize depends decisively on a vast knowledge about the system, how its different parts interact to accomplish the system's goal.

Unfortunately, in the case of legacy systems, such knowledge isn't available. Depending on its size, it might take months to understand the system so well as to find a good modularization. XXX [2]

POR ISSO SURGIRAM software modularization recovery algorithms, also known as software clustering algorithms or software architecture recovery algorithms. In its most common flavor, these algorithms analyze the dependencies between implementation components, such as classes, and then group them into modules such as there are few dependencies between classes in distinct modules.

Software modularization recovery algorithms can, therefore, do in minutes what a person would spend weeks or months. The question is: are the found modularizations good? Are they similar to what a person would find? To answer this question it's essencial to perform empirical evaluations envolving systems with known reference modularizations.

The empirical evaluations consist of selecting a collection of systems with known reference modularizations and then applying the algorithms to the systems. The modularizations found by the algorithms are then compared to the reference decompositions by a metric such as MoJo [3] or Precision-Recall.

Unfortunately there are few systems with known reference modularizations and, because to obtain reference modularizations is costly, there are few empirical studies, and most of them consider a couple of small and medium systems.

We therefore propose to use synthetic, i.e., computer-generated, software dependency networks, to evaluate software modularization recovery algorithms. These networks are generated by parametrizable models and have an embedded reference modularizations. The goal of an algorithm is, thus, to find modularizations that are similar to the reference modularization embedded in the network. With this approach we can CONTAR COM a large volume of test data that is composed of networks of different sizes and controllable characteristics.

Of course the success of this approach depends on the realism of the synthetic networks, ie, how well they resemble networks extracted from real software systems. In this paper we study three models and show that all of them are, by means of a careful parameter choosing, capable of producing realistic software networks.

The remaining sections are organized as follows. .... Section 2, ...

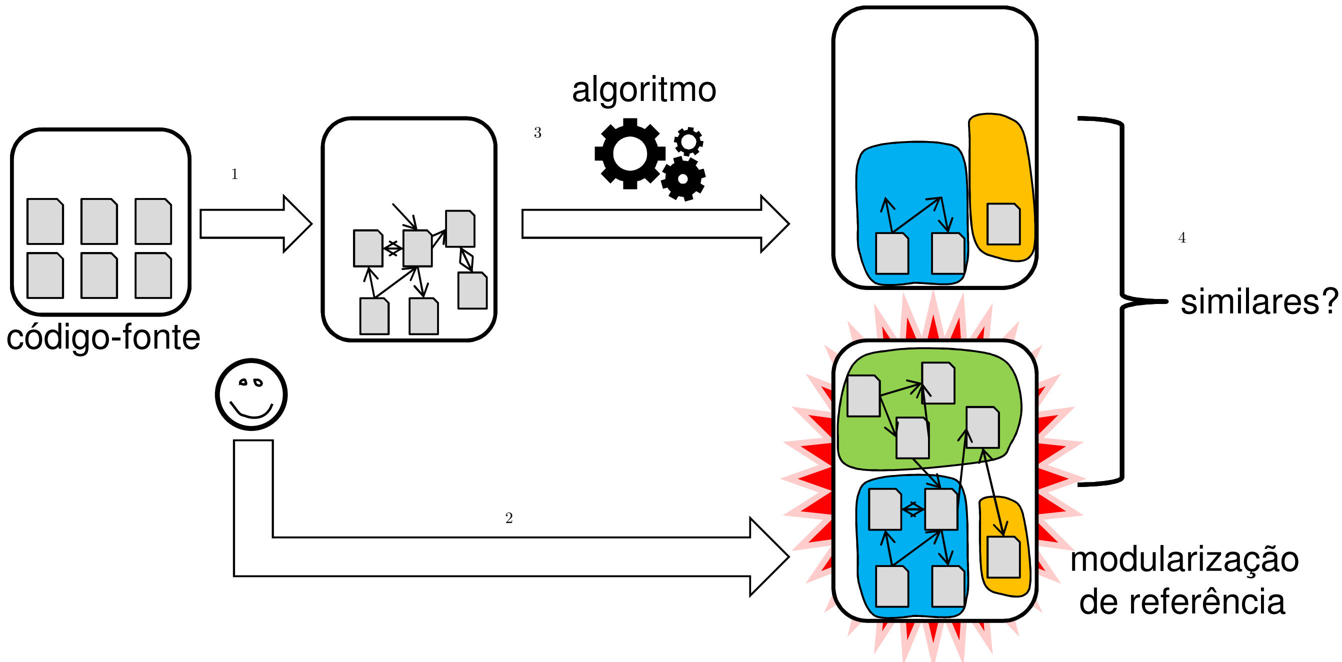

Figure 1. Evaluation of a software modularization recovery algorithm

III. Related Work

IV. Software Modularization Recovery: an Overview

Aka software architecture recovery, software architecture reconstruction, software clustering...

It's an task of reverse engineering, as defined by Tonella [4]...

DEFINITIONS

external edge...

directed graph, (un)weighted

V. Network Theory

Network theory research studies general properties of many types of networks by using statistical analysis. In the last decade, it has been found that many networks arising from sociology, biology, technology and other domains present remarkable structural similarities. It has been shown that, in these networks, the number of vertices connected to k edges, N(k), is proportional to k^{gamma}, where γ is a positive constant. These networks were called scale-free networks.

Network theory has been applied to software networks and it was shown that they are also scale-free networks [5], [6].

(in fact we can't argue the degree distribution is perfectly fit by a power law. Anyway, the distribution is much more assymetric than normal ou Poisson's)

software indegree distribution (power law), outdegree distribution (not so power law)

VI. Network Models

Many models were proposed to explain the formation of scale-free networks. These models are simple algorithms that can be proven, either formally or empirically, to generate networks that are scale-free. In this section we present three models that generate directed networks with built-in modular decomposition: BCR+, CGW and LR. The first two models grow networks using a mechanism called preferential attachment CITE Barabasi, by which nodes with many edges tend to receive more edges in the process.

A. BCR plus

The BCR model aims to model the network of hyperlinks between web pages as a directed graph without modules [7]. It was proven analitically to generate scale-free networks. We have developed an extension to this model, which we will call BCR+, that adds the concept of module. The model accepts the following parameters:

- number of vertices, n;
- a graph, G;
- three probabilities, p, q, and r, such as $p + q + r = 1$;
- a probability, mu;
- two real numbers, din and dout.

In a network with modules, one can define a MDG as a graph where the two following conditions hold: * each vertex represents a module in the original network; * there is an edge from M1 to M2 in the MDG only if there is an edge from v1 to v2 in the original network, where v1 in M1 and v2 in M2.

The BCR+ model generates networks whose MDG is equal to G by adding vertices and edges to an initial network until it reaches n vertices. The initial network is isomorphic to G: it contains one vertex for each module and one edge for each edge in G, connecting vertices whose corresponding modules are are connected. Thus, the networks's MDG is equal to G from the very beginning.

After that, the algorithm consists of successive applications of one out of three operations on the network: (1) adding a vertex with an outgoing edge; (2) adding a vertex with an ingoing edge; (3) adding a edge between existing vertices. The choice of the vertices that will be connected by a new edge, although non-deterministic, is not fully random. The probability that a particular vertex v is choosen, P(v), is proportional to a function of the in-degree or of the out-degree of the node. We say that we choose a vertex within a set V according to a function f if

P(choose v) = f(v) / sum(v in V, f(v))

The denominator is a normalizing factor that assures that the probabilities sum to 1.

Before we present the algorithm in detail, using pseudocode, we must explain some definitions. V is the set of vertices in the network being generated. This set grows as the algorithm is executed. Being v a vertex, we define the following three functions:

* out-neighbors(v): the set of all vertices that are connected to v by an edge starting in v. * same-module(v): the set of all vertices that are in the same module as v (except v itself). * other_modules(v): the set of all vertices that are in modules that are connected to v's module (in the graph G) by an edge starting in v's module.

After the initial network is created, the algorithm proceeds as follows:

We can see that the probabilities p, q and r control how often each operation is performed. Because the operation associated with probability r does not add any vertices, greater values of r imply more edges in the resulting network. It is easy to see that nodes connected to many ingoing edges are more likely to get another ingoing edge, and the same reasoning can be applied to outgoing edges. The parameter din can alleviate the handicap by providing a "base in-degree" that is applied to all vertices when computing the probabilities. Consider two vertices, v1 with in-degree 4, and v2 with in-degree 8. If din = 0, v2 is twice more likely to receive a new incoming edge; if, otherwise, din = 4, v2 is only 3/2 more likely to receive the edge.

The parameter mu controls the proportion of edges between vertices in distinct modules. Lower values of mu lend to networks that are more modular.

The BCR+ model is a growth model, meaning that the network is generated vertex by vertex, growing from an initial network. It can, therefore, simulate the evolution of a software network. Moreover, it can simulate the evolution of a software system subject to constraints in module interaction, as is the case with top-down design methodologies CITE.

B. CGW

The CGW model was proposed to model the evolution of software systems organized in modules. It was proven formally to generate scale-free networks. [8] It accepts the following parameters:

* n, m * Probabilities p1, p2, p3, p4, summing 1 * Natural numbers e1, e2, e3, e4 * alpha

Just like BCR+, this is a growth model. Its initial network is composed of two vertices belonging to the same module and a directed edge between them. The remaining m - 1 modules are initially empty. Because the original implementation of the model is not available, we describe in detail the algorithm we implemented:

Unlike BCR+, this model does not allow constraints on the connection between modules, however it accounts for the rewiring and the removal of edges.

C. LF

The LF model is a very flexible model that can generated weighted directed networks with overlapping modules, that is, in which a vertex can belong to more than one module. Unlike the previous models, this is not a growth model: all vertices are generated at once and then the edges are added.

There is also a special version of the model in which the edges weights are discarded and the modules are non overlapping. We used the original implementation of this version, available at http://.

VII. Characterization of Software Networks

Our research hypothesis is that at least one of the presented models can synthesize networks that resemble software networks. A central issue, thus, is how to measure similarity between networks. In order to be useful, the metric must be able to differentiate between software and non-software networks. In this section we present such a metric, together with an experiment that evaluates its usefulness by applying it to both software and non-software networks.

A. Similarity Between Networks

In a recent work, Milo et al. [9] proposed to characterize networks by analyzing their triad concentration. A triad is a network with three vertices in which all vertices are connected. There are only 13 distinct triads, one for each configuration of directed edges, as shown in Figure 2.

By counting how many times each triad appears in a network, one can build a triad concentration profile (TCP), which is a vector with 13 numbers that summarize the local structure of the network. Figure 3 shows the TCP for three distinct networks.

Following the work by Milo et al. [9], similarity between two networks can be measured by computing Pearson's

```
while the network has less than n vertices:
  choose one of the operations according to probabilities (p, q, r)
  operation 1: (add a vertex with an outgoing edge)
    choose a vertex w within V according to f(x) = din + in-degree(x)
    add a new vertex v to w's module
    add an edge from v to w
  operation 2: (add a vertex with an ingoing edge)
    choose a vertex w within V according to f(x) = dout + out-degree(x)
    add a new vertex v to w's module
    add an edge from w to v
  operation 3: (add an edge between two existing vertices)
    choose a vertex v within V according to f(x) = dout + out-degree(x)
    choose a case according to probabilities (mu, 1 - mu)
    case 1: (distinct modules)
   choose a vertex w within (other\_modules(v) - neighbors(v)) according to f(x) = din + in-de
      add an edge from v to w
    case 2: (same module)
      choose w within (same-module(v) - neighbors(v)) according to f(x) = din + in-degree(x)
      add an edge from v to w
  end
```

correlation coefficient between the corresponding TCPs, which yields a value between -1 (most dissimilar) and 1 (most similar):

$$\mathrm{sim}(a, b) \ = \ \mathrm{cor}(\mathrm{TCP}(a), \mathrm{TCP}(b)),$$

where a and b are networks, TCP(x) is the triad concentration profile for network x, and cor(x, y) is Pearson's correlation coefficient.

B. Data Set

To support the evaluation of the metric, we have collected 131 networks. The networks are described in detail in Appendix A.

Software networks. We have collected 65 software systems written in Java, with size ranging from 111 to 35,363 classes. Java was chosen for being a popular programming language in which many open source systems have been written. The software networks, representing dependencies between classes, were extracted with the tool Dependency Finder CITE.

Non-software networks. We have collected 66 networks from distinct domains, such as biology, sociology, technology, and linguistics. These networks are freely available on the Internet and have been used in previous researches.

C. Evaluation of the Similarity Metric

In order to evaluate the similarity metric, we measured the similarity between the networks in the data set. A suitable metric must fullfil two conditions: (i) it must yield high similarity between software networks, and (ii) it must yield lower similarity between software networks and networks from other domains.

Using the data set we can define S-score, a metric that represents how much a particular network resemble software networks. It is defined as the average similarity between the network and a sample of software networks:

$$\text{S-score}(a) = \frac{\sum_{s \in S} \mathrm{sim}(a, s)}{|S|},$$

where S is the set of sample software networks, and $|S|$ is the cardinality of S. In this work we use the full software data set consisting of 65 software networks.

We measured the S-score for each software network, which ranged from 0.83 to 0.98. The average S-score was 0.97 and the standard deviation, 0.03. The high average S-score and the low standard deviation show that the metric successfully captures common structural patterns in software networks.

TODO: Boxplot by network class (software, metabolic, neural, social etc.)

Then we measured the S-score for each non-software network. The majority of the networks (X%) have a S-score lower than 0.83, which shows that they are ... Networks extracted from the social network Facebook have negative S-score.

A few networks, though, showed high S-score. The network polblogs, showing links between blogs on politics, had similarity 0.97. The neural network of C Elegans also had a high similarity (0.88). Further investigation is needed in order to discover why does it happen and whether auxiliary metrics can differentiate these networks from software networks.

```
while the network has less than n vertices:
  choose operation (p1, p2, p3, p4)
  operation 1: (adding a vertex with e1 edges)
    create a new vertex v and add it to a randomly chosen module
    do e1 times:
      choose a vertex w according to mbpa(v)
      add an edge from v to w
  operation 2: (adding e2 edges)
    do e2 times:
      choose a vertex v randomly
      choose a vertex w according to mbpa(v)
      add edge from v to w
  operation 3: (rewiring e3 edges)
    do e3 times:
      choose a vertex v randomly
      choose an edge e randomly within edges that start in v
      choose w according to mbpa(v)
      remove e
      add an edge from v to w
  operation 3: (removing e4 edges)
    do e4 times:
      remove and randomly chosen edge
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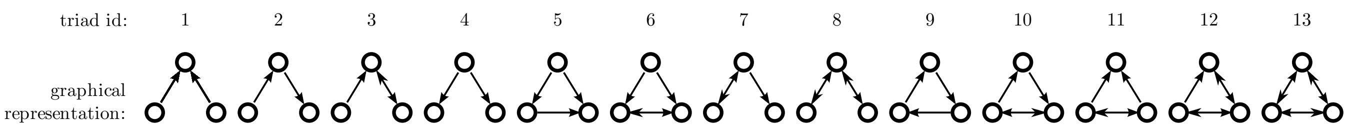
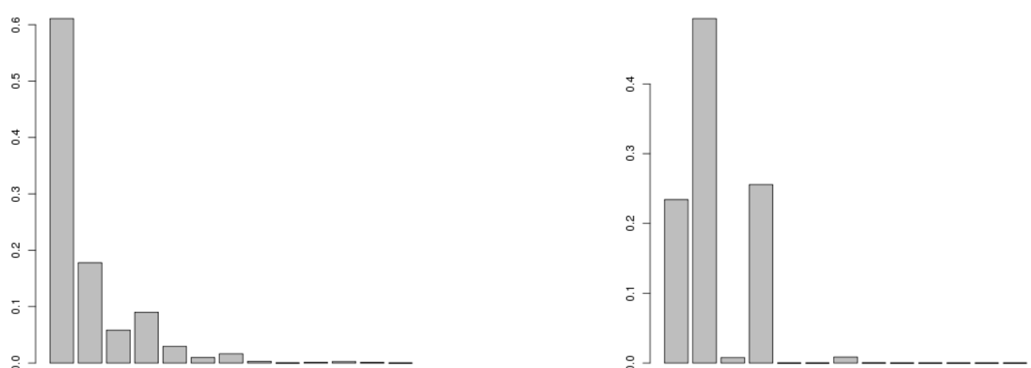


Figure 2. Triads (id vs. graph. reprs.)



(a) Software network

(b) Non-software network

Figure 3. Triad profiles

D. A Network Classification Model

Although the S-score of a network tells how close it is from software networks, it does not tell whether a network is close enough that it can be considered software-like. What is needed is a binary classification model that distinguishes software-like networks from the other networks. The distinction can be made by choosing a suitable S-score threshold. Networks with S-score below the threshold are considered dissimilar from software networks; only networks with S-score above the threshold are considered software-like.

As we have shown on the previous section, there are non-software networks with high S-scores, hence it is impossible to build a perfect classification model, regardless of the threshold. Nonetheless, such a model can be evaluated by its precision and recall. Consider a data set with both software and non-software networks. Let S be the set of all software networks, and L the set of all networks that were classified as software-like. The precision of the model is

$$precision : \frac{S \cap L}{L}$$

and the recall is

$$recall : \frac{S \cap L}{S}$$

Increasing the threshold has the effect of reducing the recall, because fewer software networks are classified as software-like. Decreasing the threshold has the effect of reducing the precision, since many non-software networks are classified as software-like.

The choice of a proper threshold, thus, depends on whether it is more important to have high precision of high recall. Because our research hypothesis is that networks synthesized by the presented models are software-like, higher precision means a stronger test, as fewer networks are classified as software-like.

To get 100% precision, the threshold needs to be 0.98, so the non-software network with highest S-score is below the threshold. The recall in this case, though, would be X%, which is too low, meaning the most software networks are misclassified. So we chose the value 0.88, that is immediatly greater than the second greater non-software network S-score. With this value, we have a high recall (X%) and a still high precision (X%).

VIII. Evaluation of Network Models

In the previous section it was shown that many networks, although scale-free, can be distinguished from software networks by a simple classification model based on triad concentration profiles. In this section we show empirically that the three network models previously presented synthesize networks that are indistinguishable from software networks.

The experiment consists of synthesizing networks using many combinations of parameters from the three models, and then classifying each network as software-like or non software-like. After that, we build a classification model for each model, based on model parameters.

A. Synthetic Data Set

We want to investigate if, with a proper choice of parameters, a model is capable of synthesizing a network that resembles software networks. Because the possible combinations of parameter values are infinite, we have set the number of vertices to 1000 and then varied the remaining parameters in discrete steps. In this section we describe the combinations of parameters values used for each model.

B. BCR+ networks

We have chosen five different module dependency networks, which where extracted from actual dependencies between archives of five different software systems of our sample. The module dependency networks are shown on Figure 4.

The probabilities p, q and r were given all possible values from 0.0 up to 1.0, in 0.2 steps, such as the sum of the probabilities was 1. Since the only events that create vertices are those associated with probabilities p and q, we imposed the additional restriction that p + q ¿ 0.

For deltain and deltaout we assigned the integer numbers from 0 to 4. TODO: why

Finally, we chose mu from 0.0 to 0.6 in 0.2 steps. It does not make sense to choose higher values since they mean that there will be more edges connecting different modules.

In total, 9,500 networks were synthesized.

C. LF networks

Like BCR, we choose mu ranging from 0.0 to 0.6 in 0.2 steps. For the remaining parameters we selected values from our sample of software systems. For degexp, ..., we picked the minimum, the median and the max values.

Total: 1,296 networks

D. CGW networks

We have varied each of the probabilities p1, p2, p3, and p4 from 0.0 to 1.0, in 0.2 steps, with $p1 > 0$ and $p1 + p2 + p3 + p4 = 1$. Each of the parameters $e1$, $e2$, $e3$, and $e4$ assumed the values 1, 2, 4, and 8.

alpha in -1, 0, 1, 10, 100, 1000. m in 2, 4, 8, 16, 32 (just like bcr and lfr)

In total, 38,790 networks were synthesized.

E. Results

We used our classifier ...

Table: Model — Number of Networks — Realistic Networks — Percent %

Show some graphs: histogram of average correlations for each model. 5

All models produce networks that resemble software networks. For some parameters, though, the networks are not realistic.

F. Parameter-Based Classification Models

1R

Naive Bayes

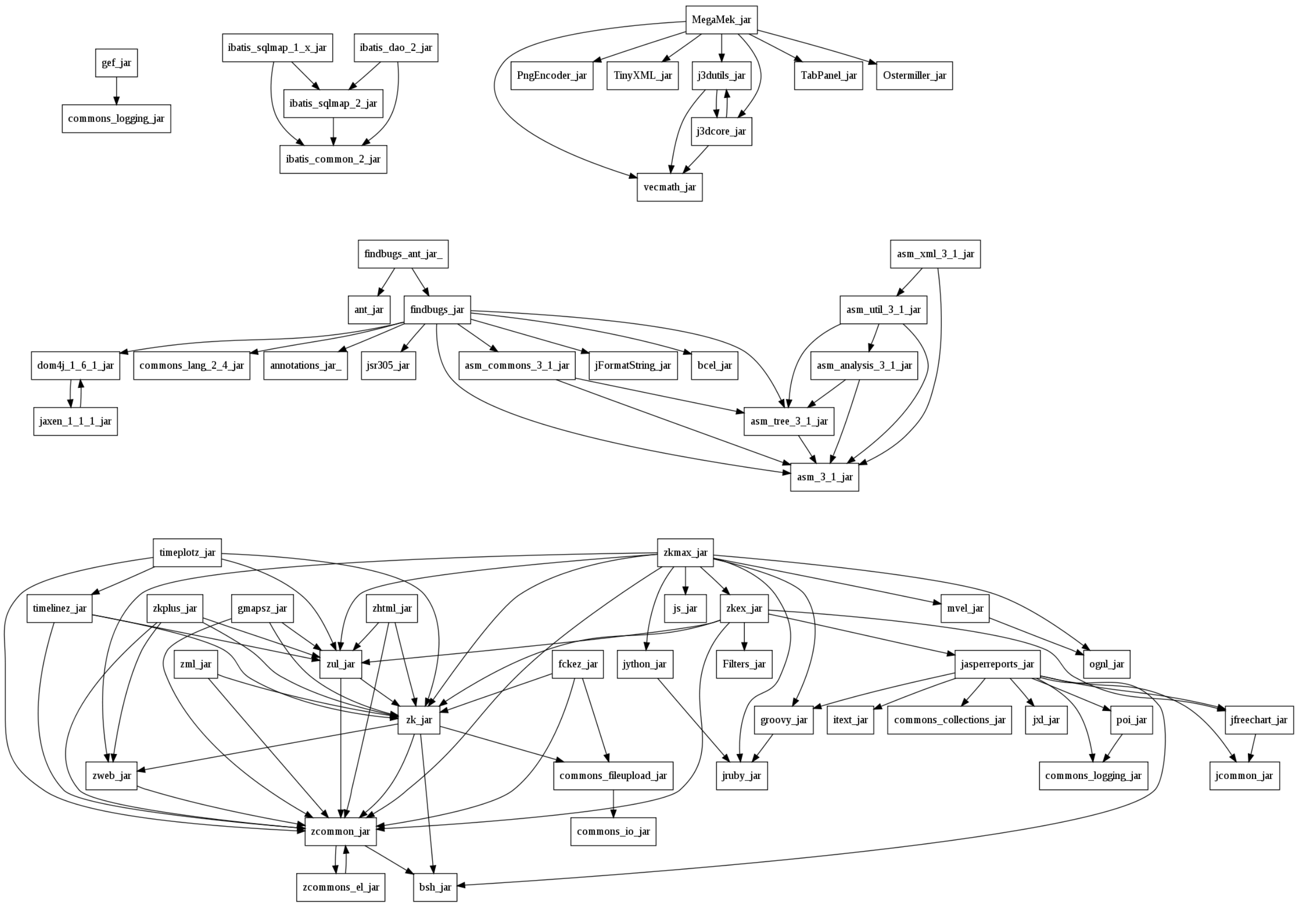


Figure 4. Module dependency graphs

G. Homogeinity

Pick realistic networks from a model. Are they similar to each other? (see standard deviation) In other words: do the parameters make a difference?

Are they similar to networks generated by the other models? In other words: are the models equivalent?

IX. Threats to validity

We generated only one network for each set of parameters. (as we've shown, some parameters are redundant as they do not change significantly the realism)

Some clustering algorithms use weights and they weren't studied here.

EV: We've only studied 65 systems, which is not that much.

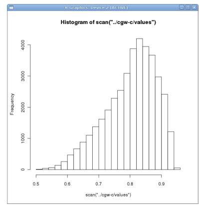
We only studied object-oriented systems implemented in Java. Maybe the results would be different if we studied systems implement in other languagens or using other paradigms. The choice of a particular technique for extracting dependencies (static analysis) may also have impact on the structure of the networks.

X. Conclusion and Future Work

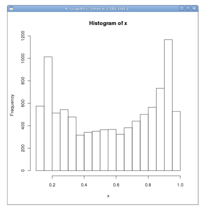
We have shown empirically that network models found in the literature can synthesize networks that resemble the network of dependencies between classes in object-oriented systems. This result supports the use of synthetic networks in the evaluation of software clustering algorithms.

The use of synthetic data is common in distributed computing research, but still underexplored in software engineering research. Because many reverse engineering tasks rely on dependency data, we expect this work to have impact beyond the software clustering community.

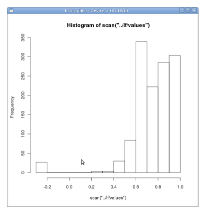
We accept that it is important to evaluate the algorithms with real software networks, but we argue that the use of synthetic networks in a complementary manner can give researchers new insights about the algorithms. First, the use of models allows the creation of large test sets, thus diminishing the small sample effects. Moreover, the networks are



(a) Software network



(b) Non-software network



(c) Non-software network

Figure 5. Triad profiles

created in a controlled way, according to model parameters, so it is possible to study the behavior of the algorithms with different parameter values.

In a future work, we intend to use synthetic networks in the evaluation of software clustering algorithms that were previously studied with real networks [10]. After that we will be able to compare the results obtained by both approaches.

XI. Appendix A: List of Networks

TODO: Show as Table: Name, Vertices, Edges

Software networks:

From SourceForge: AbaGuiBuilder-1.8 alfresco-labs-deployment-3Stable aoi272 stendhal-0.74 battlefieldjava-0.1 checkstyle-5.0 dom4j-1.6.1 findbugs-1.3.8 freetts-1.2.2-bin ganttproject-2.0.9 geoserver-2.0-beta1-bin geotools-2.5.5-bin gfp_0.8.1 hibernate-distribution-3.3.1.GA-dist hsqldb_1_8_0_10 iBATIS_DBL-2.1.5.582 iReport-nb-3.5.1 JabRef-2.5b2-src jailer_2.9.9 jalopy-1.5rc3 jasperreports-3.5.2-project jfreechart-1.0.13 pentaho-reporting-engine-classic-0.8.9.11 jGnash-2.2.0 jgraphpad-5.10.0.2 jmsn-0.9.9b2 juel-2.1.2 JXv3.2rc2deploy makagiga-3.4 MegaMek-v0.34.3 iFreeBudget-2.0.9 mondrian-3.1.1.12687 oddjob-0.26.0 openxava-3.1.2 pdfsam-1.1.3-out pjirc_2_2_1_bin pmd-bin-4.2.5 proguard4.3 smc_6_0_0 squirrel-sql-3.0.1-base squirrel-sql-3.0.1-standard tvbrowser-2.7.3-bin villonanny-2.3.0.b02.bin rapidminer-4.4-community zk-bin-3.6.1

From other places:

ArgoUML-0.28 GEF-0.13-bin Hl7Comm.1.0.1 IRPF2009v1.1 broker-4.1.5 dbwrench ec2-api-tools ermodeller-1.9.2-binary flyingsaucer-R8 gdata-src.java-1.31.1 guice-2.0 gwt-windows-1.6.4 jai-1_1_4-pre-dr-b03-lib-linux-i586-08_Jun_2009 jakarta-tomcat-5.0.28-embed juxy-0.8 myjgui_0.6.6 peer-4.1.5 subethasmtp-3.1 thinkui_sqlclient-1.1.2 worker-4.1.5

Other networks:

3 circuit networks (circuit-s208 circuit-s420 circuit-s838)

5 facebook networks (facebook-Caltech36 facebook-Georgetown facebook-Oklahoma facebook-Princeton facebook-UNC28)

5 language networks (lang-english lang-french lang-japanese lang-spanish)

43 metabolic networks

3 protein networks (protein-a4j protein-AOR protein-eaw)

2 social networks (social-leader social-prison)

other networks:

polblogs

yeast

beta3sreduced celegansneural

czech ecoli-metabolic

XII. Conclusion

The conclusion goes here. this is more of the conclusion

Acknowledgment

Dalton, Jorge, Christina, Garcia, Charles, Fabiola, Italo, Roberto, Jemerson, Sandra.

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