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Abstract

A graph drawing library is like a toolbox, allowing experts to select and configure a specialized algorithm in order to meet the requirements of their diagram visualization application. However, without expert knowledge of the algorithms the potential of such a toolbox cannot be fully exploited. This gives rise to the question whether the process of selecting and configuring layout algorithms can be automated such that good layouts are produced. In this paper we call this kind of automation "*meta layout*." We propose a genetic representation that can be used in meta heuristics for meta layout and contribute new metrics for the evaluation of graph drawings. Furthermore, we examine the use of an evolutionary algorithm to search for optimal solutions and evaluate this approach both with automatic experiments and a user study. The results confirm that our methods can actually help users to find good layout configurations.

Contents

1 Introduction

There are many different approaches for drawing graphs, and all have their specific strengths and weaknesses. Therefore successful graph drawing libraries include multiple algorithms, and usually they offer numerous configuration options to allow users to tailor the generated layouts to their needs. However, the proper choice of a layout algorithm as well as its configuration often require detailed knowledge of the background of these algorithms. Acquiring such knowledge or simply testing all available configuration options is not feasible for users who require quick results.

An inspiring idea was communicated by Biedl et al. [5]: by displaying multiple layouts of the same graph, the user may select those that best match her or his expectations. In this paper we build on that idea and apply meta heuristics for generating a variation of layouts using existing layout libraries.

We introduce the notion of *abstract layout*, which denotes the annotation of graphs with directives for layout algorithm selection and configuration. *Concrete layout* is a synonym for the *drawing* of a graph and is represented by the annotation of graph elements with position and size data. When a layout algorithm is executed on a graph, it transforms its abstract layout into a concrete layout. By *meta layout* we denote an automatic process of generating abstract layouts.

Our contributions are a genetic representation of abstract layouts, metrics for convenient evaluation of *aesthetic criteria* [20] of the concrete layouts, and operations for applying an evolutionary algorithm for meta layout. Furthermore, we propose a simple method for adapting the weights of aesthetic criteria according to the user-selected layouts, supporting the approach of Biedl et al. mentioned above. We performed automated as well as user-based experiments in order to evaluate our proposed methods. The results indicate that evolutionary meta layout can actually help inexperienced users to find good layouts for their graphs.

The remainder of this paper is organized as follows. In Chapter 2 we discuss related work on evolutionary graph layout and layout configuration. Chapter 3 introduces the necessary data structures and fitness function that enable the evolutionary process, which is described in Chapter 4. In Chapter 5 we report experimental results on the effectiveness and applicability of these methods. We conclude and outline prospective work in Chapter 6.

2 Related Work

Several authors have proposed evolutionary algorithms where the individuals are represented by lists of coordinates for the positions of the nodes of a graph [2, 6, 13, 15, 21, 22, 24]. Here, in contrast, we do not include any specific graph in our encoding of individuals, but we build on meta data of the available algorithms and their parameters, hence we can apply the result of our evolutionary algorithm to any graphs, even if they were not considered during the evolutionary process. Furthermore, we benefit from all features that are already supported by the existing algorithms, while previous approaches for evolutionary layout were usually restricted to draw edges as straight lines and did not consider additional features such as edge labels.

Other works have focused on integrating meta heuristics in existing layout methods. De Mendonça Neto and Eades proposed a system for automatic learning of parameters of a simulated annealing algorithm [9]. Utech et al. introduced a genetic representation that allows to combine the layer assignment and node ordering steps of the layer-based drawing approach with an evolutionary algorithm [23]. Such a combination of multiple NP-hard steps is also applied by Neta et al. for the *topology-shape-metrics* approach [18]. They use an evolutionary algorithm to find planar embeddings (*topology* step) for which the other steps (*shape* and *metrics*) are able to create good layouts.

Bertolazzi et al. proposed a system for automatic selection of layout algorithms that best match the user's requirements [4]. The system is initialized by evaluating the available algorithms with respect to a set of aesthetic criteria using randomly generated graphs of different sizes. The user has to provide a ranking of the criteria according to her or his preference. When a layout request is made, the system determines the difference between the user's ranking and the evaluation results of each algorithm for graphs of similar size as the current input graph. The algorithms with the lowest difference are offered to the user.

Similarly, Niggemann and Stein proposed to build a data base that maps vectors of structural graph features, e. g. the number of nodes and the number of connected components, to the most suitable layout algorithm with respect to some predefined combination of aesthetic criteria [19]. These data are gathered by applying the algorithms to a set of "typical" graphs. A suitable algorithm for a given input graph is chosen by measuring its structural features and comparing them with the entries present in the data base. The main problem of the approaches of Bertolazzi et al. and Niggemann and Stein is that the result of layout algorithm selection may vary a lot depending on the set of graphs used to evaluate the algorithms. In particular, randomly generated graphs are often structurally very different from those that occur in an actual application. Our method, in contrast, evaluates layout algorithms using the same graphs for which layouts are requested.

Archambault et al. combined graph clustering with layout algorithm selection in a

multi-level approach [1]. The clustering process is tightly connected with the algorithm selection, since both aspects are based on topological features of the input graph. When a specific feature is found, e. g. a tree or a clique, it is extracted as a subgraph and processed with a layout algorithm that is especially suited for that feature: a tree is processed with tree layout, and a clique is processed with circular layout. This kind of layout configuration depends on detailed knowledge of the behavior of the algorithms, which has to be encoded explicitly in the system, while the solution presented here can be applied to any algorithm independently of their behavior.

3 Genotypes and Phenotypes

The *genotype* of an individual is its genetic code, while the *phenotype* is the total of its observable characteristics. In biology a phenotype is formed from its genotype by growing in a suitable environment. We propose to use abstract layouts (configurations) as genotypes, and concrete layouts (drawings) as phenotypes. The "environment" for this kind of phenotypes is a graph. We generate the concrete layout $L(\lambda)$ that belongs to a given abstract layout λ by applying all parameters encoded in λ to the chosen layout algorithm A, which is also encoded in λ, and executing A on the graph given by the environment. This encoding of parameters and algorithm selection is done with a set of *genes*, which together form a *genome*. A gene consists of a *gene type* with an assigned value. The gene type has an identifier, a data type (integer, floating point, Boolean, or enumeration), optional lower and upper bounds, and an optional parameter controlling the standard deviation of Gaussian distributions.

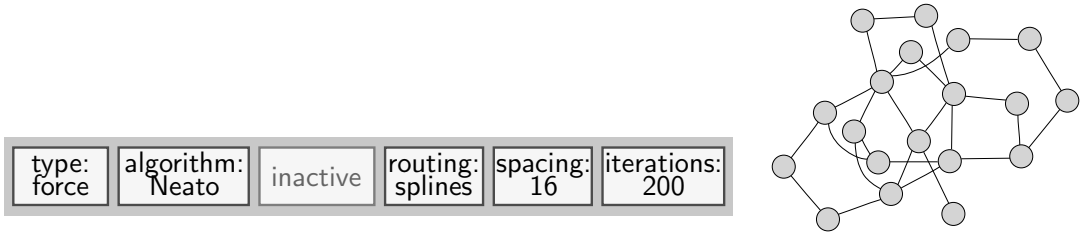
We assign each layout algorithm to a *layout type* depending on the underlying approach implemented in the algorithm. The main layout types are *layer-based*, *force-based*, *circular*, *orthogonal*, *tree*, and *planar*. Each algorithm A has a set P_A of parameters that control the behavior of A. We consider the union $\mathcal{P} = \bigcup P_A$ of all parameters, which we call the set of *layout options*. Each genome contains a gene g_T for selecting the layout type, a gene g_A for selecting the layout algorithm, and one for each layout option in $\mathcal{P}$. It is also possible to use only a subset of these genes, as long as all generated genomes contain the same subset. Such a restriction can serve to focus on the selected layout options in the optimization process, while other options are kept constant.

Some genes of a genome are dependent of each other. The gene g_A, for instance, is constrained to be set to a layout algorithm that belongs to the layout type selected in g_T. Furthermore, the layout algorithm A selected in g_A does not support all layout options in $\mathcal{P}$, therefore the options in $\mathcal{P} \setminus P_A$, i. e. those not supported by A, are marked as *inactive*. A genome with six genes and a possible phenotype are shown in Figure 1.

Inactive genes of a genome G do not contribute to the characteristics of the phenotype of G, i. e. of its drawing, hence two genomes that differ only in their inactive genes may produce the same drawing. On the other hand, some layout algorithms are randomized and produce different drawings when executed twice with the same configuration, even when applied to the same graph.

The genetic representation introduced above requires meta data about available layout algorithms and their supported parameters. We express these data in an XML format using *extension points* of the Eclipse platform.[1]

[1] `http://www.eclipse.org/resources/resource.php?id=495`



(a) Genotype (b) Phenotype

Figure 1: (a) A genome with six genes. The layout type gene is set to force-based algorithms, the layout algorithm gene is set to a specific algorithm named "Neato", and three parameters of that algorithm are set with the remaining genes. One gene is inactive because the corresponding layout option is not supported by Neato. (b) A phenotype of the genome, represented by a layout generated by Neato for an arbitrary graph.

3.1 Fitness Function

Our genotypes have a completely different representation compared to previous evolutionary layout algorithms. The phenotypes, in contrast, are commonly represented by graph layouts, hence we can apply the same fitness evaluation methods as many other previous solutions. The most obvious approach is the evaluation of aesthetic criteria [20]. This process requires an evaluation graph G, to which all layout algorithms are applied, and a selection of criteria for judging the generated layouts.

Some authors used a linear combination of specific criteria as fitness function [3, 6, 13]. For instance, given a graph layout L, the number of edge crossings $\kappa(L)$, and the standard deviation of edge lengths $\delta(L)$, the optimization goal could be to minimize the cost function $f(L) = w_c\kappa(L) + w_d\delta(L)$, where suitable scaling factors w_c and w_d are usually determined experimentally. The problem of this approach is that the values resulting from $f(L)$ have no inherent meaning apart from the general assumption "the smaller $f(L)$, the better the layout L." As a consequence, the cost function can be used only as a relative measure, but not to determine the absolute quality of layouts.

Huang et al. proposed to compute the difference of aesthetic criteria x to their mean value $\bar{x}$ among all considered layouts and to scale it by their standard deviation $\sigma(x)$ [16]. The fitness is then determined as $f(L) = \sum_i \frac{x_i(L)-\bar{x}_i}{\sigma(x_i)}$, where $x_1, \ldots, x_q$ are the included criteria. This approach has the disadvantage that the mean values and standard deviations can vary greatly depending on the set of considered layouts. Therefore it cannot be used as an absolute quality measure.

An improved variant, proposed by several authors, is to normalize the criteria to the range between 0 and 1 [11, 20, 21, 22, 24]. However, this is still not sufficient to effectively measure absolute layout quality. For instance, Tettamanzi normalizes the edge crossings $\kappa(L)$ with the formula $\mu_c(L) = \frac{1}{\kappa(L)+1}$ [22]. For the complete graph K_5, which is not planar, event the best layouts yield a result of $\mu_c(L) = 50\%$, suggesting that the layout is only half as good as it could be. Purchase proposed to scale the number of crossings against an upper bound κ_{max} defined as the number that results when all

pairs of edges that are not incident to the same node cross each other [20]. Her formula is $\mu_c(L) = 1 - \frac{\kappa(L)}{\kappa_{max}}$ if $\kappa_{max} > 0$ and $\mu_c(L) = 1$ otherwise. Purchase herself notes that this definition "is biased towards high values." For instance, the graph N14 used in her evaluations has 24 nodes, 36 edges, and $\kappa_{max} = 558$. All layouts with up to 56 crossings would result in $\mu_c(L) > 90\%$. When tested with a selection of 28 layout algorithms, all of them resulted in layouts with less that 56 crossings (the best had only 11 crossings), hence the formula of Purchase would assign a very high fitness to all these generated layouts.

We propose new normalization functions that aim at well-balanced distributions of values among typical results of layout algorithms. A *layout metric* is a function μ that maps graph layouts L to values $\mu(L) \in [0, 1]$. Given layout metrics $\mu_1, \ldots, \mu_k$ with weights $w_1, \ldots, w_k \in [0, 1]$, we compute the fitness of a graph layout L by

$$f(L) = \frac{1}{\sum_{i=1}^{k} w_k} \sum_{i=1}^{k} w_k \mu_k(L) \ . \tag{3.1}$$

In the following we describe some of the metrics we have used in conjunction with our proposed genotype representation and evolutionary algorithm. The goal of these metrics is to allow an intuitive assessment of the respective criteria, which means that the worst layouts shall have metric values near 0%, the best ones shall have values near 100%, and moderate ones shall score around 50%. The metrics should be parameterized such that this spectrum of values is exhausted for layouts that are generated by typical layout algorithms, allowing to clearly distinguish them from one another. Additionally to the metrics presented here, we adopt previously proposed metrics that already meet our requirements, e. g. for the number of edge bends and the number of edges pointing in a specific direction as given by Purchase [20].

The basic idea behind each of our formulae is to define a certain *input split value* x_s such that if the value of the respective criterion equals x_s, the metric is set to a defined *output split value* μ^*. Values that differ from x_s are scaled towards 0 or 1, depending on the specific criterion. This approach involves several constants, which we determined experimentally.

Let $G = (V, E)$ be a directed graph with a layout L. Let $n = |V|$ and $m = |E|$.

Number of crossings. Similarly to Purchase we define a virtual upper bound $\kappa_{max} = m(m-1)/2$ on the number of crossings [20]. We call that bound virtual because it is valid only for straight-line layouts, while layouts where edges have bend points can have arbitrarily many crossings. Based on the observation that crossings tend to be more likely when there are many edges and few nodes, we further define an input split value

$$\kappa_s = \min \left\{ \frac{m^3}{n^2},\ (1 - \mu_c^*)\kappa_{max} \right\} \ . \tag{3.2}$$

μ_c^* is the corresponding output split value, for which we chose $\mu_c^* = 10\%$. The exponents of m and n are chosen such that the split value becomes larger when the m/n ratio is

high. We denote the number of crossings as $\kappa(L)$. Layouts with $\kappa(L) < \kappa_\mathrm{s}$ yield metric values above μ_c^*, while layouts with $\kappa(L) > \kappa_\mathrm{s}$ yield values below μ_c^*. This is realized with the formula

$$\mu_\mathrm{c}(L) = \begin{cases} 1 & \text{if } \kappa_\mathrm{max} = 0, \\ 0 & \text{if } \kappa(L) \geq \kappa_\mathrm{max} > 0, \\ 1 - \frac{\kappa(L)}{\kappa_\mathrm{s}}(1 - \mu_\mathrm{c}^*) & \text{if } \kappa(L) \leq \kappa_\mathrm{s}, \\ \left(1 - \frac{\kappa(L) - \kappa_\mathrm{s}}{\kappa_\mathrm{max} - \kappa_\mathrm{s}}\right)\mu_\mathrm{c}^* & \text{otherwise.} \end{cases} \tag{3.3}$$

Area. Let $w(L)$ be the width and $h(L)$ be the height of the drawing L. The area required to draw a graph depends on the number of nodes and edges, hence we define a *relative area*

$$\alpha(L) = \frac{w(L)h(L)}{(n+m)^2} \tag{3.4}$$

that takes into account the number of elements in the graph. We square that number because we observed that many drawings of larger graphs require a disproportionately high area. We split the output values at two points $\mu_\mathrm{a}^* = 10\%$ and $\mu_\mathrm{a}^{**} = 95\%$, with corresponding input split values α_s1 and α_s2. Values below μ_a^* are met when $\alpha(L) > \alpha_\mathrm{s1}$, values above μ_a^{**} are met when $\alpha(L) < \alpha_\mathrm{s2}$, and values in-between are scaled proportionally. The constants α_s1 and α_s2 have been determined experimentally as 1000 and 50, respectively. We define the area metric as

$$\mu_\mathrm{a}(L) = \begin{cases} \frac{\alpha_\mathrm{s1}}{\alpha(L)}\mu_\mathrm{a}^* & \text{if } \alpha(L) > \alpha_\mathrm{s1}, \\ 1 - \frac{\alpha(L)}{\alpha_\mathrm{s2}}(1 - \mu_\mathrm{a}^{**}) & \text{if } \alpha(L) < \alpha_\mathrm{s2}, \\ \left(1 - \frac{\alpha(L) - \alpha_\mathrm{s2}}{\alpha_\mathrm{s1} - \alpha_\mathrm{s2}}\right)(\mu_\mathrm{a}^{**} - \mu_\mathrm{a}^*) + \mu_\mathrm{a}^* & \text{otherwise.} \end{cases} \tag{3.5}$$

Aspect ratio. The aspect ratio $r(L)$ of a drawing is the ratio of its width $w(L)$ to its height $h(L)$. This measure is important to effectively display graphs on typical media such as computer screens or sheets of paper. We choose the *golden ratio* $r_\mathrm{g} \approx 1.618$ as the optimal value for aspect ratios. The computation of a metric from this optimum is rather simple:

$$\mu_\mathrm{r}(L) = \begin{cases} \frac{r_\mathrm{g}}{r(L)} & \text{if } r(L) \geq r_\mathrm{g}, \\ \frac{r(L)}{r_\mathrm{g}} & \text{otherwise.} \end{cases} \tag{3.6}$$

Edge length. Many force-based layout algorithms aim at ideal edge lengths [12]. Similar formulae as those used in these algorithms could be applied to compute a layout metric for the edge length. Here we propose a formula based on the average edge length $\bar{\lambda}(L)$ and an ideal edge length λ_opt:

$$\mu_\mathrm{l}(L) = \begin{cases} \frac{\lambda_\mathrm{opt}}{\bar{\lambda}(L)} & \text{if } \bar{\lambda}(L) \geq \lambda_\mathrm{opt}, \\ \sqrt{\frac{\bar{\lambda}(L)}{\lambda_\mathrm{opt}}} & \text{otherwise.} \end{cases} \tag{3.7}$$

We chose $\lambda_{\text{opt}} = 60$ experimentally. The square root for values below the ideal length serves to raise the metric result for drawings with very short edges.

Edge length uniformity. We measure this criterion with the standard deviation $\sigma_\lambda(L)$ of edge lengths and compare it against the average edge length $\bar{\lambda}(L)$, which we use as input split value. We define

$$\mu_{\text{u}}(L) = \begin{cases} \frac{\bar{\lambda}(L)}{\sigma_\lambda(L)}\mu_{\text{u}}^* & \text{if } \sigma_\lambda(L) \geq \bar{\lambda}(L), \\ 1 - \frac{\sigma_\lambda(L)}{\bar{\lambda}(L)}(1 - \mu_{\text{u}}^*) & \text{otherwise,} \end{cases} \tag{3.8}$$

where the output split value $\mu_{\text{u}}^* = 20\%$ corresponds to the metric value that results when the standard deviation equals the average.

3.2 Distance Function

The difference between two solutions can be determined either on the genotype level or on the phenotype level. The latter means comparing the drawings of the two individuals, which can be done with *difference metrics* [7]. Such metrics, however, are rather expensive in terms of computation time. Therefore we propose a distance function that compares solutions by their genomes, which is much more efficient because it is independent of the size of the graphs given by the environment.

The distance $d(X_1, X_2)$ of two genomes X_1 and X_2 is determined by the sum of the differences of all genes. We assume that for each gene in X_1 a corresponding gene of the same type is contained in X_2. Given values g_1 and g_2 of two genes with the same type t, we define their difference as

$$d(g_1, g_2) = \frac{|g_1 - g_2|}{\sigma_t} \tag{3.9}$$

if t has integer or floating point values, where σ_t is the standard deviation assigned to the type t. Genes with other data types have no inherent ordering, therefore we define their difference as $d(g_1, g_2) = 0$ if $g_1 = g_2$, and $d(g_1, g_2) = 1$ otherwise.

4 Evolutionary Process

The genetic encoding presented in Chapter 3 can serve as basis for numerous meta heuristics. In this section we discuss one possible heuristic with the goal of creating a starting point of further research, without claiming that this is the ultimate solution. We use an evolutionary algorithm, a popular method for searching large solution spaces.

A *population* is a set of genomes. An *evolution cycle* is a function that modifies a population with four steps, which are explained below. The evolutionary algorithm executes the evolution cycle repeatedly, checking some terminating condition after each execution. Simple conditions for fully automatic optimization are to limit the number of iterations and to check whether the fitness of the best individual exceeds a certain threshold. Alternatively, the user can be involved by manually controlling when to execute the next evolution cycle and when to stop the process. The four steps of the evolution cycle are discussed in the following and exemplified in Figure 2.

1. Recombination. New genomes are created by crossing random pairs of existing genomes. A crossing of two genomes is created by crossing all their genes. Two integer or floating point typed genes are crossed by computing their average value, while for other data types one of the two values is chosen randomly. Only a selection of the fittest individuals is considered for mating.

When the parent genomes have different values for the layout algorithm gene, the child is randomly assigned one of these algorithms. As a consequence, the *active / inactive* statuses of the other genes of the child must be adapted such that they match the chosen algorithm A: each gene g is made active if and only if A supports the layout option associated to g.

2. Mutation. Genomes have a certain probability of mutating. A mutation is done by randomly modifying its genes, where each gene g has an individual mutation probability p_g depending on its type. We assign the highest p_g values to genes with integer or floating point values, medium values to genes with Boolean or enumeration values, and the lowest values to the layout algorithm and layout type genes. Let g be a gene with value x. If the data type of g is integer or floating point, the new value x' is determined using a Gaussian distribution using x as its average and the standard deviation assigned to the gene type of g. If x' exceeds the upper or lower bound assigned to the gene type of g, it is corrected to a value between x and the respective bound. For genes with other types, which have no specific order, a new value is chosen based on a uniform distribution over the finite set of values, excluding the previous value. When the layout algorithm gene mutates, the *active / inactive* statuses of other genes must be updated

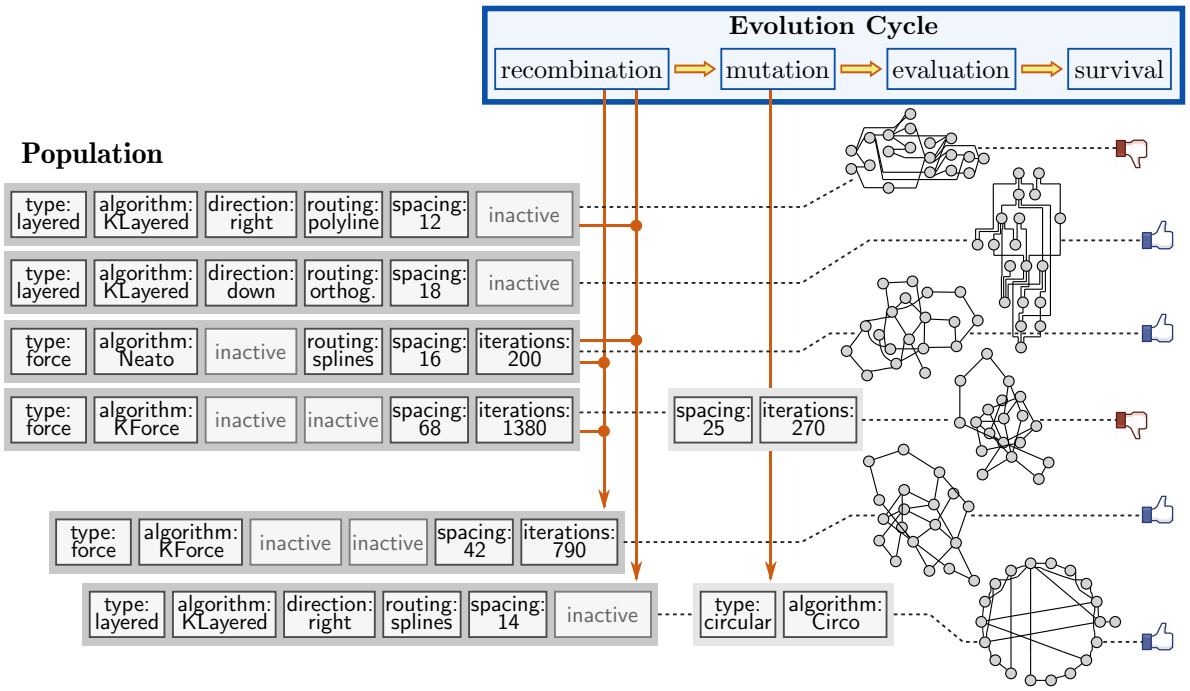


Figure 2: Evolutionary meta layout example: starting with a population of four genomes, two new genomes are created through recombination, two genomes are mutated, and four of the resulting genomes survive after their evaluation.

as described for the recombination step.

3. Evaluation. A fitness value is assigned to each genome that does not have one yet (see Section 3.1), which involves executing the encoded layout algorithm in order to obtain a corresponding phenotype. The population is sorted using these fitness values.

4. Survival. Only the fittest individuals survive. Checking all genomes in order of descending fitness, we include each genome X in the set of survivors if and only if it meets the following requirements: (i) its fitness exceeds a certain minimum, (ii) the maximal number of survivors is not reached yet, and (iii) the distance of X to other individuals is sufficient. The latter requirement serves to support the diversity of the population. Comparing all pairs of individuals would require a quadratic number of distance evaluations, therefore we apply the distance function d introduced in Section 3.2 only to some random samples X' from the current set of survivors. In order to meet the third requirement, $d(X, X') \geq d_{\min}$ must hold for a fixed minimal distance $d_{\min}$.

4.1 Choosing Metric Weights

The fitness function discussed in Section 3.1 uses layout metrics $\mu_1, \ldots, \mu_k$ and weights $w_1, \ldots, w_k \in [0, 1]$, where each w_i controls the influence of μ_i on the computed fitness.

The question is how to choose suitable weights. Masui proposed to apply genetic programming to find a fitness function that best reflects the user's intention [17]. The computed functions are evolved as Lisp programs and are evaluated with layout examples, which have to rated as "good" or "bad" by the user. A similar approach is used by Barbosa and Barreto [2], with the main difference that the fitness function is evolved indirectly by modifying a set of weights with an evolutionary algorithm. Additionally, they apply another evolutionary algorithm to create concrete layouts of a given graph. Both algorithms are combined in a process called *co-evolution*: the results of the weights evolution are used for the fitness function of the layout evolution, while the fitness of the weights is determined based on user ratings of sample layouts.

We have experimented with two much simpler methods, both of which involve the user: (a) the user directly manipulates the metric weights with sliders allowing values between 0 and 1, and (b) the user selects good layouts from the current population and the metric weights are automatically adjusted according to the selection. This second method builds on the assumption that the considered layout metrics are able to compute meaningful estimates of the absolute quality of any given layout (see Section 3.1). Let $\bar{\mu}_1, \ldots, \bar{\mu}_k$ be the average values of the layout metrics $\mu_1, \ldots, \mu_k$ for the selected layouts. Furthermore, let $w_1, \ldots, w_k$ be the current metric weights. For each $i \in \{1, \ldots, k\}$ we determine a *target weight*

$$w_i^* = \begin{cases} 1 - \frac{1}{2}\left(\frac{1-\bar{\mu}_i}{1-\mu_{\mathrm{w}}^*}\right)^2 & \text{if } \bar{\mu}_i \geq \mu_{\mathrm{w}}^*, \\ \frac{1}{2}\left(\frac{\bar{\mu}_i}{\mu_{\mathrm{w}}^*}\right)^2 & \text{otherwise,} \end{cases} \tag{4.1}$$

where μ_{w}^* is a constant that determines which metric result is required to reach a target weight of 50%. We chose $\mu_{\mathrm{w}}^* = 70\%$. The new weight of the layout metric μ_i is $w_i' = \frac{1}{2}(w_i + w_i^*)$.

4.2 User Interface

We have experimented with a user interface that includes both variants for modifying metric weights, shown in Figure 3. The window visualizes populations by presenting up to 16 small drawings of the evaluation graph, which represent the fittest individuals of the current population. 13 metrics are shown on the side of the window. The user may use the controls in the window to

- view the computed values of the layout metrics for an individual,
- directly set the metric weights,
- select one or more favored individuals for indirect adjustment of weights,
- change the population by executing an evolution cycle ("Evolve" button),
- restart the evolution with a new initial population ("Restart" button), and

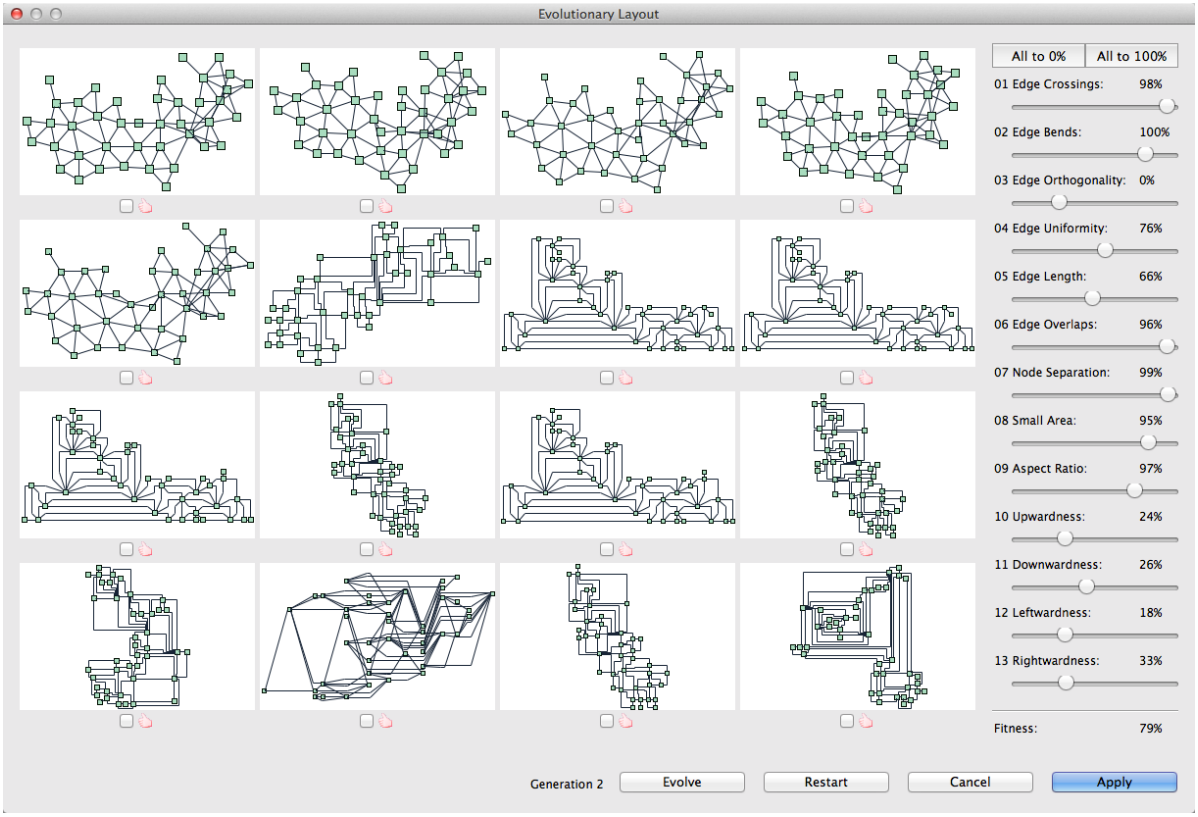


Figure 3: User interface for evolutionary meta layout, showing drawings for 16 individuals of the current population. The check box below each proposed graph drawing is used to select favored layouts for automatic adaption of metric weights. The sliders on the right offer direct manipulation of the weights.

- finish the process and select the abstract layout encoded in a selected individual ("Apply" button).

The indirect method for choosing weights, which adapts them according to the user's selection of favored layouts, is in line with the *multidrawing* approach introduced by Biedl et al. [5]. The main concept of that approach is that the user can select one of multiple offered drawings without the need of defining her or his goals and preferences in the first place. The multidrawing system reacts on the user's selection and generates new layouts that are similar to the selected ones. In our proposed method, this similarity is achieved by adjusting the fitness function such that the selected layouts are assigned a higher fitness, granting them better prospects in the competition against other layouts.

5 Evaluation

The methods presented in this paper have been implemented and evaluated in KIELER, an Eclipse-based open source project.[1] Our experiments included four layout algorithms from KIELER as well as five algorithms from the Graphviz library [14] and 22 algorithms from the OGDF library [8]. The total number of genes in each genome was 79.

5.1 Execution Time

We tested the performance of evolutionary meta layout on a set of 100 generated graphs with varying number of nodes $2 \leq n \leq 100$ and $e = 1.5\,n$ edges. The tests have been executed with an Intel Xeon 2.5 GHz CPU. The population contained 16 genomes, the recombination operation bred 13 new genomes, and the mutation operation affected 60% of the whole population, thus 22.6 new genomes were created on average. This means that about 23 layout algorithm executions had to be performed for the evaluation operation of each evolution cycle, and each layout metric has been evaluated just as often. We measured the average execution time of one evolution cycle, which led to the results shown in Figure 4. The vast majority of time is spent in the evaluation step: on average 74% is taken by layout algorithm execution, and 20% is taken by metrics evaluation. The rather high execution time limits the number of evolution cycles that can be performed in an interactive environment. The consequence is that the evolutionary algorithm has to converge to an acceptable solution within few iterations. However, the evaluation step is very suitable for parallelization, since the evaluations are all independent. As seen in Figure 4, the total execution time can be reduced by half when run with multiple threads on a multicore machine (eight cores in this example).

5.2 Programmatic Experiments

Layout metrics. We evaluated the layout metrics proposed in Section 3.1 using the set of 1277 graphs collected by North [10]. For each of these graphs, we created 100 random layout configurations, executed the respective layout algorithms to obtain concrete layouts, and computed the metric values for those layouts. In order to fulfill the goals stated in Section 3.1, the metrics should yield low values for bad layouts and high values for good layouts, hence, with an ideal formula, all values between 0 and 1 should occur when applied to layouts generated by layout algorithms. We evaluated this by measuring the standard deviations, minima, and maxima of the layout metric results. A uniform

[1] `http://www.informatik.uni-kiel.de/rtsys/kieler/`

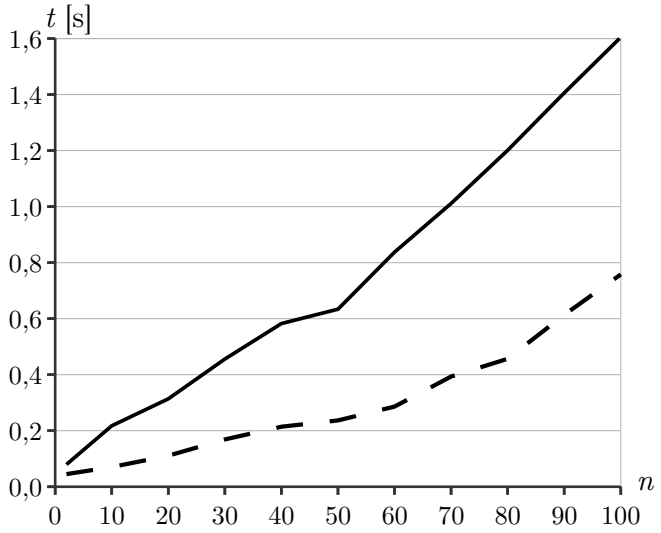


Figure 4: Execution time t plotted by number of nodes n with single core execution (solid line) and multicore execution (dashed line).

Metric	$\bar{\mu}$	$\sigma(\mu)$	$\bar{\sigma}(\mu)$	$\bar{\mu}_{\min}$	$\bar{\mu}_{\max}$
Crossings	82.3%	27.6%	23.3%	9.4%	99.9%
Area	82.8%	23.7%	22.8%	5.1%	99.8%
Aspect Ratio	58.0%	21.5%	20.9%	7.7%	97.5%
Edge Length	47.7%	28.4%	26.3%	5.0%	98.1%
Uniformity	45.6%	24.1%	22.2%	13.0%	88.7%

Table 1: Results of layout metrics evaluations for the North graphs. $\bar{\mu}$ is the total average of the respective metric, $\sigma(\mu)$ is its standard deviation, $\bar{\sigma}(\mu)$ is the average of the standard deviations determined for each graph, $\bar{\mu}_{\min}$ is the average of the minimum values for each graph, and $\bar{\mu}_{\max}$ is the average of the maximum values for each graph.

distribution over the range $[0, 1]$ has the standard deviation 0.289 (28.9%), the minimum 0%, and the maximum 100%. The values measured for the North graphs are shown in Table 1. These values are quite close to the ideal values of the uniform distribution, in particular those of the edge crossings and the edge length metrics. We conclude that our proposed formula for layout metrics computation are suitable as absolute quality measures for drawings generated by typical graph layout algorithms.

Evolutionary algorithm. We carried out three experiments in order to verify the effectiveness of the evolutionary approach. The experiments had different optimization goals: minimal number of edge crossings, maximal number of edges pointing left, and optimal uniformity of edge lengths. In each experiment the corresponding layout metric was given a weight of 100%, while all other metrics were deactivated. 30 randomly generated graphs were used as evaluation graphs. In the crossing minimization experi-

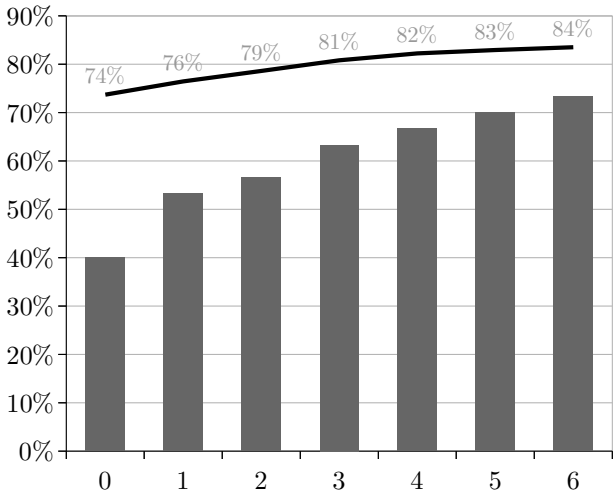


Figure 5: Result of the edge uniformity experiment. The line on top shows the fitness values of the best genomes for iterations 0 to 6 (horizontal axis), while the bars show the fractions of genomes that are set to force-type algorithms.

ment, for 60% of the graphs a planarization-based algorithm was selected as the genome with highest fitness after three or less iterations. This confirms the intuitive expectation, since planarization methods are most effective in minimizing edge crossings. In the experiment that aimed at edges pointing left, for 90% of the graphs a layer-based algorithm was selected as the genome with highest fitness after three or less iterations. Additionally, the layout option that determines the main direction of edges had to be set to *left*, which was accomplished in 83% of the cases. In the edge uniformity experiment, for 77% of the graphs a force-based algorithm was selected as the genome with highest fitness after six or less iterations (see Figure 5). This result matches the expectation, too, because force-based methods aim at drawing all edges with uniform length. In all experiments it could be observed that the average rating of genomes was consistently rising after each iteration of the evolutionary cycle. We conclude that our proposed evolutionary meta layout approach can effectively optimize given aesthetic criteria, and in most cases the kind of layout algorithm that is automatically selected is consistent with the intuition. A very relevant observation is that the process tends to converge very quickly, often yielding good solutions after few iterations, e. g. as illustrated in Figure 5. On the other hand, in some cases the computation is trapped in local optima, which could possibly be avoided by improving the parameters of the evolutionary computation.

5.3 User Study

We have conducted a user study to determine the practical usefulness of our approach. The study is based on a set of 8 graphs, inspired by real-world examples that were found on the web, with between 15 and 43 nodes and 18 to 90 edges. 25 persons participated in the study: four members of our research group, 17 computer science students, and four

persons who were not involved in computer science. For novice users we expected that the evolutionary meta layout approach would lead to a significantly higher efficiency in graph readability compared to direct manipulation of layout configurations. We did not expect such an improvement for the research group members, who are experts in graph layout technology and are likely to have predetermined opinions about which layout configurations to use in certain contexts.

For each graph, the participants were presented three tasks regarding connectivity, e. g. finding the shortest path between two given nodes. The participants then had to find a layout configuration which they regarded as useful for working on the tasks. The test instructions encouraged the participants to improve the layout configuration until they were sure they had found a well readable layout.

Four of the graphs were treated with the user interface of the evolutionary meta layout, presented in Section 4.2 and named Evol in the following, which evolves a population of layout configurations and lets users pick configurations by their previews. For the other four graphs, the participants were required to find layout configurations manually by choosing from a list of available layout algorithms and modifying parameters of the chosen algorithms. For each participant we determined randomly which graphs to treat with Evol and which to configure with the manual method, called Manual in the following. After the participants had accepted a layout configuration for a graph, they worked on the respective tasks by inspecting the drawing that resulted from the configuration.

After all graphs were done, the participants were asked 6 questions about their subjective impression of the evolutionary approach. The overall response to these questions was very positive: on a scale from -2 (worst rating) to 2 (best rating), the average ratings were 1.0 for the quality of generated layouts, 0.8 for their variety, 1.2 for the time required for finding suitable layouts, 0.6 for the effectiveness of manually setting metric weights, and 1.5 for the effectiveness of adjusting metric weights by favoring individuals. Most notably, the indirect adjustment of metric weights was rated much higher than their direct manipulation. This indicates that most users prefer an intuitive interface based on layout proposals instead of manually setting parameters of the fitness function, since the latter requires to understand the meaning of all layout metrics.

The objective results of the user study confirm the subjective evaluation: the average rate of correct answers of non-expert users to the tasks was 77.4% for Manual and 79.8% for Evol. Furthermore, the average time used to work on each task was lower by 7.5% with Evol (131 seconds) compared to Manual (142 seconds). When comparing the median values, which tend to eliminate the influence of outliers, the improvement of the working times is even more significant: 18.6% lower with Evol compared to Manual. Expert users, in contrast, did not benefit from the evolutionary approach: on average, their rate of correct answers was equal for both methods, and the time for working on the tasks did not improve, but was even higher with Evol than with Manual. This confirms the assumption that the method proposed in this paper is more suitable in applications used by persons without expert knowledge on graph drawing.

Table 2 shows the results for each of the eight graphs that were chosen for the user study. The values in the row labeled “Average” differ from the total averages given

Graph	Rate of correct answers			Average working time (seconds)		
	Man. (r_M)	Evol (r_E)	$r_E - r_M$	Man. (t_M)	Evol (t_E)	$t_E - t_M$
afcon	61.1%	92.6%	**31.5%**	226.6	144.2	**−82.4**
climate	87.5%	89.7%	**2.2%**	117.6	129.8	**12.2**
mysql	100.0%	100.0%	**0.0%**	85.0	80.4	**−4.6**
nz-threat	93.3%	87.9%	**−5.4%**	63.1	71.9	**8.8**
presocrat	50.0%	35.6%	**−14.4%**	161.2	184.2	**23.0**
salamand	85.7%	95.2%	**9.5%**	126.9	116.7	**−10.1**
sanskrit	59.0%	66.7%	**7.7%**	188.8	184.9	**−4.0**
time	82.0%	87.5%	**5.5%**	131.9	139.6	**7.7**
Average	77.3%	81.9%	**4.6%**	137.6	131.5	**−6.2**

Table 2: Rate of correct answers and average time for working on the tasks for the 21 non-expert participants of the experiment. Results that confirm the assumption that layouts created with Evol are more readable than those created with Manual are highlighted in green, while results that do not confirm the assumption are highlighted in red.

above because for each graph the ratio of the number of participants who worked with Manual and those who worked with Evol was different. This is due to the random assignment of configuration methods to the graphs. However, the overall averages shown in Table 2 confirm the already discussed results.

Many participants commented that they clearly preferred Evol over Manual. It could be observed that novice users were overwhelmed by the number of configuration parameters shown for the manual method. In many cases, they stopped trying to understand the effects of the parameters after some unsuccessful attempts to fine-tune the layout. For the Evol interface, on the other hand, similarly frustrating experiences were observed in few cases where the evolutionary algorithm apparently ran into local optima that did not satisfy the users' expectations.

6 Conclusion

We introduced the notion of meta layout, which means creating an abstract layout by choosing and parameterizing a layout algorithm, which in turn generates a concrete layout of a graph. We presented a genetic representation of abstract layouts, metrics for building a fitness function, and an evolutionary algorithm for developing a population of abstract layouts. Furthermore, we proposed a simple method for the indirect adjustment of weights of layout metrics for the fitness function. Since the result of the evolutionary computation is not a concrete layout, but a layout configuration, it can be applied to any graph without repeating the process.

Our experiments confirmed the usefulness of the presented methods. Participants of the user study clearly preferred the evolutionary approach over the manual setting of parameters for layout algorithms, and they were more effective at working on tasks about graph connectivity using the layout generated by the evolutionary method compared to the manual method.

The evolutionary algorithm presented here is not the only heuristic for optimizing abstract layouts. Further work could evaluate other optimization heuristics that build on our genetic representation and compare them to the results of this paper. For instance, using a divide-and-conquer approach one could separately optimize each parameter of the layout algorithms, one after another.

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