



Project no. 288570

# PARAPHRASE

Strategic Research Partnership (STREP)

**PARALLEL PATTERNS FOR ADAPTIVE HETEROGENEOUS MULTICORE SYSTEMS**

## **User Manual of the Pattern Candidate Browser D4.3**

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# Chapter 1

## Pattern Candidate Browser

### 1.1 ParaPhrase Refactoring Tool includes RefactorErl

The ParaPhrase–Enlarged project targets the identification of pattern candidates that can be transformed into the application of high-level parallel patterns in an Erlang program by the ParaPhrase Refactoring Tool. The analyses for pattern candidate identification can be implemented with RefactorErl, which is a static analysis and transformation tool for the Erlang language. Therefore we have integrated RefactorErl into the ParaPhrase Refactoring Tool. After this integration Wrangler and RefactorErl can be used together, RefactorErl providing analyses, and Wrangler executing transformations requested by users. The integration makes it possible to call RefactorErl from within Wrangler, i.e. (the user interface of) the ParaPhrase Refactoring Tool. More precisely, Wrangler and RefactorErl are connected with each other by a duplex communication channel, therefore more sophisticated collaboration of the tools is possible. We provide an installation bundle that can be used to install the extended ParaPhrase Refactoring Tool containing both Wrangler and RefactorErl.

#### 1.1.1 Installation guide

To be able to install the integrated ParaPhrase Refactoring Tool on Unix platforms (including different versions of OS X), the following packages should have been successfully installed:

- gcc ( $\geq 4.5$ )
- make
- tar
- bash
- m4

- ncurses
- Erlang/OTP (>= R15B02)

First download and unpack the zip file containing the ParaPhrase Refactoring Tool installation files into an arbitrary directory (the “root directory” of the tool). This root directory will contain a script named `para_script`. To install the tool, the following command should be executed in that directory:

```
./para_script -refactorerl /path/to/refactorerl
-wrangler /path/to/wrangler -build tool
```

Some non-mandatory options also exist and can be used to customize the installation process. These are the following:

- `-wrangler_dest PATH`: where to install Wrangler. The default is the root directory of the tool.
- `-qc PATH`: a path to a custom Quick Check library that can be used by the tool. By default, the tool uses a “Quick Check mini” shipped with the tool. If a custom Quick Check library is preferred, make sure that the app file of that library suits the requirements of a valid Erlang app file.

After a successful installation, 3 generated scripts will be placed in the root directory of the tool. These scripts should be used for starting, building and uninstalling the tool. All the scripts should be executed in the root directory of the tool. Use

- `./generated_start_script` to start the tool,
- `./generated_build_script` to rebuild the tool, and
- `./generated_clean_script` to uninstall the tool.

## 1.2 Users’ manual

Parts of the Users’ Manual are available as interactive help in the tool.

### 1.2.1 Usage of the integrated ParaPhrase Refactoring Tool

The tool can be started by executing the generated start script, named `generated_start_script`, located in the root directory of the tool. It is important to note that only one instance of the tool can be run at a time. After a successful start up, a named Erlang shell is given to the user. From this shell every Wrangler command can be invoked.

In order to search for candidates, the source code to analyze has to be loaded into the database of the tool. This can be done by executing the following command in the given Erlang shell:

```
referl_api:request({add, "/absolute/path/to/source"}).
```

If a list of loaded files are needed, the following command should be executed:  
`referl_api:request({sem_query, "files"}).`

If an empty database is requested, the following command should be executed:  
`referl_api:request({reset}).`

If some contents of the loaded files have been changed since the last addition operation, their contents may be refreshed in the database of the tool. This can be done by executing the following command:

`referl_api:request({db_sync}).`

The tool can be stopped by executing the following command:  
`referl_api:stop().`

To start pattern discovery, the following command should be executed:  
`referl_api:request({search_and_show_candidates}).`

After pattern discovery and the cost analysis have been finished, a web browser (Safari on OS X, Firefox on Linux) starts displaying a web application with the transformation sequences recommended by the cost analysis. This web application is detailed in the rest of the section.

## 1.2.2 Features provided by the web-based user interface

The interface is responsible for storing and displaying the suggested transformation sequences. These sequences can also be exported in different formats for further usage.

Pattern discovery and cost analysis can be time and resource consuming tasks, therefore the results of the analysis are stored permanently until a new analysis is started. The stored results can be displayed via the web-based interface. Multiple users (for example, a developer team) can browse its results at the same time.

The tool presents the transformation sequences to our users in a way that avoids overloading them with unnecessary detail, but which highlights the key decisions that must be made. Thus, transformation sequences are displayed partially. The sequences are sorted based on their expected speedups, so the top 10 of the most valuable transformation sequences are displayed in a table at first sight. Only those properties of each sequence are shown with which decisions can be made. If a user is interested in the details of a sequence, a fully detailed view can be requested. In this detailed view, all of the information can be found with which the transformations can be done, and the prediction of the tool can be validated.

For further studying the suggested transformation sequences, the results can be exported in CSV file format. By choosing this format, a CSV file is sent to the browser, which contains either all of the sequences (even the hidden ones), or the details of a selected transformation sequence, depending on the request of the user.

For further processing the results, XML format should be chosen. By choosing this format, an XML file is sent to the browser, which contains both the properties and the defined transformations of all of the sequences (even the hidden ones).

### 1.2.3 Usage of the web-based user interface

Note that the tool can only be used correctly when JavaScript is enabled in the browser!  
Help messages are available in the web page, and can be activated by clicking on the `i` icons.

The web-based interface starts automatically after pattern discovery and cost analysis have been finished. The interface also starts when the previously stored results are requested to be shown. To show the previous results without re-running static analyses, the following command should be executed:

```
referl_api:request({show_candidates}).
```

Whether a new pattern discovery has been started, or the previously stored results have been requested, a table appears in the top of the web page. An example is shown in Figure 1.1. The table is already sorted initially, but this initial ordering can be changed by clicking on a column of the table.



ID	Configuration	Module	Function	Arity	Number of workers	Expected speedup (CPU)	Expected speedup (GPU)	Recommended?
6 ((e1190))		matMult	theSkel	2	170	304.23	1.00	✓
3 ((e1424))		matMult	genmat	2	257	176.90	1.00	✓
2 ((e1339))		matMult	randmat	3	257	170.11	1.00	✓
4 ((e1252))		matMult	cols	1	69	11.80	1.00	✓
1 ((e1190))		matMult	mult_prime2	2	69	11.80	1.00	✓
5 ((e894))		matMult	theSkel	2	47	6.29	1.00	✓
7 ((e972))		matMult	mult	4	43	5.61	1.00	✓

Figure 1.1: Displaying the top 10 transformation sequences via the web-based interface

The columns of the table mean:

- *Configuration*: The algorithmic structure in the form of an abstract skeletal configuration, which encapsulates the structure of the algorithm together with its component information, showing the relationships and dependencies among the components.
- *Module, Function and Arity*: The function, identified by the given M:F/A, which contains the entry point of the algorithmic structure.
- *Number of workers*: The maximum number of workers required by this transformation sequence.
- *Expected speedups*: After applying all the transformations, the tool predicts that the analysed source can achieve these speedups. The prediction is based on the measured sequential execution times.

- *Recommended?:* A transformation sequence is recommended if the analysed source can accomplish either real CPU speedup or real GPU speedup by applying the defined transformations. (Note that GPU estimates have not been implemented so far.)

By clicking on the combo-box labelled `Chart options`, and selecting the requested file format from the appearing local-menu, data export can be initiated.

By clicking on a transformation sequence, its detailed view, containing all of the transformation descriptions, appears in a table in the bottom of the web page. An example is shown in Figure 1.2.

Details of the transformation sequence

Configuration	Location information	Program text	Number of workers	Sequential CPU time	Sequential GPU time	Parallel CPU time	Parallel GPU time	Expected speedup (CPU)	Expected speedup (GPU)	Used stream length
e1190	/home/v/work/paraphrase /repo/refer/tool/matrix /matMut.eri : {{71.31}, {71.40}} - {71.46}, {71.46}	mut_prime(R, C)	1	1.00	0.00	1.00	0.00	1.00	1.00	1
(e1190)	/home/v/work/paraphrase /repo/refer/tool/matrix /matMut.eri : {{70.1}, {70.11}} - {71.72}, {71.72}	mut_prime2([], C) -> []; mut_prime2([R Rows], C) -> [ mut_prime(R, C) ] mut_prime2(Rows, C) ] .	2	10,000.00	0.00	5,555.50	0.00	1.80	1.00	10,000
((e1190))	/home/v/work/paraphrase /repo/refer/tool/matrix /matMut.eri : {{18.41}, {18.45}} - {18.88}, {18.88}	lists:map(fun(X) -> mut_prime2(Y, X) end, Cols)	170	100,000,000.00	0.00	328,699.20	0.00	304.23	1.00	10,000

Chart options ▼

Figure 1.2: Detailed view of a transformation sequence

The columns of the table mean:

- *Configuration:* The algorithmic structure in the form of an abstract skeletal configuration, which encapsulates the structure of the algorithm together with its component information, showing the relationships and dependencies among the components.
- *Location information:* How to find the corresponding code fragments on which the suggested transformation can be applied.
- *Program text:* The program text of the corresponding code fragment.
- *Number of workers:* The maximum number of workers required by this code fragment after applying the suggested transformation.
- *Sequential CPU/GPU times:* The average of the measured execution times of the corresponding code fragments.
- *Parallel CPU/GPU times:* After applying all the transformations, the tool predicts that the corresponding code fragment can be executed within these time bounds. The prediction is based on the measured sequential execution times.

- *Expected speedups*: After applying all the transformations, the tool predicts that the analysed source can achieve these speedups.
- *Used stream length*: The length of the stream with which the tool has measured the sequential execution times and has predicted the parallel execution times.

This table can also be sorted by clicking on any of its columns, and its data can also be exported in CSV file format.

### 1.2.4 Data types of the exported formats

In order to correctly import the CSV file, the following delimiters should be used:

- Text delimiter: ` `
- Field delimiter: ,
- Row delimiter: \n

```
-<tr_seq_entities timestamp="{2013,9,23},{12,25,21}" db_hash="{1379,938935,432742},60487398">
-<tr_seq_entity id="6" configuration="(11e1192)" module="matMult" function="theSkel" arity="2" numberofworkers="170"
  expectedspeedupcpu="307.01158795553397" expectedspeedupgpu="1.0" recommended="true">
-<tr_comp_entities>
  <tr_comp_entity id="0" configuration="e1192" locationinformation="/home/v/work/paraphrase/repo/referl/tool/matrix/matMult.erl : {{71,31},
    {71,40}} - {{71, 46}, {71, 46}}" programtext="mult_prime(R, C)" numberofworkers="1" sequentialcputime="1" sequentialgputime="0"
    parallelcputime="1" parallelgputime="0" expectedspeedupcpu="1.0" expectedspeedupgpu="1.0" usedstreamlength="1"/>
  <tr_comp_entity id="1" configuration="(1e1192)" locationinformation="/home/v/work/paraphrase/repo/referl/tool/matrix/matMult.erl : {{70,1},
    {70,11}} - {{71, 72}, {71, 72}}" programtext="mult_prime2(I, C) -> [I, mult_prime2([R|Rows], C)] -> [mult_prime(R, C) | mult_prime2(Rows, C)]"
    numberofworkers="2" sequentialcputime="10000" sequentialgputime="0" parallelcputime="5506.614616920685" parallelgputime="0"
    expectedspeedupcpu="1.8159977945927201" expectedspeedupgpu="1.0" usedstreamlength="10000"/>
  <tr_comp_entity id="2" configuration="(11e1192)" locationinformation="/home/v/work/paraphrase/repo/referl/tool/matrix/matMult.erl :
    {{18,41}, {18,45}} - {{18, 88}, {18, 88}}" programtext="lists:map(fun(X) -> mult_prime2(Y, X) end, Cols)" numberofworkers="170"
    sequentialcputime="10000000" sequentialgputime="0" parallelcputime="325720.60444338503" parallelgputime="0"
    expectedspeedupcpu="307.01158795553397" expectedspeedupgpu="1.0" usedstreamlength="10000"/>
  </tr_comp_entities>
</tr_seq_entity>
+<tr_seq_entity id="7" configuration="(1e974)" module="matMult" function="mult" arity="4" numberofworkers="47"
  expectedspeedupcpu="5.945201816782893" expectedspeedupgpu="1.0" recommended="true"></tr_seq_entity>
+<tr_seq_entity id="5" configuration="(1e886)" module="matMult" function="theSkel" arity="2" numberofworkers="47"
  expectedspeedupcpu="5.97298797764636" expectedspeedupgpu="1.0" recommended="true"></tr_seq_entity>
+<tr_seq_entity id="4" configuration="(1e1254)" module="matMult" function="cols" arity="1" numberofworkers="73"
  expectedspeedupcpu="12.813481926778527" expectedspeedupgpu="1.0" recommended="true"></tr_seq_entity>
+<tr_seq_entity id="3" configuration="(1e1426)" module="matMult" function="genmat" arity="2" numberofworkers="257"
  expectedspeedupcpu="191.46378557610327" expectedspeedupgpu="1.0" recommended="true"></tr_seq_entity>
+<tr_seq_entity id="2" configuration="(1e1341)" module="matMult" function="randmat" arity="3" numberofworkers="257"
  expectedspeedupcpu="189.36324520713706" expectedspeedupgpu="1.0" recommended="true"></tr_seq_entity>
+<tr_seq_entity id="1" configuration="(1e1192)" module="matMult" function="mult_prime2" arity="2" numberofworkers="73"
  expectedspeedupcpu="12.813481926778527" expectedspeedupgpu="1.0" recommended="true"></tr_seq_entity>
</tr_seq_entities>
```

Figure 1.3: XML document exported from the web-based interface

A document exported in XML format (see Figure 1.3 for example) has a root element, named `tr_seq_entities`, whose attributes hold the timestamp of the XML generation and a hash value of the database contents. Each child element of the `tr_seq_entities` container element corresponds to a transformation sequence. These elements, named `tr_seq_entity`, have attributes that hold the properties shown in the table of the transformation sequences. They also have a child element, `tr_comp_entities`, which also acts as a container. Its child elements, named `tr_comp_entity`, represent transformation descriptions. The attributes of `tr_comp_entity` hold the properties that are shown in the table of the detailed view.

## Chapter 2

# Implementation Details

### 2.1 UI workflow

The user interface of the ParaPhrase Refactoring Tool should be able to present pattern candidates, i.e. code fragments amenable to parallelization by transforming into applications of skeletons. This presentation should be detailed enough so that the user can make refactoring decisions upon, and it should be well-organised so that unnecessary details and useless information do not prevent the user from making good decisions. In particular, the user interface should filter out candidates that are definitely worse than others, and prioritise the good ones.

In order to achieve this, we have created software components that present pattern candidates to users of the ParaPhrase Refactoring Tool on a web-based user interface, after sorting the candidates based on the expected performance benefits of parallelization. Performance benefits are estimated by a cost model that takes the sequential execution time of certain expressions as input. Figure 2.1 explains how these components are interconnected, and the rest of this section explains each component in more details. Note that the Static Analysis component is being developed in WP2, providing input to components that have been developed in T4.2.

#### 2.1.1 Static Analysis for Pattern Discovery

The pattern discovery component analyses the source code and points out the potential candidates for parallelization. Additionally, it takes into account the nesting of candidates, and computes the different combinations of transformation sequences. With this approach the user can select not only a single transformation, but also transformation sequences for parallelization.

A simple example from the matrix multiplication module:

```
mult_seq(Rows, Cols) ->
  lists:map(fun(R) ->
             lists:map(fun(C) -> mult_sum(R, C) end,
```

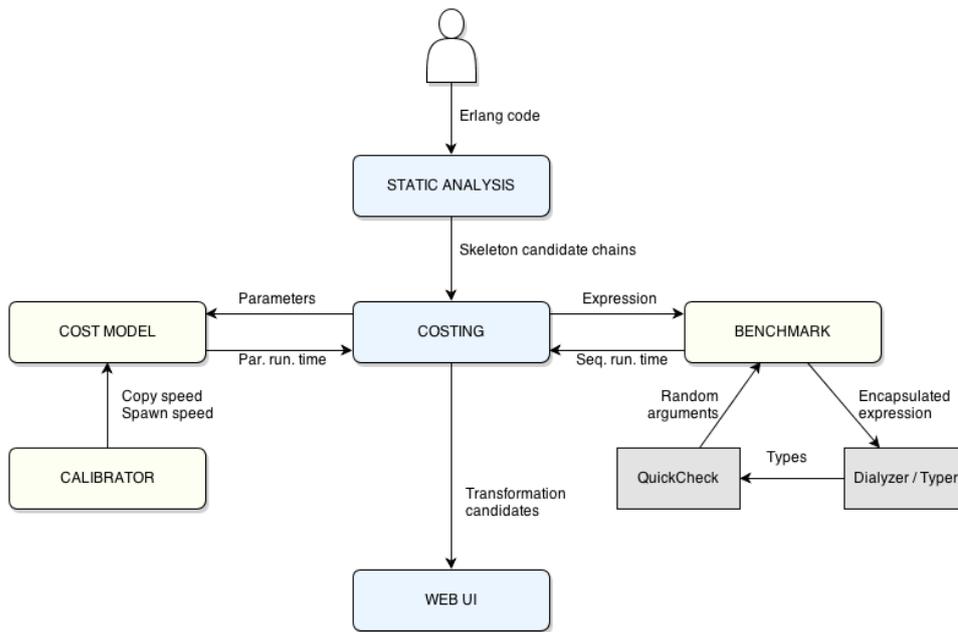


Figure 2.1: Components to present pattern candidates to users

```

    Cols)
end, Rows) .

```

Possible options for transformation sequences are the following.

- Transform the top-level lists:map/2 application into a farm.
- Transform the inner lists:map/2 application into a farm.
- Transform both lists:map/2 applications, and obtain a farm of farms.

### 2.1.2 Cost Analysis

The pattern discovery phase finds source code segments that can be transformed into applications of parallel skeletons, and generates combinations of those pattern candidates that belong to the same code segment, and can be embedded into each other. In other words, it identifies possible transformation sequences that could result in parallelized code that uses the skeleton library.

The aim of the cost analysis component is to select transformation sequences which are expected to result in significant speedup when comparing the execution time of the original and the transformed (parallelized) code segment. Therefore, during the cost analysis phase we measure the sequential execution time of code segments, and calculate the parallel execution time using a cost model (Section

2.1.2.1). In some cases we also need to determine some missing input for the cost model.

After the pattern discovery phase we have a *list of transformation sequences*. A *transformation sequence* consists of *transformation descriptions*, where a transformation description describes which code segment could be transformed into which kind of skeleton (for now we take into account only the farm and the pipeline skeletons). In the cost analysis phase we process every transformation sequence individually, and refine their transformation descriptions with some heuristic information:

- Estimated sequential execution time – the measured/calculated execution time of the original code segment;
- Estimated parallel execution time – the predicted execution time after parallelization;
- Additional information for the transformation, for example the optimal number of workers in the case of a farm.

After we have extended all of the transformation descriptions in a transformation sequence, we highlight the outermost transformation, because its description contains information concerning the whole sequence. This follows from the fact that we calculate its parallel execution time assuming that all of the embedded transformations will be applied. In the following we briefly introduce the calculation method of the heuristic information. The transformation description may belong to either a map or a pipeline candidate.

**Pipeline** In the case of a pipeline candidate we need the number of stages, the execution time of the stages and the length of the data stream as input for the cost model. From the given code segment we identify the stages of the pipeline and ask the benchmarking component (Section 2.1.2.2) to measure the execution time for each. We also identify the expression that belongs to the data stream, and following the dataflow in the source code, we try to estimate its length. If it is not possible, we use a default stream length in the further calculations. After we have collected all the needed information for the cost model, we can calculate the predicted parallel execution time.

**Farm** In the case of a farm candidate we need the execution time of the function that is applied to each element of the data stream, the length of the data stream and the number of the workers as input for the cost model. From the given code segment we identify the worker function, and ask the benchmarking component to measure the execution time for it. We try to estimate the length of the data stream similarly as in the case of a pipeline. The last step is to determine the optimal number of workers: we calculate the parallel execution time for every possible number of workers within a well-founded interval, and we choose the worker number which results in the best execution time.

### 2.1.2.1 Cost Model

For the estimation of parallel execution time of Erlang expressions, we use a cost model that has been derived from the cost models of the pipeline and the farm skeletons already published by the ParaPhrase consortium [3,4]. In order to make our estimations more precise (namely, to cover implementation-level costs better), we have slightly modified the published cost models. The cost model used for evaluating pattern candidates is the following.

#### Pipeline

- $M$  : the number of stages
- $T_{stages}$  : time costs of the stages ( $|T_{stages}| = M$ )
- $T_{copy}(L)$  : time cost of sending  $L$  pieces of data between processes

The sequential execution time of calculating all the  $M$  stages on  $L$  pieces of data takes  $L * \text{sum}(T_{stages})$ , while the same computation in parallel (assuming that we have at least as many computing units as stages) will only take

$$\text{sum}(T_{stages}) + (L - 1) * \text{max}(T_{stages})$$

time units. In the case of parallel execution, however, we need to deal with the communication and process starting costs as well: setting up  $M$  workers and pushing every data item through the whole pipeline takes  $(T_{spawn} + T_{copy}(L)) * M$  extra time units.

Therefore, we get the following time costs for pipelines:

$$T_{seq} := L * \text{sum}(T_{stages})$$

$$T_{par} := \text{sum}(T_{stages}) + (L - 1) * \text{max}(T_{stages}) + (T_{spawn} + T_{copy}(L)) * M$$

---

```

timecost_pipe(L, T_stages) ->
  M = length(T_stages),
  sum(T_stages) + (L - 1) * max(T_stages)
  + (timecost_spawn() + timecost_copy(L)) * M.

```

---

#### Farm

- $T_{work}$  : time cost of the operation to be performed
- $T_{copy}(L)$  : time cost of sending  $L$  pieces of data between processes
- $N_p$  : number of computing units
- $N_w$  : number of workers started

In the case of algorithms transformable into the farm skeleton, the sequential execution time of the computation on  $L$  elements is  $T_{work} * L$ , while in parallel, we can theoretically finish in  $T_{work} * \lceil L / \min(N_p, N_w) \rceil$  time units.

---

```

timecost_farm(N_p, N_w, L, T_work) ->
  T_work * ceiling(L / min(N_p, N_w))
  + timecost_emitter(N_w, L)
  + timecost_collector(N_w, L).

```

---

However, we have additional costs related to communication and process setup:

- Emitting takes  $T_{spawn} * (N_w + 2) + T_{copy}(L) * 3$  time units: spawning  $N_w$  workers, the data source process and the emitter process, plus copying the data to the data source, then to the emitter, and finally to the worker.

---

```

timecost_emitter(N_w, L) ->
  timecost_spawn() * (N_w + 2) + timecost_copy(L) * 3.

```

---

- The collection of the results has two phases: the spawned collector process receives the results from the workers, then it sends the data towards the final destination. Formally, the cost is  $T_{spawn} + T_{copy}(L) * 2$ .

---

```

timecost_collector(N_w, L) ->
  timecost_spawn() + timecost_copy(L) * 2.

```

---

That is, for the farm skeleton we get the following costs:

$$\begin{aligned}
T_{seq} &:= T_{work} * L \\
T_{par} &:= T_{work} * \lceil L / \min(N_p, N_w) \rceil + \\
&\quad T_{spawn} * (N_w + 2) + T_{copy}(L) * 3 + T_{spawn} + T_{copy}(L) * 2
\end{aligned}$$

**Calibration** Apparently, spawning and copy speeds may highly influence the parallel execution time of skeletons. In order to compute reasonably accurate costs, a calibration module has been integrated into the cost model. The calibration checks both the process spawning and the heap copy speed of the actual machine. Note that, for the moment, we have omitted GPU-related costs.

The copy operation is benchmarked as follows. We spawn a process whose only purpose is to receive data, and send back an acknowledgement; then we generate lists with varying sizes (up to 128MB), and measure the time it takes to transfer the lists (10 times repeatedly, of which we take the average). The result of the measurement is the microsecond/byte rate of the Erlang node.

Benchmarking the process spawning operation consists of measuring the time needed for starting  $N/4$ ,  $N/2$  and  $N$  processes (10 times repeatedly, of which we take the average). In this setting,  $N$  is the maximum number of processes that can be spawned on the current Erlang node. The result of the measurement is the microseconds needed to start a single process.

### 2.1.2.2 Benchmarking

The key factor of the parallel cost model is the sequential execution time of the work to be done on the stream of data ( $T_{stages}$  and  $T_{work}$  in the case of pipelines and farms, respectively). In order to supply our cost formula with a good estimation of the sequential time cost, we have created a benchmarking component that can measure the execution time of individual Erlang expressions.

**Expression encapsulation, typing** The expressions selected for benchmarking are put together with all their dependencies (functions, records, type specifications) so that they are encapsulated into an Erlang module. This module has only one exported function, parametrised by the free variables of the expressions in question. The module, on one hand, is turned into Erlang Abstract Code and is fed into TypEr, resulting in the types of the arguments; on the other hand, we compile the synthesised module and load it into the runtime system.

As an intermediate phase, we turn the type information returned by TypEr into a QuickCheck data generator. We then apply the QuickCheck property based tester as a systematic random generator for the free variables of the expressions to be benchmarked: the values returned by the generator will be passed to the module just compiled and loaded into the virtual machine.

**Timing strategy** We execute the function to be measured multiple times (at least twice, at most one million times), and take the average of the results. The execution time is accumulated, and if it reaches at least 0.2 seconds, we terminate the benchmark and calculate some statistics.

### 2.1.3 Web UI

After cost analysis has finished, all transformation sequences including their detailed transformation descriptions are determined. These results should be stored and should be converted into such a representation that can be interpreted as easily as possible by the users. The last phase of the tool, called *Web UI*, meets these requirements and even more.

The Web UI prior aim is to provide a web-based user interface, where users can browse and can export results. Due to the server-client architecture of the interface, multiple users (for instance, a developer team) can browse its results at the same time.

The Web UI is responsible for:

- handling persistence,
- managing its web server,
- displaying the results in a user-friendly manner.

### 2.1.3.1 Building components of the Web UI

The data flow between the building components of the Web UI is shown in Figure 2.2.

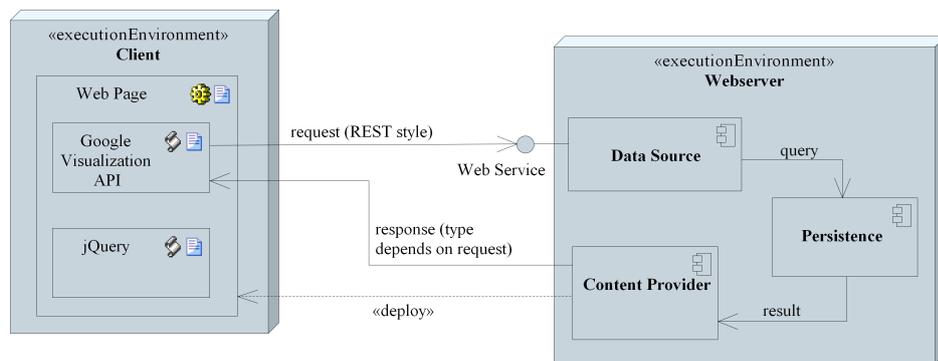


Figure 2.2: Deployment diagram of the Web UI

The main tasks of the Web UI at the server side are detailed below.

- *Persistence*: This component is responsible for producing the final representation of transformation sequences. The transformation sequences stored previously can be queried by other components.
- *Provided services*: A minimal web server, which needs no extra dependencies, is utilised transparently. This web server provides some web services responsible for serving contents via separate protocols and handling user inputs.

Contents generated by one of the services are sent to the browser by the managed web server via the HTTP protocol. These contents can be HTML pages, XML or CSV files containing the exported transformation sequences or transformation descriptions, JSON data or generated JavaScript scripts.

### 2.1.3.2 Used techniques

The Google Visualization API [1] provides a toolkit with which data can be presented to the user in various formats, for instance in a table with pre-defined actions and style-sheets. The API has many built-in features and the ability to:

- query and display data in a formatted, fancy style;
- define an initial order for the displayed data;
- reorder the displayed data based on the user's choice;

- decompose large amounts of data by displaying them page by page;
- handle user events, and
- export data in a user given format.

The API also gives the chance to use an own data source by implementing its protocol. SQL-like queries can be sent via HTTP protocol to the data source to retrieve data. It is important to note that no data is sent to Google, every data manipulations are done within the client's browser.

By utilising this API and implementing an own data source the results are displayed to the users in the web browser of the user. The implemented data source can interpret requests defined by the query language of Google and can serve the requested contents in different formats (special JSON, CSV, XML, JavaScript script) based on the request.

By handling user events, two tables can be shown in a joint view, where one element of the first table can be detailed in the second table. Transformation sequences and their transformation descriptions can be visualised by applying this joint view.

For other purposes, for example showing help dialogues to the users, jQuery [2] is utilised. jQuery is a widely-used JavaScript framework, which allows the programmer to concentrate on real problems by hiding the differences in the behaviour of different JavaScript engines. The programmer can choose from a wide variety of DOM selectors, iterators, event listeners and so on.

## 2.2 Further improvements

Some of the features of the tool have not yet been completely implemented. Most importantly, benchmarking is only performed on CPUs; benchmarking on GPUs is under development.

For benchmarking an expression, we generate test data into its free variables. Test data generation is implemented using QuickCeck, which needs type information on the data to be generated. Currently we compute the type of the free variables with TypEr – this tool sometimes fails to find the appropriate type for these variables: it finds a more general type than the one that could be used with QuickCheck without running into a type error. We are currently working on some improvements of the typing mechanism.

The cost model used for computing parallel execution time estimates from measured sequential execution times only supports the pipe and the farm skeletons. Further skeletons will be added once pattern discovery will be able to return those skeletons as well.

The tool is capable of displaying pattern candidates provided by the pattern discovery component. However, this component (being developed in another work package) has only an initial implementation. Improvements in this component will have to be reflected in the other components of our tool.

# Bibliography

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