

Package: mergingTools (via r-universe)

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Title Tools to Merge Hardware Event Monitors (HEMs) Coming from Separate Subexperiments into One Single Dataframe

Version 1.0.1

Description Implementation of two tools to merge Hardware Event Monitors (HEMs) from different subexperiments. Hardware Reading and Merging (HRM), which uses order statistics to merge; and MULTi-Correlation HEM (MUCH) which merges using a multivariate normal distribution. The reference paper for HRM is: S. Vilardell, I. Serra, R. Santalla, E. Mezzetti, J. Abella and F. J. Cazorla, ``HRM: Merging Hardware Event Monitors for Improved Timing Analysis of Complex MPSoCs," in IEEE Transactions on Computer-Aided Design of Integrated Circuits and Systems, vol. 39, no. 11, pp. 3662-3673, Nov. 2020, <doi:10.1109/TCAD.2020.3013051>. For MUCH: S. Vilardell, I. Serra, E. Mezzetti, J. Abella, and F. J. Cazorla. 2021. ``MUCH: exploiting pairwise hardware event monitor correlations for improved timing analysis of complex MPSoCs". In Proceedings of the 36th Annual ACM Symposium on Applied Computing (SAC '21). Association for Computing Machinery. <doi:10.1145/3412841.3441931>. This work has been supported by the European Research Council (ERC) under the European Union's Horizon 2020 research and innovation programme (grant agreement No. 772773).

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NeedsCompilation no

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Contents

code2hem	2
correlation_matrix	3
data_hrm_raw_vignette	3
data_much_raw_vignette	4
generate_mvg_params	4
get_independent_matrix	5
HRM_merge	6
MUCH_merge	7
process_raw_experiments	9
simulate_and_merge	9
T2080_code2name	10

Index	12
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code2hem	<i>Code to HEM name</i>
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Description

code2hem returns the name of the HEM corresponding to the code of the T2080 manual. When gathering experimental data the captured HEMs will be coded with a number. This functions transforms the number into the reference name in the T2080 manual.

Usage

```
code2hem(cod = NULL)
```

Arguments

cod HEM code on the T2080 manual.

Value

Returns the name of the HEM that corresponds to the input code.

Examples

```
code <- 1
hem <- code2hem(code)
hem
```

correlation_matrix *Compute correlation matrix*

Description

Compute correlation matrix

Usage

```
correlation_matrix(splitted_data = NULL)
```

Arguments

splitted_data Sample data.

Value

Returns a merged dataframe as stated in the description

References

S. Vilardell, I. Serra, R. Santalla, E. Mezzetti, J. Abella and F. J. Cazorla, "HRM: Merging Hardware Event Monitors for Improved Timing Analysis of Complex MPSoCs," in IEEE Transactions on Computer-Aided Design of Integrated Circuits and Systems, vol. 39, no. 11, pp. 3662-3673, Nov. 2020, <doi:10.1109/TCAD.2020.3013051>.

Examples

```
n_pmcs <- 6
data_much <- mergingTools::process_raw_experiments(data = data_much_raw_vignette,
                                                  n_pmcs = n_pmcs)
cor_matrix <- mergingTools::correlation_matrix(splitted_data = data_much)
```

data_hrm_raw_vignette *Data generated for HRM merging*

Description

Data from a hardware platform experiment

Usage

```
data_hrm_raw_vignette
```

Format

An object of class dataframe

data_much_raw_vignette

Data generated for MUCH merging

Description

Data from a hardware platform experiment

Usage

data_much_raw_vignette

Format

An object of class dataframe

generate_mvg_params

Generate multivariate Gaussian distribution parameters

Description

generate_mvg_params takes as input the experimental data along its correlation matrix to estimate the Sigma matrix and the vector of means to compute the multivariate Gaussian distribution

Usage

```
generate_mvg_params(splitted_data = NULL, cor_matrix = NULL)
```

Arguments

splitted_data Splitted experimental data.

cor_matrix Correlation matrix

Value

Returns the parameters of the multivariate Gaussian distributions as well as a list of concatenated HEM readings

Examples

```
n_pmcs <- 6
data_much <- mergingTools::process_raw_experiments(data = data_much_raw_vignette,
                                                  n_pmcs = n_pmcs)
cor_matrix <- mergingTools::correlation_matrix(splitted_data = data_much)
dep_lvl <- 0.85
# Remove the HEMs which are linearly dependant on other HEMs
cor_matrix_independent <- mergingTools::get_independent_matrix(cor_matrix = cor_matrix,
                                                            dep_lvl = dep_lvl)
mvg_params <- mergingTools::generate_mvg_params(splitted_data = data_much,
                                                cor_matrix = cor_matrix_independent)
```

```
get_independent_matrix
```

Generate independent HEMs

Description

There may be some HEMs which are linear dependent on another HEM. This produces conflicts when generating the multivariate Gaussian distribution as the Sigma matrix will not be invertible, causing an error. To avoid this, `get_independent_matrix` tells the user which HEMs are independent so they can choose which HEMs to use. To do so the user must input the maximum correlation between HEMs by `dep_lvl`. If `dep_lvl` is too high (>0.95) the user may leave very dependent HEMs and thus the Sigma matrix will not be invertible. We advise the user to lower the `dep_lvl` until the Sigma matrix is invertible.

Usage

```
get_independent_matrix(cor_matrix = NULL, dep_lvl = NULL)
```

Arguments

<code>cor_matrix</code>	Correlation matrix
<code>dep_lvl</code>	Dependency level allowed. A number between 0 and 1 indicating the maximum correlation allowed between HEMs.

Value

Returns a list of independent HEMs

Examples

```
n_pmcs <- 6
data_much <- mergingTools::process_raw_experiments(data = data_much_raw_vignette,
                                                  n_pmcs = n_pmcs)
cor_matrix <- mergingTools::correlation_matrix(splitted_data = data_much)
dep_lvl <- 0.85
# Remove the HEMs which are linearly dependant on other HEMs
```

```
cor_matrix_independent <- mergingTools::get_independent_matrix(cor_matrix = cor_matrix,
                                                              dep_lvl = dep_lvl)
```

 HRM_merge

HRM merge

Description

HRM_merge merges HEMs coming from separate subexperiments into one single dataset. A Subexperiment is a measurement of a group of HEMs the size of the allowed PMCs by the machine. For HRM there is a designated anchor HEM that will be included on each subexperiment. For more details check the reference paper below. The input data must be in a specific format:

1	2	3	1	4	5
30	15	20	40	10	12
35	16	25	25	13	15
32	14	30	21	11	17

where the numbers on top are the codes for the HEMs on the T2080. In this case we have two subexperiments: subexp1 = (1, 2, 3), subexp2 = (1, 4, 5); and H1 is the anchor HEM that should be included in each subexperiment. The data will be processed into:

H1	H2	H3	H1	H4	H5
30	15	20	40	10	12
35	16	25	25	13	15
32	14	30	21	11	17

The processing transforms the code of the HEMs to the reference name on the T2080 manual. merge_hems sorts each subexperiment by the anchor HEM, and the substitutes the anchor HEM by its quantiles. If one inputs the example dataset, merge_hems will return:

H1	H2	H3	H4	H5
21	15	20	11	17
31	14	30	13	15
40	16	25	10	12

Usage

```
HRM_merge(data = NULL, anchor_hem = NULL)
```

Arguments

data	Sample data.
anchor_hem	Reference HEM for merging

Value

Returns a merged dataframe as stated in the description

References

S. Vilardell, I. Serra, R. Santalla, E. Mezzetti, J. Abella and F. J. Cazorla, "HRM: Merging Hardware Event Monitors for Improved Timing Analysis of Complex MPSoCs," in IEEE Transactions on Computer-Aided Design of Integrated Circuits and Systems, vol. 39, no. 11, pp. 3662-3673, Nov. 2020, <doi:10.1109/TCAD.2020.3013051>.

Examples

```
library(mergingTools)
n_pmcs <- 6
data_hrm <- mergingTools::process_raw_experiments(data = data_hrm_raw_vignette, n_pmcs = n_pmcs)
merged_data <- mergingTools::HRM_merge(data = data_hrm, anchor_hem = "PROCESSOR_CYCLES")
```

MUCH_merge

MUCH Merge

Description

MUCH_merge merges HEMs coming from separate subexperiments into one single dataset. A Subexperiment is a measurement of a group of HEMs the size of the allowed PMCs by the machine. For MUCH you need to measure each HEM against the rest of them. For instance, let's say that one has 2 PMCs and 3 HEMs to measure. The input data coming from the experiments should look like this:

1	2	1	3	2	3
30	15	20	54	15	24
35	16	25	32	10	29
32	14	30	45	9	32

where the numbers on top are the codes for the HEMs on the T2080. In this case we have three subexperiments: subexp1 = (1, 2), subexp2 = (1, 3, 6), subexp3 = (2, 3); The data will be processed into:

H1	H2	H1	H3	H2	H3
30	15	20	54	15	24
35	16	25	32	10	29
32	14	30	45	9	32

The processing transforms the code of the HEMs to the reference name on the T2080 manual. Now with this data, MUCH_merge computes the correlation matrix of all HEMs and with it it constructs a

`process_raw_experiments`*Process raw experimental data*

Description

`process_raw_experiments` splits the data into separate dataframes. The number of different dataframes is the number of subexperiments and the number of variables on each one is the number of PMCs. The validation data is on the form of several subexperiments that don't need to be merged together. The intent of the data is to provide information on how each HEM behaves when put against another HEM. The validation data them is a collection of subexperiments where each HEM is put against each other.

Usage

```
process_raw_experiments(data = NULL, n_pmcs = NULL)
```

Arguments

<code>data</code>	Validation data.
<code>n_pmcs</code>	Number of PMCS used on the experiment

Value

Returns a list of dataframes as stated in the description.

Examples

```
n_pmcs <- 6
data_much <- mergingTools::process_raw_experiments(data = data_much_raw_vignette,
                                                    n_pmcs = n_pmcs)
```

`simulate_and_merge`*Simulate the MVG and merge the HEMs*

Description

`simulate_and_merge` takes as input the parameters of the multivariate Gaussian distribution and simulates multiple samples. The number of samples is determined by `n_sims`. On each simulation, each HEM of the experimental data is sorted from lowest to highest independently. Then, the simulated MGD is used as the model to arrange the experimental data. For instance, if on the MGD the 10th highest value of HEM 1 is paired with the 2nd highest and the 4th highest values of HEMs 2 and 3 respectively, Then, we modify the experimental data to copy this arrangement. After merging and arranging, the 10th highest value of HEM 1 on the experimental data will be paired with the 2nd highest and the 4th highest values of HEMs 2 and 3 respectively. The algorithm does multiple simulations of the MGD and keeps the sample that gives the lowest error on the correlation matrix when the data is merged w.r.t. the correlation matrix of the experimental data.

Usage

```
simulate_and_merge(  
  mvg_params = NULL,  
  n_runs = NULL,  
  n_sims = NULL,  
  cor_matrix = NULL  
)
```

Arguments

mvg_params	parameters from the multivariate Gaussian distribution
n_runs	Number of rows for the output merged data
n_sims	Number of simulations for the multivariate Gaussian distribution to find the optimal merge
cor_matrix	Correlation matrix

Value

Returns a merged dataframe as stated in the description

Examples

```
n_pmcs <- 6  
data_much <- mergingTools::process_raw_experiments(data = data_much_raw_vignette,  
                                                  n_pmcs = n_pmcs)  
cor_matrix <- mergingTools::correlation_matrix(splitted_data = data_much)  
dep_lvl <- 0.85  
# Remove the HEMs which are linearly dependant on other HEMs  
cor_matrix_independent <- mergingTools::get_independent_matrix(cor_matrix = cor_matrix,  
                                                             dep_lvl = dep_lvl)  
mvg_params <- mergingTools::generate_mvg_params(splitted_data = data_much,  
                                                cor_matrix = cor_matrix_independent)  
  
n_sims <- 10  
n_runs <- 1000  
merged_data <- mergingTools::simulate_and_merge(mvg_params = mvg_params,  
                                              n_runs = n_runs,  
                                              n_sims = n_sims,  
                                              cor_matrix = cor_matrix_independent)
```

T2080_code2name

T2080 HEM codes to HEM names

Description

Dataset used to transform the codes from the T2080 manual into readable HEM names.

T2080_code2name

11

Usage

`T2080_code2name`

Format

An object of class `data.frame` with 262 rows and 2 columns.

Examples

`data(T2080_code2name)`

Index

- * **HEM**
 - code2hem, [2](#)
- * **HRM**
 - correlation_matrix, [3](#)
 - HRM_merge, [6](#)
 - process_raw_experiments, [9](#)
- * **MUCH**
 - generate_mvg_params, [4](#)
 - get_independent_matrix, [5](#)
 - MUCH_merge, [7](#)
 - process_raw_experiments, [9](#)
 - simulate_and_merge, [9](#)
- * **datasets**
 - data_hrm_raw_vignette, [3](#)
 - data_much_raw_vignette, [4](#)
 - T2080_code2name, [10](#)

code2hem, [2](#)

correlation_matrix, [3](#)

data_hrm_raw_vignette, [3](#)

data_much_raw_vignette, [4](#)

generate_mvg_params, [4](#)

get_independent_matrix, [5](#)

HRM_merge, [6](#)

MUCH_merge, [7](#)

process_raw_experiments, [9](#)

simulate_and_merge, [9](#)

T2080_code2name, [10](#)