S-FRULER: aprendizaje automático escalable de reglas de predicción en Big Data

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Acknowledgements

- This work was supported by the Spanish Ministry of Economy and Competitiveness under project TIN2014-56633-C3-1-R, the Galician Ministry of Education under the projects EM2014/012 and CN2012/151, and Mestrelab Research S.L. under project IN852A 2013/75

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Motivation

- Genetic Fuzzy Systems (GFSs): fuzzy rules + evolutionary algorithms
  - Fuzzy rules: knowledge representation
  - Evolutionary algorithms: optimization
  - Accuracy + readability/interpretability

- TSK-1 fuzzy rules

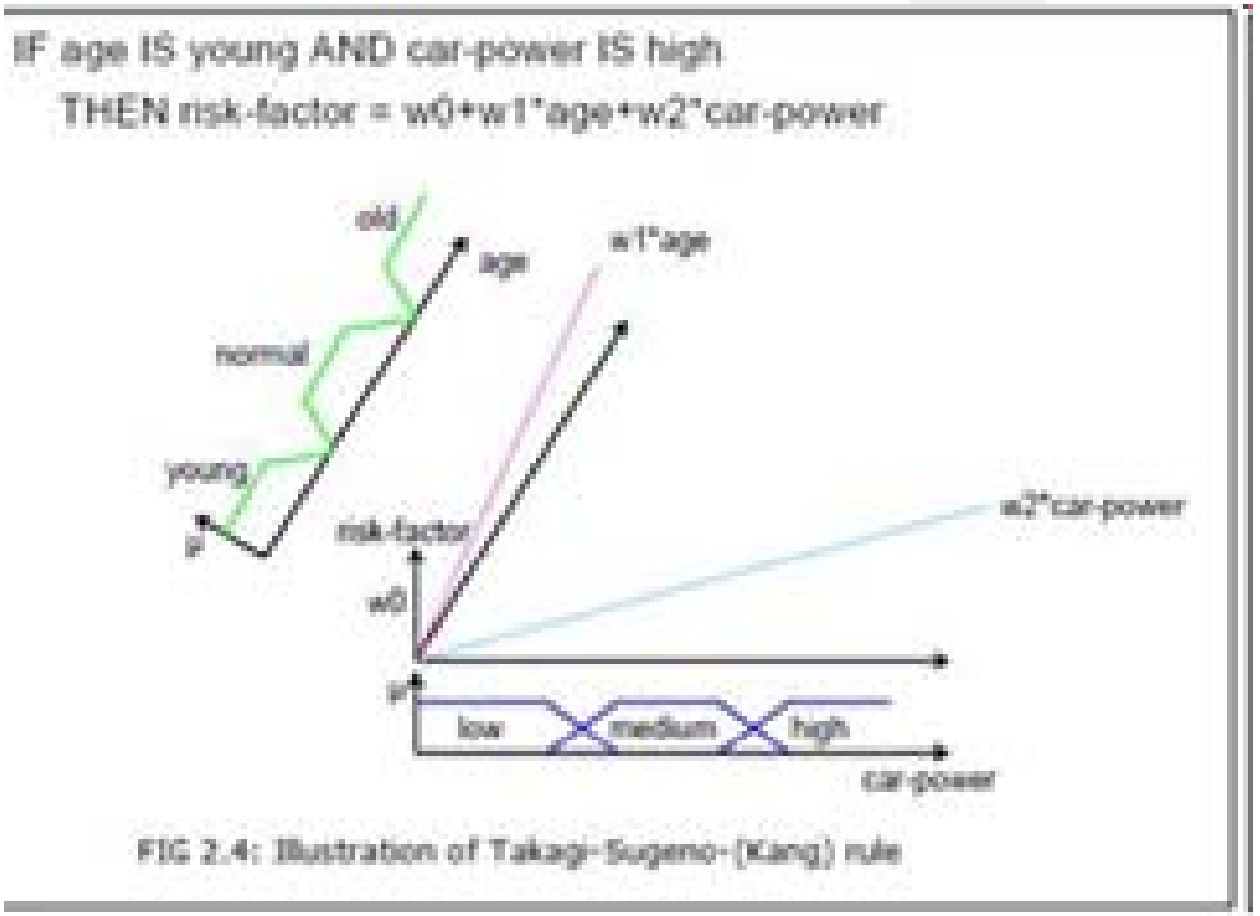

FIG 2.4: Illustration of Takagi-Sugeno-(Kang) rule

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Motivation (ii)

- FRULER: accurate and simple TSK-1 fuzzy rule base models for regression

$$\text{If } X_1 \text{ is } A_1 \text{ and } X_2 \text{ is } A_2 \text{ and } \ldots \text{ and } X_p \text{ is } A_p \text{ then}$$
$$Y = \beta_0 + X_1 \cdot \beta_1 + X_2 \cdot \beta_2 + \cdots + X_p \cdot \beta_p$$

- Simplicity: improve readability/interpretability and generalization ability
  - Linguistic fuzzy partitions with a low number of labels
  - Low number of rules
  - Regularization of the consequents

- S-FRULER: scalable version of FRULER for Big Data

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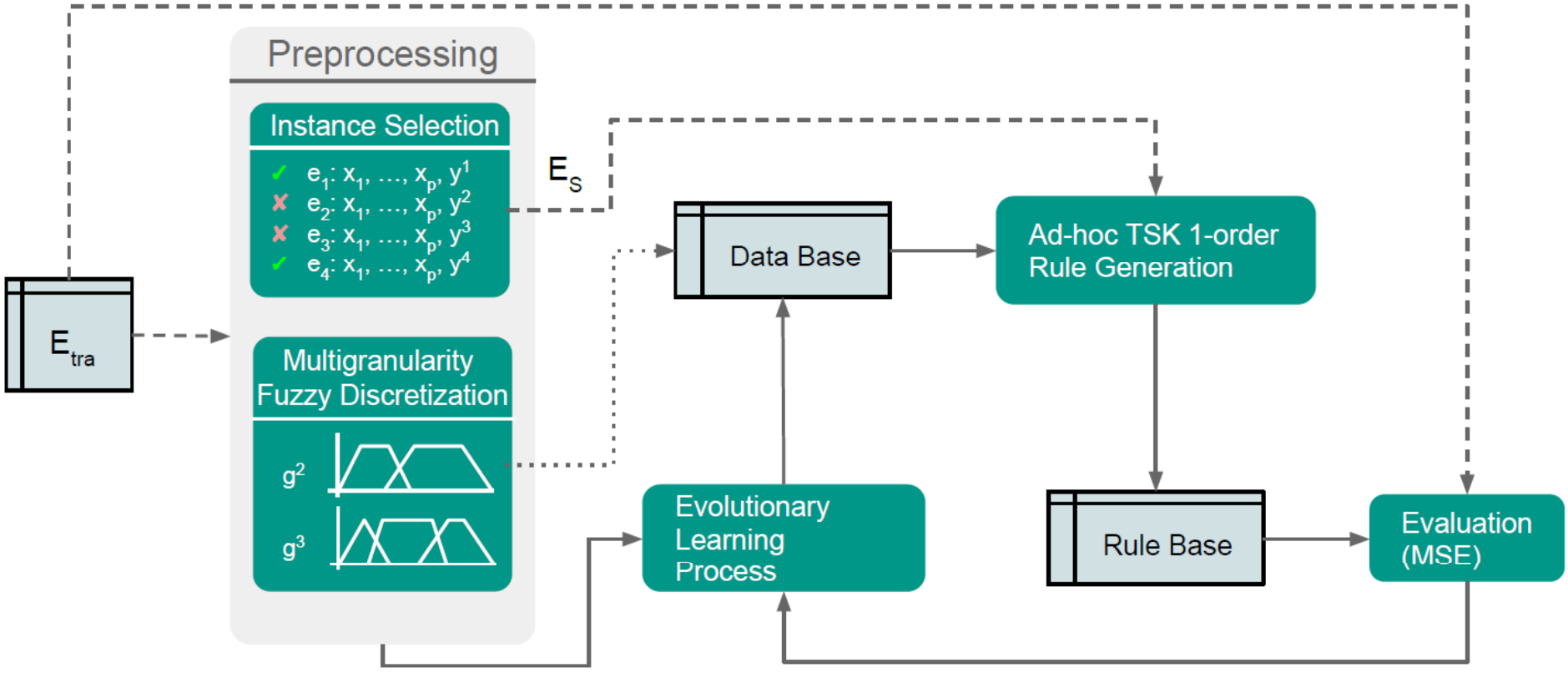
FRULER
Fuzzy Rule Learning through Evolution for Regression



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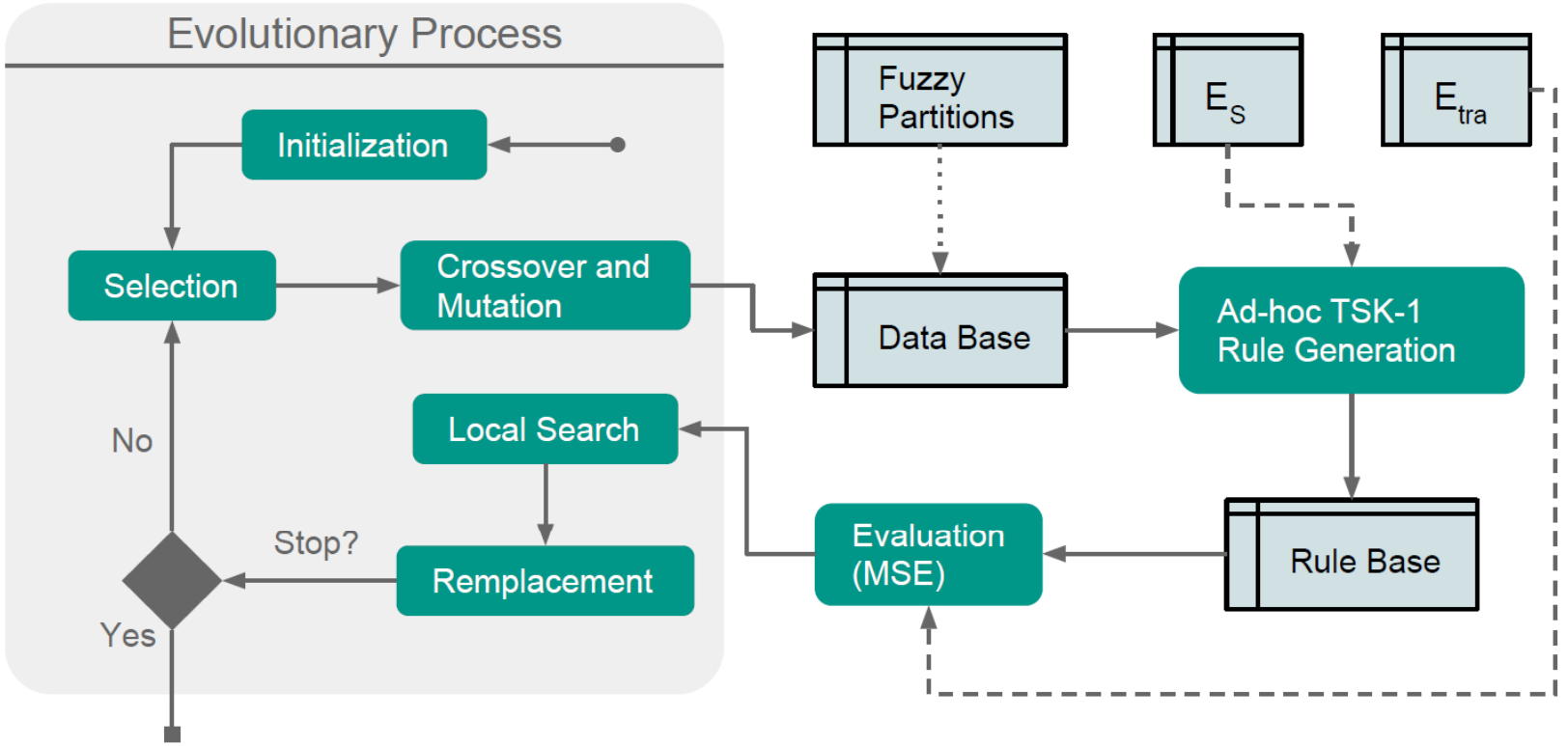
Genetic algorithm

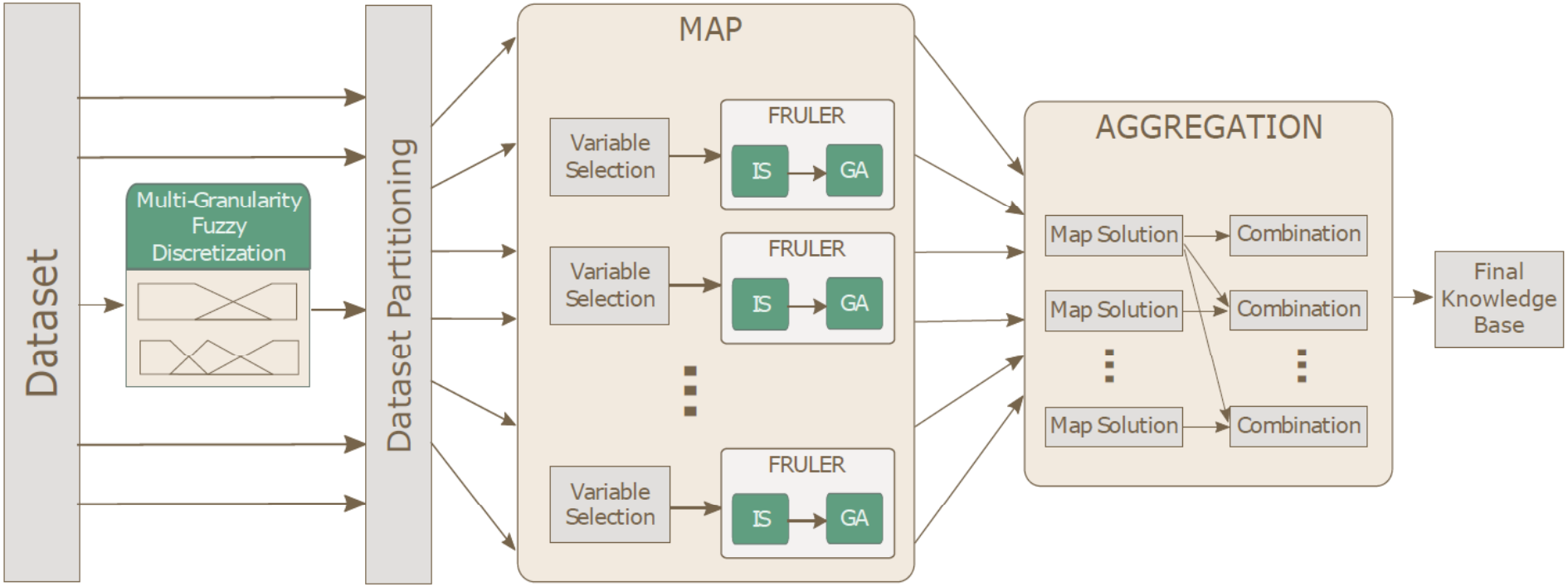
- Codification: $C_1 = (g_1, g_2, \ldots, g_{p_m})$ $C_2 = (\alpha_1^1, \ldots, \alpha_1^{g_1-1}, \ldots, \alpha_p^1, \ldots, \alpha_p^{g_p-1})$



- Generation of the KB: Wang & Mendel + Elastic Net (selected instances)
- Evaluation: training examples

S-FRULER

Scalable Fuzzy Rule Learning through Evolution for Regression



- Number of partitions: $n_{map} = log_2(p^2 * l * n)$
  - Depends on the number of input variables, the maximum granularity of the input variables, and the number of instances

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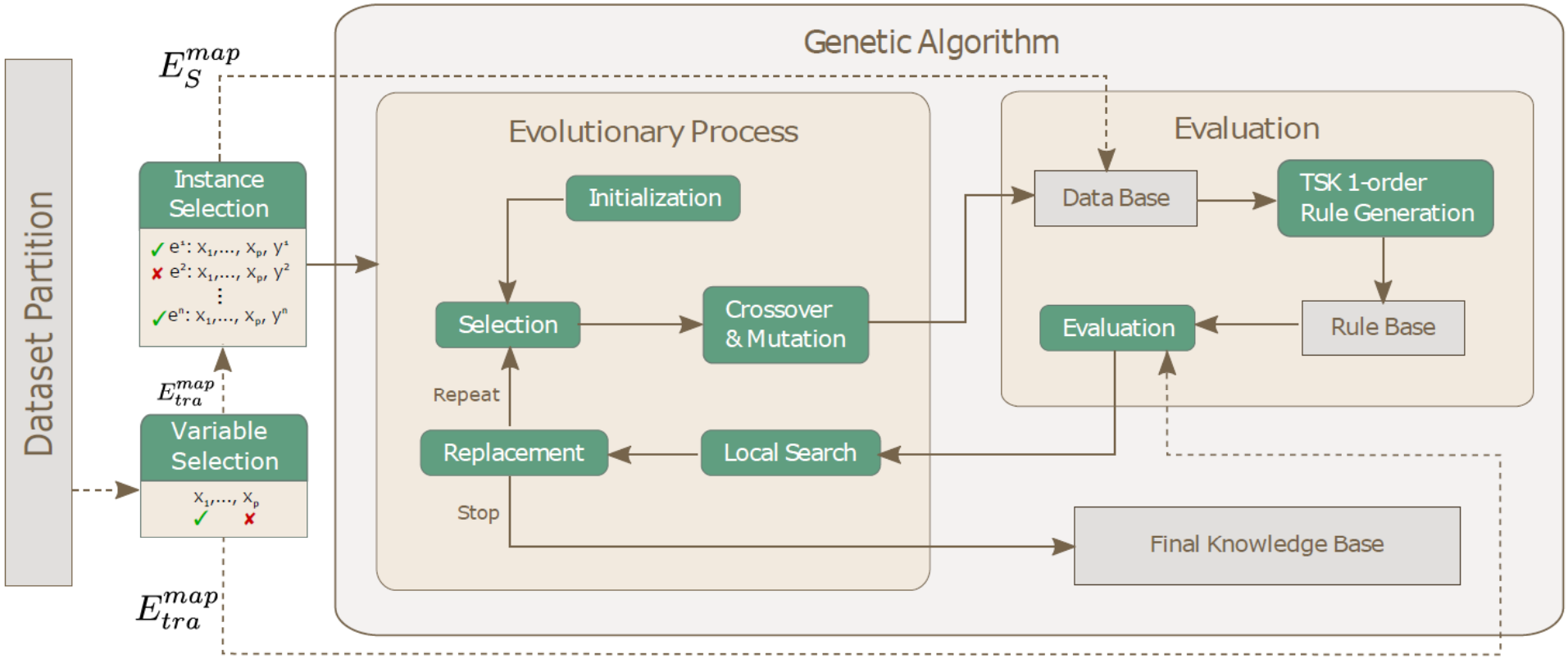
S-FRULER: Map function



- For each node select randomly a subset of variables:
  - p_m: number of variables for each mapper

$$p_m \geq -p \cdot ((1 - \alpha_{p_m})^{1/n_{map}} - 1)$$

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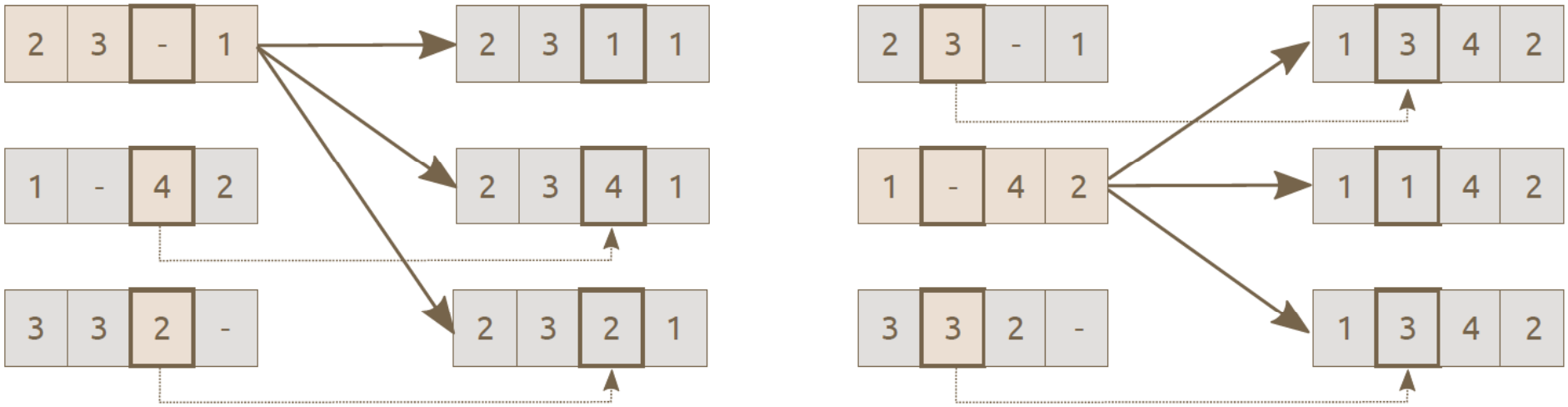
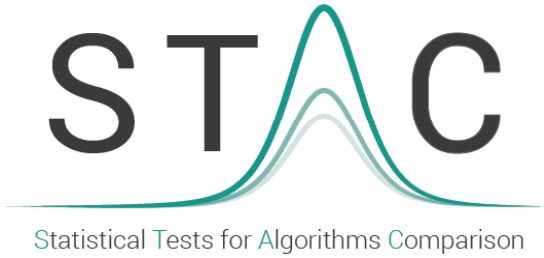
S-FRULER: aggregation function

- Keep the KB simple: combine the granularities of the different solutions
  - Maximum of n^2_{map} solutions
- Generate the TSK rule bases using the combination of selected instances



Results: FRULER

- 28 datasets
- **FRULER ranks first**



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algorithms	FRULER		FS_{MOGFS}^{e}+TUN^{e}		L-METSK-HD^{e}		A-METSK-HD^{e}	
	#Rules	Test Error	#Rules	Test Error	#Rules	Test Error	#Rules	Test Error
ELE1	**4.1**	2.012	8.1	**1.954**	15	1.925	11.4	2.022
PLA	**1.4**	1.219	18.6	1.194	23	1.218	19.2	**1.136**
QUA	7.8	0.0181	**3.2**	**0.0178**	35.9	0.019	18.3	0.0181
ELE2	**4.3**	6,729	8	10,548	59	20,095	36.9	**3,192**
FRIE	**8.0**	**0.731**	22	3.138	95.1	3.084	66	1.888
MPG6	**13.7**	**3.727**	20	4.562	99.6	4.469	53.6	4.478
DELAIL	**2.5**	1.458	6.2	1.528	98.3	1.621	36.8	**1.402**
DEE	**7.9**	**0.080**	18.3	0.093	96.4	0.095	50.6	0.103
DELELV	**5.8**	1.045	7.9	1.086	91	1.119	39.1	1.031
ANA	**3.9**	0.008	10	**0.003**	48.9	0.006	33.3	0.004
MPG8	**12.7**	**4.084**	23	4.747	98.7	5.61	64.2	5.391
ABA	**4.5**	2.393	8	2.509	42.4	2.581	23.1	**2.392**
CON	**8.9**	**20.598**	15.4	32.977	96.5	38.394	53.7	23.885
STP	42.4	**0.353**	**23**	0.912	100	0.78	66.4	0.387
WAN	**5.6**	**0.888**	8	1.635	91.1	1.773	48	1.189
WIZ	**8.9**	**0.663**	10	1.011	55.4	1.296	29.1	0.944
FOR	**5.6**	**2,214**	10	2,628	93.7	4,633	40.6	5,587
MOR	7.9	**0.007**	7	0.019	40.9	0.028	27.2	0.013
TRE	**4.5**	**0.027**	9	0.044	42.8	0.052	28.1	0.038
BAS	**6.2**	305,777	17	**261,322**	95.7	320,133	59.8	368,820
CAL	15.4	2.110	**8.4**	2.95	99.8	2.638	55.8	**1.71**
MV	**6.0**	0.083	14	0.158	76.4	0.244	56.5	**0.061**
HOU	12.1	**8.005**	**11.7**	9.4	68.9	10.368	30.5	8.64
ELE	**5.4**	**2.934**	8	9	76.4	8.9	34.9	7.02
CA	**7.1**	**4.634**	14	5.216	71.3	5.88	32.9	4.949
POLE	40.8	110.898	**13.1**	102.816	100	150.673	46.3	**61.018**
PUM	**7.8**	0.367	17.6	0.292	87.5	0.594	63.3	**0.287**
AIL	**8.5**	**1.404**	15	2	99.1	1.822	48.4	1.51

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Results: FRULER for energy optimization

- Model the energy-building behavior and optimize energy efficiency
- OPERE(EU LIFE program)
- Monte da Condesa building:
  - 25,000 m^2
  - 2013 power consumption: 5,747 MWh
  - SCADA system with 469 variables
  - Dorm: 6 floors, > 400 students

	$\%R$		$\% < T_{setpoint}$		Temperature diff.
	oldSys	*newSys*	*oldSys*	*newSys*	Diff
07th to 10th of March	26.36%	16.67%	3.54%	3.33%	0.16 °C
05th to 08th of April	27.95%	10.42%	0.42%	0.21%	0.57 °C
04th to 07th of May	23.61%	0.00%	0.42%	0.00%	0.60 °C
02th to 05th of June	0.00%	1.04%	2.08%	0.00%	0.28 °C
Average	19.48%	7.03%	1.62%	0.89%	0.37 °C

Results: FRULER vs. S-FRULER

Dataset	FRULER	S-FRULER
DELAIL	1.46	**1.44**
DELELV	**1.04**	1.12
CAL	**2.11**	2.18
MV	0.08	**0.05**
HOU	**8.0**	8.2
ELV	**2.9**	3.2
CA	**4.6**	**4.6**
POLE	**111**	124
PUM	0.367	**0.349**
AIL	**1.4**	**1.4**

- "medium-sized" datasets: <40k examples, <40 variables
- FRULER best in 5, S-FRULER best in 3, equal in 2

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Results: runtime of FRULER vs. S-FRULER

Algorithms	FRULER	S-FRULER	Standalone		Cluster	
	Time	n_{map}	Time	Speedup	Time	Speedup
DELAIL	0:09:58	21	0:01:18	8	0:00:48	12
DELELV	0:25:01	22	0:01:38	15	0:01:13	21
CAL	1:57:03	23	0:04:20	27	0:03:22	35
MV	1:17:02	23	0:09:27	8	0:05:49	13
HOU	4:15:17	25	0:04:06	62	0:03:09	81
ELV	3:01:30	26	0:03:10	57	0:03:14	56
CA	0:38:12	25	0:03:46	10	0:01:48	21
POLE	1:53:15	27	0:10:20	11	0:05:14	22
PUM	31:14:27	24	0:01:58	956	0:01:39	1,139
AIL	12:50:38	28	0:07:13	107	0:03:32	218

- Standalone: HP Proliant with 4 AMD Opteron 6262 HE (64 cores and 128 GB)
- Spark Cluster: Amazon Elastic MapReduce (EMR) 4.0.0 with m3.xlarge machines (Intel Xeon E5-2670 v2, 4 cores, 15 GB)

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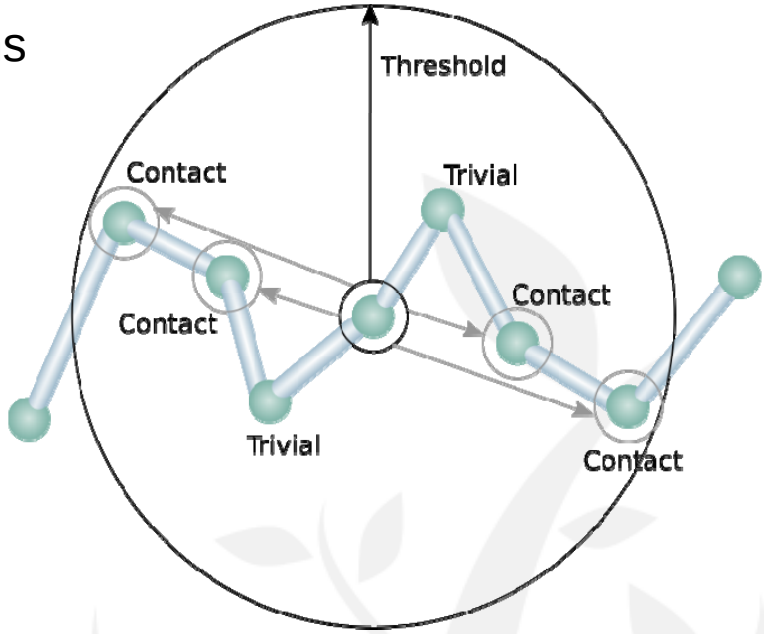
Results: large dataset

- Prediction of the 3D structure of protein chains
  - Estimate the coordination number of a protein



- Regression: comparison with Mllib
  - Runtimes for standalone mode

			S-FRULER		Ridge SGD		Lasso SGD	
Datasets	# Cases	# Variables	Test Error	Time	Test Error	Time	Test Error	Time
w1	257,560	60	12.45	04:42:08	15.09	00:42:56	19.01	00:45:05
w2	257,560	100	12.15	05:32:33	14.20	01:00:44	18.91	01:01:25
w3	257,560	140	12.23	05:48:42	14.18	01:04:36	18.89	01:04:43
w4	257,560	180	12.30	12:17:42	13.62	01:06:42	18.93	01:05:46

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Results: large dataset (ii)

- Classification:

Algorithm	S-FRULER	BioHEL	GAssist	PART	C4.5
w1	76.9	75.8	74.8	70.9	68.6
w2	77.3	76.0	74.7	70.9	68.6
w3	77.7	76.4	74.6	69.9	68.1
w4	77.4	76.5	74.8	76.0	68.2

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Chemical Shift Prediction

- Predict the chemical shift of the atoms in a molecule
- More than 54,000 examples, 985 input variables
- RF for regression

Error	< 0.1	< 0.2	< 0.3	< 0.4	< 0.5	< 0.6	< 0.7	< 0.8	< 0.9	< 1	> 1	> 2
Porcentaje de instancias	72.14	84.63	90.41	93.63	95.81	96.98	97.90	98.61	98.98	99.37	0.63	0.02
Desviación	0.03	0.05	0.07	0.09	0.10	0.11	0.13	0.14	0.14	0.15	0.27	0.00
% de instancias en 4 desviaciones	99.77	99.67	99.67	99.64	99.62	99.61	99.58	99.55	99.55	99.53	94.12	100

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Conclusions

- FRULER obtains simple models with high precision
  - Small and medium-sized datasets
- S-FRULER is a distributed version of FRULER implemented with Apache Spark
- S-FRULER has speedups usually larger than the number of dataset partitions used, showing an scalability higher than linear in both standalone and cluster modes
- Results demonstrate the capability of S-FRULER to obtain precise and simple models in large scale problems.

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I. Rodríguez-Fdez, M. Mucientes, and A. Bugarín. Fuzzy Rule Learning through Evolution for Regression. Information Sciences, 354:1-18, 2016.

I. Rodríguez-Fdez, M. Mucientes, and A. Bugarín. S-FRULER: Scalable fuzzy rule learning through evolution for regression. Knowledge-Based Systems, 110:255-266, 2016.

Software disponible en: http://tec.citius.usc.es/fruler/

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