NRC as a formal model for expressing bioinformatics workflows

A. Gambin [1], J. Hidders [2], N. Kwasnikowska [3], S. Lasota [1], J. Sroka [1], J. Tyszkiewicz [1], J. Van den Bussche [3]
[1] Warsaw University, [2] University of Antwerp, [3] Hasselt University

Context

- bioinformatics workflows
  - network of data centered processing steps
- processing steps involve
  - large amounts of complex data
    - sequence files, BLAST reports
    - XML data
  - a variety of tools
    - EMBOSS suite, BioPerl scripts
    - webservices, Mascot searches

Problems

- workflows execute as a mix of automated scripts and manual intervention
  - difficult to maintain
- results are stored in ad-hoc ways, e.g. files, Excel sheets
  - difficult to manage

Existing solutions

- workflow execution engines
  - Kepler [2], Taverna [3]
- not based on a formal data model, or too complicated and not data oriented

Our contribution

- using Nested Relational Calculus [1] for modeling data oriented workflows
- many bioinformatics workflows can be modeled in NRC
- advantages of using NRC
  - puts data oriented workflows on a firm foundation
  - formalism is already well understood
- natural approach
  - BioKleisli [4] is also based on NRC

Nested Relational Calculus

- established formalism for querying over complex objects [1]
- complex objects are arbitrarily nested collections and tuples
- collections can be sets, multi-sets and lists
- set-based model: sets {} and tuples ⟨⟩
- typed query language
  - extensible repertoire of base types
    - Boolean, String, Number
    - FASTA sequence file
    - XML, based on a DTD or XML Schema
  - complex types: nested sets and tuples

Workflow example – description

- 3D signal maps from LC-MS analysis of blood samples
- two groups: diseased and normal
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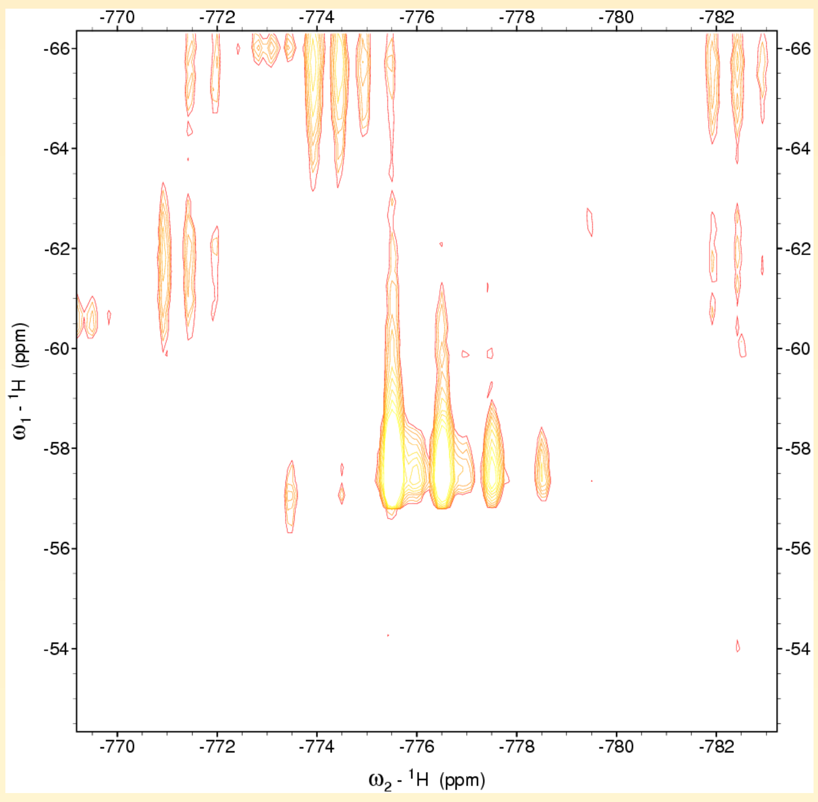

- choosing classifiers, defined by a feature selection method
  - t-statistic, correlation
- and a classification algorithm
  - Decision Trees (DT), Random Forest (RF), Support Vector Machine (SVM)
- k-fold cross validation to obtain the following performance statistics for each classifier
  - sensitivity, specificity

Workflow example – data types

- base types

  String, Number, Boolean, Sample
- complex types
  - input type

    PatSample = ⟨ id: String, sample: Sample, diseased: Boolean ⟩
  - output type

    FSelCAlg = ⟨ tstat: {CAlg}, corr: {Calg} ⟩

    with CAlg = ⟨ dt: PStats, rf: PStats, svm: PStats ⟩

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    TestTrain = ⟨ test: PepClusters, train: PepClusters ⟩

    PepClusters = { ⟨ clustermass: Number, patlist: PatList ⟩ }

    PatList = { ⟨ patid: String, diseased: Boolean, intensity: Number ⟩ }

NRC core operations

- constant value of a base type — "John", true, 89
- variable of any type, either base type or complex — $patient
- tuple construction — ⟨ name: "John", condition: true, age: 89 ⟩
- tuple projection — $patient.name
- empty set construction — ∅
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- set union — $patientList = $healthy ∪ $diseased
- flattening of a nested set
  - $patientList = flatten({$healthy, $diseased})
- iteration over a set
  - for $patient in $patientList return $patient.name
- named program definition — pBLAST: FASTA → {AccessionNr}
  - external programs, used as a "black box"
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- equality test for base types — $patient.name = "John"
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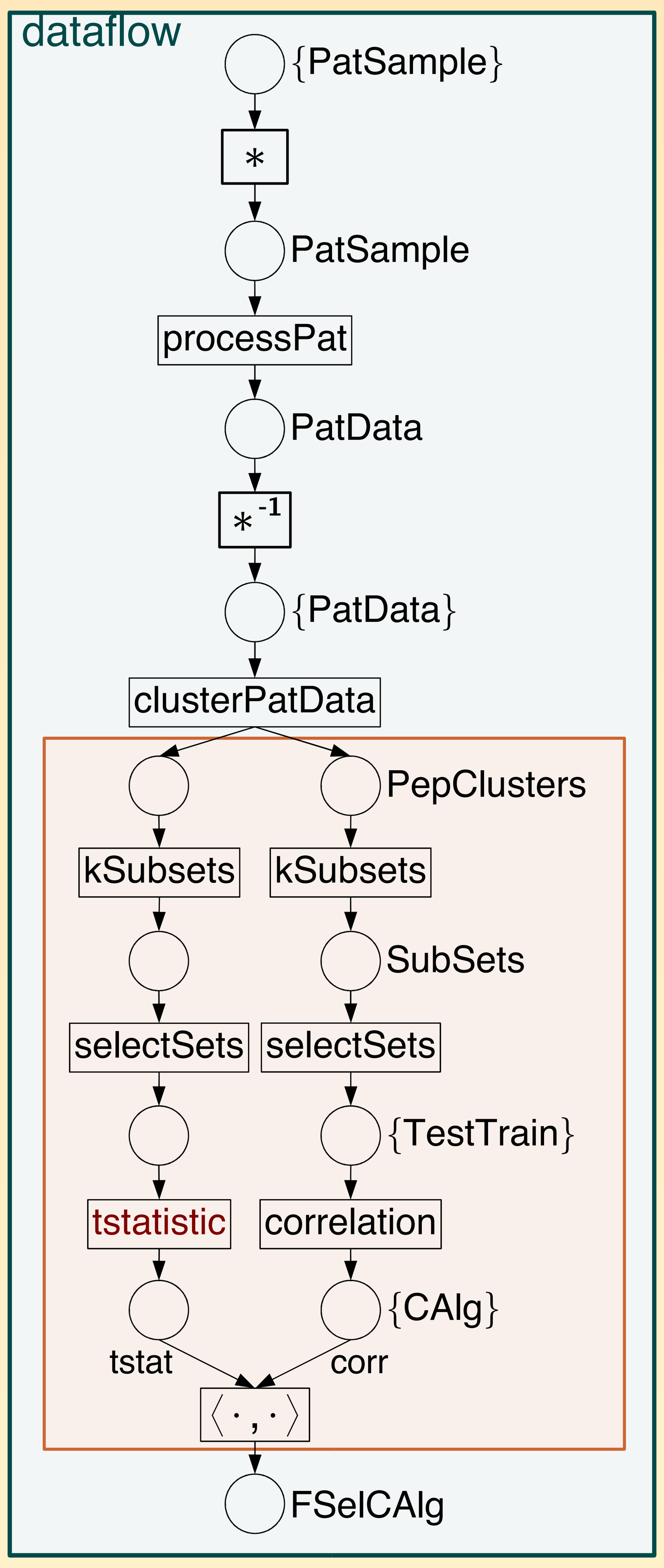
- core operations can be combined into programs



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define dataflow($s: {PatSample}): FSelCAlg as
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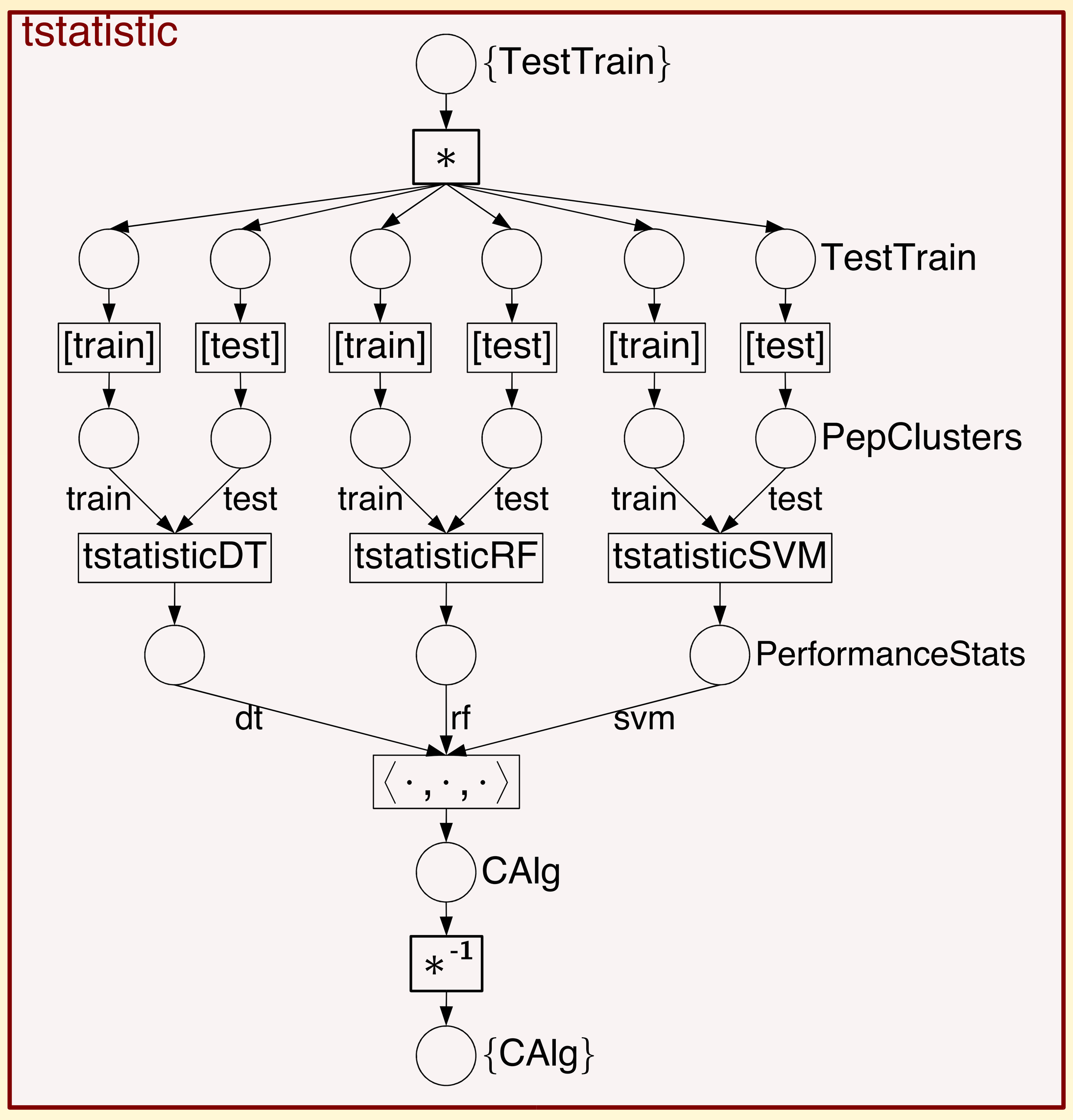

Graphical representation

- dataflow language based on Petri nets and Nested Relational Calculus [6]
- typing system and core operations from NRC
- top-down, hierarchical design of the data flow

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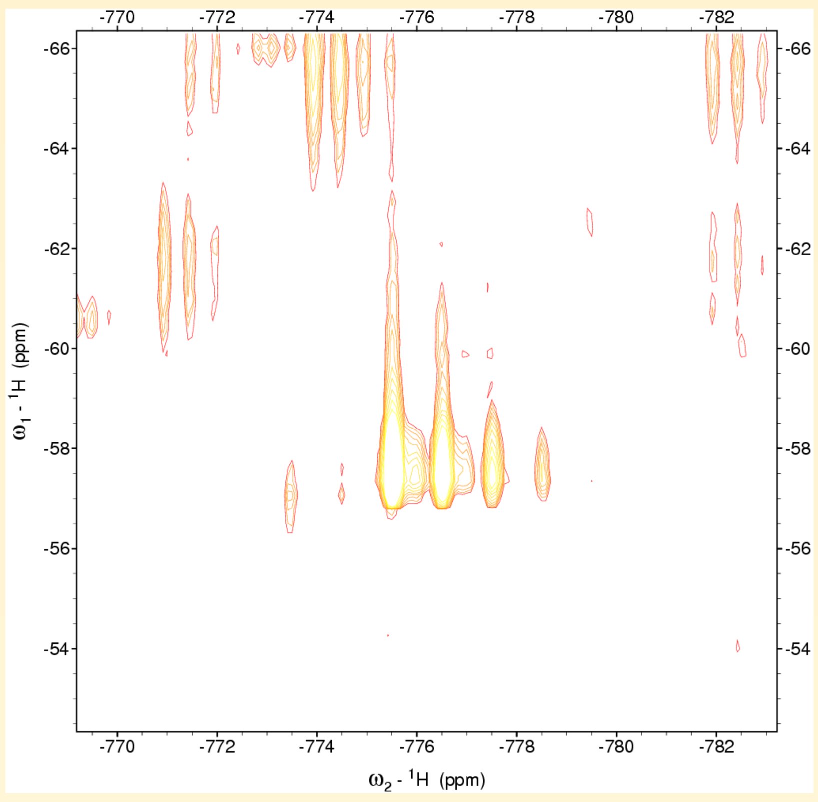

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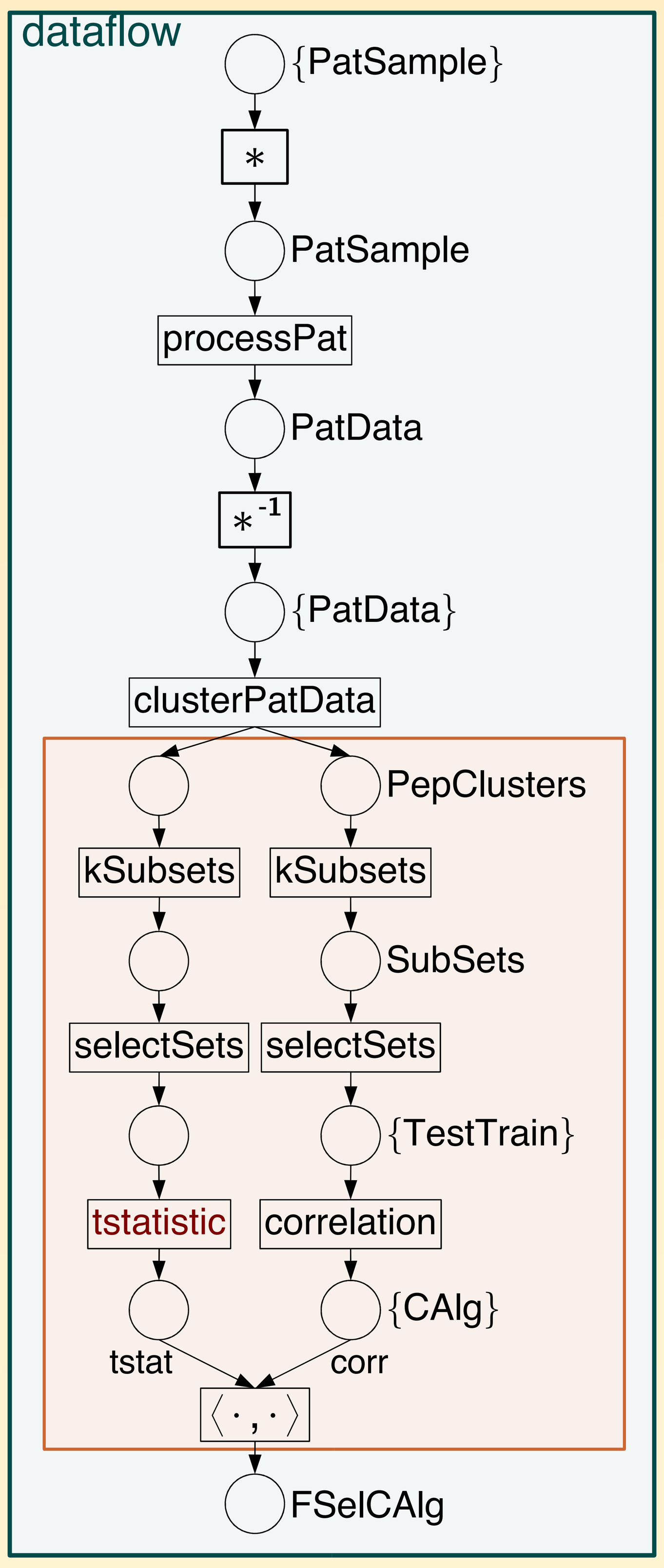

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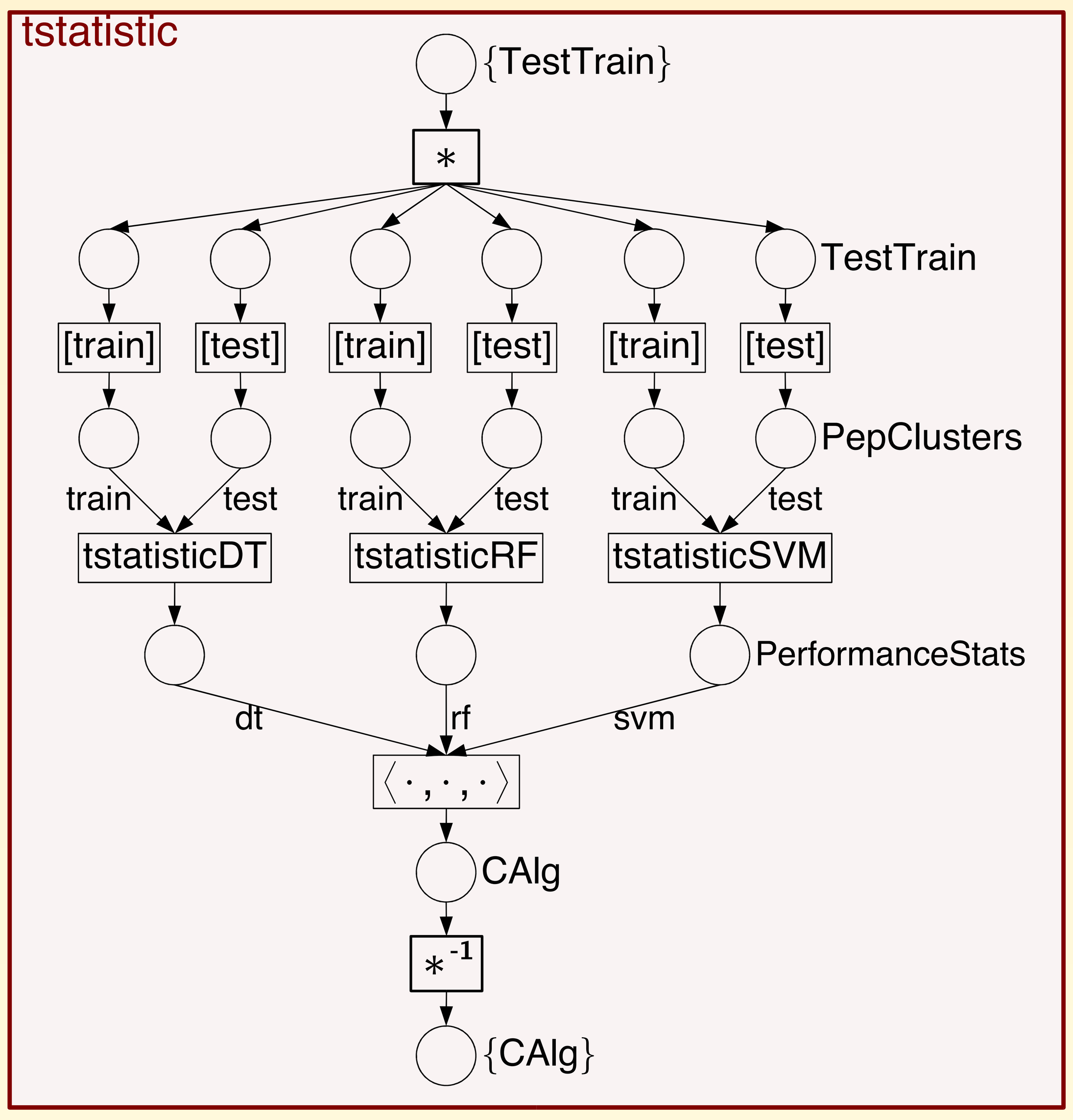

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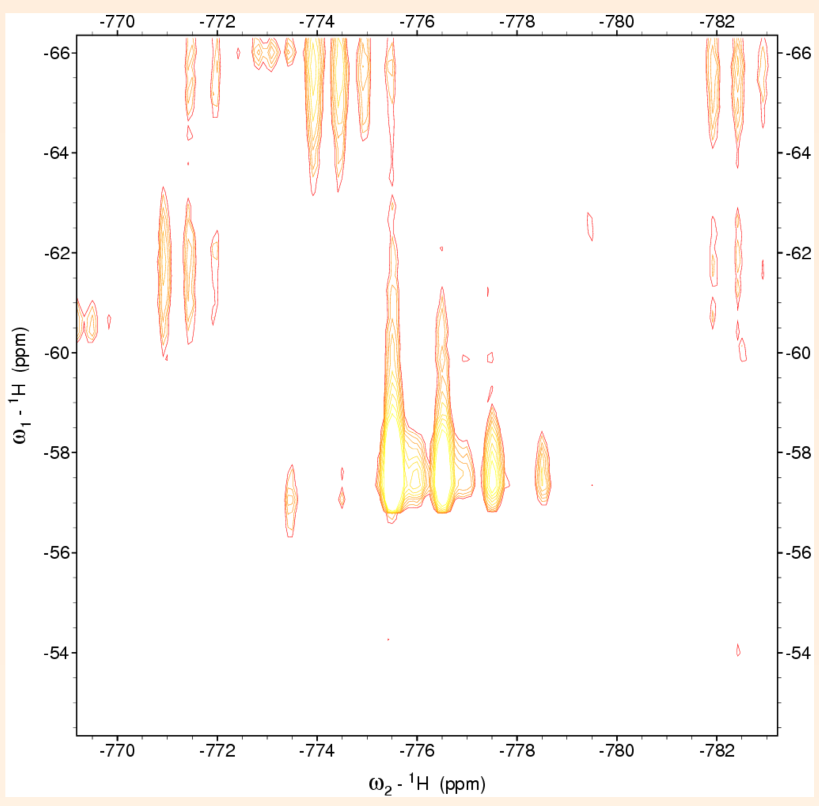

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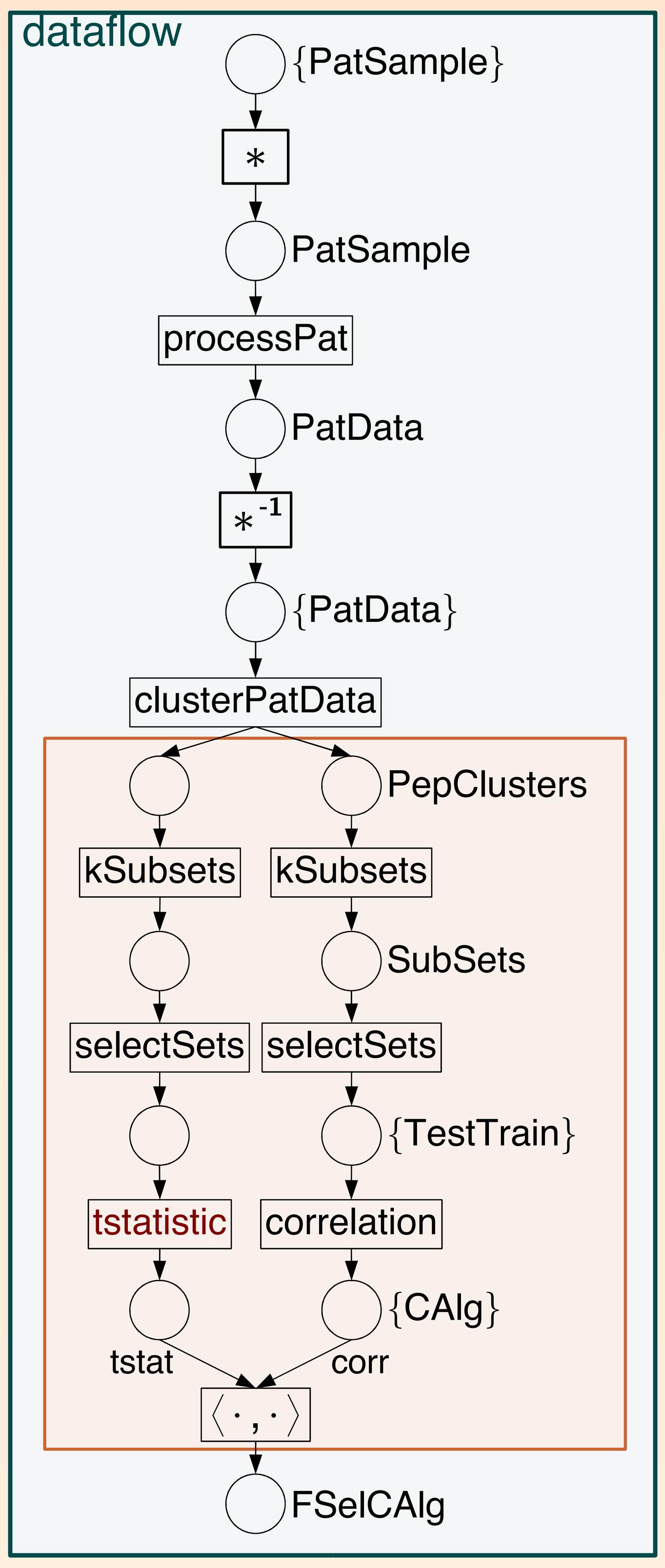

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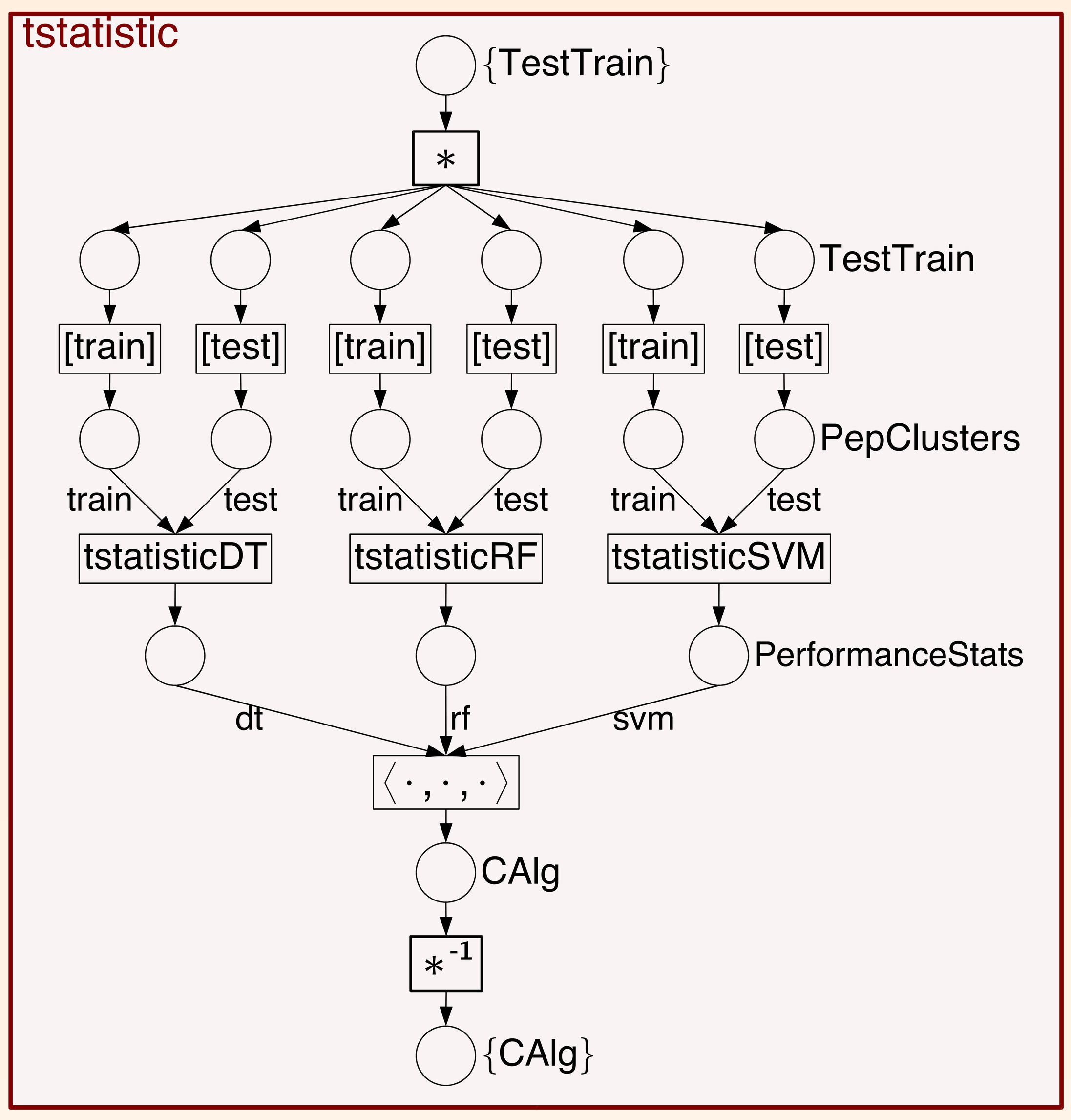

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