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# **inferelator**

***Release v0.6.1***

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The **Inferelator 3.0** is a package for gene regulatory network inference that is based on regularized regression. It is an update of the **Inferelator 2.0**, which is an update of the original **Inferelator**. It is maintained by the Bonneau lab in the Systems Biology group of the Flatiron Institute.

This repository is the actively developed inferelator package for python. It works for both single-cell and bulk transcriptome experiments. Includes **AMuSR** (Castro et al 2019), elements of **InferCLaDR** (Tchourine et al 2018), and single-cell workflows (Jackson et al 2020).

We recommend installing this package from PyPi using `python -m pip install inferelator`. If running locally, also install `joblib` by `python -m pip install joblib` for parallelization. If running on a cluster, also install `dask` by `python -m pip install dask[complete] dask_jobqueue` for dask-based parallelization.

This package can also be installed from the github repository. Clone the **inferelator** [GitHub](#) repository and run `python setup.py install`.

Documentation is available at <https://inferelator.readthedocs.io>, and basic workflows for ***Bacillus subtilis*** and ***Saccharomyces cerevisiae*** are included with a tutorial.

All current example data and scripts are available from Zenodo

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## 1.1 Workflow Constructor

Construct inferelator workflows from preprocessing, postprocessing, and regression modules

```
inferelator.workflow.inferelator_workflow (regression=<class 'inferelator.regression.base_regression._RegressionWorkflowMixin'>,
                                           workflow=<class 'inferelator.workflows.workflow_base.WorkflowBase'>)
```

Create and instantiate an Inferelator workflow.

### Parameters

- **regression** (*str*, *RegressionWorkflow subclass*) – A class object which implements the `run_regression` and `run_bootstrap` methods for a specific regression strategy. This can be provided as a string.
  - ”base” loads a non-functional regression stub.
  - ”bbsr” loads Bayesian Best Subset Regression.
  - ”elasticnet” loads Elastic Net Regression.
  - ”sklearn” loads scikit-learn Regression.
  - ”stars” loads the StARS stability Regression.
  - ”amusr” loads AMuSR Regression. This requires multitask workflow.
 Defaults to “base”.
- **workflow** (*str*, *WorkflowBase subclass*) – A class object which implements the necessary data loading and preprocessing to create design & response data for the regression strategy, and then the postprocessing to turn regression betas into a network. This can be provided as a string.
  - ”base” loads a non-functional workflow stub.
  - ”tfa” loads the TFA-based workflow.

”single-cell” loads the Single Cell TFA-based workflow.

”multitask” loads the multitask workflow.

Defaults to “base”.

**Returns** This returns an initialized object which has both the regression workflow and the preprocessing/postprocessing workflow. This object can then have settings assigned to it, and can be run with `.run()`

**Return type** Workflow instance

## 1.2 Common Workflow

**class** `inferelator.workflow.WorkflowBaseLoader`

WorkflowBaseLoader is the class to load raw data. It does no processing; it only takes data from files.

**append\_to\_path** (*var\_name*, *to\_append*)

Add a string to an existing path variable

### Parameters

- **var\_name** (*str*) – The name of the path variable (*input\_dir* or *output\_dir*)
- **to\_append** (*str*) – The path to join to the end of the existing path variable

**print\_file\_loading\_arguments** (*file\_name*)

Print the settings that will be used to load a given file name.

**Parameters** **file\_name** (*str*) – The name of the variable containing the file name (from *set\_file\_properties*)

**set\_expression\_file** (*tsv=None*, *hdf5=None*, *h5ad=None*, *tenx\_path=None*, *mtx=None*, *mtx\_barcode=None*, *mtx\_feature=None*, *h5\_layer=None*)

Set the type of expression data file. Current loaders include TSV, hdf5, h5ad (AnnData), and MTX sparse files. Only one of these loaders can be used; passing arguments for multiple loaders will raise a ValueError.

### Parameters

- **tsv** (*str*, *optional*) – A path to a TSV (or tsv.gz) file which can be loaded by `pandas.read_csv()`
- **hdf5** (*str*, *optional*) – A path to a hdf5 file which can be loaded by `pandas.HDFStore`
- **h5ad** (*str*, *optional*) – A path to an AnnData h5 file
- **tenx\_path** (*Path*, *optional*) – A path to the folder containing the 10x mtx, barcode, and feature files
- **mtx** (*str*, *optional*) – A path to an mtx file
- **mtx\_barcode** (*str*, *optional*) – A path to a list of observation names (i.e. barcodes, etc) for the mtx file
- **mtx\_feature** (*str*, *optional*) – A path to a list of gene names for the mtx file
- **h5\_layer** (*str*, *optional*) – The layer (in an AnnData h5) or the store key (in an hdf5) file to use. Defaults to using the first key.

**set\_file\_loading\_arguments** (*file\_name*, *\*\*kwargs*)

Update the settings for a given file name. By default we assume all files, except expression data, can be



read in as TSV files. Any arguments provided here will be passed to *pandas.read\_csv()* for the file name provided.

*set\_file\_loading\_arguments('expression\_matrix\_file', sep=",")* will read the *expression\_matrix\_file* as a CSV.

#### Parameters

- **file\_name** (*str*) – The name of the variable containing the file name (from *set\_file\_properties*)
- **kwargs** – Arguments to be passed to *pandas.read\_csv()*

**set\_file\_paths** (*input\_dir=None, output\_dir=None, expression\_matrix\_file=None, tf\_names\_file=None, meta\_data\_file=None, priors\_file=None, gold\_standard\_file=None, gene\_metadata\_file=None, gene\_names\_file=None*)

Set the file paths necessary for the inferelator to run

#### Parameters

- **input\_dir** (*str*) – A path containing the input files
- **output\_dir** (*str, optional*) – A path to put the output files
- **expression\_matrix\_file** (*str*) – Path to the expression data If set here, this expression file will be assumed to be a TSV file. Use *set\_expression\_file()* for other file types
- **meta\_data\_file** (*str, optional*) – Path to the meta data TSV file
- **tf\_names\_file** (*str*) – Path to a list of regulator names to include in the model
- **priors\_file** (*str*) – Path to a prior data file TSV file [Genes x Regulators]
- **gold\_standard\_file** (*str*) – Path to a gold standard data TSV file [Genes x Regulators]
- **gene\_metadata\_file** (*str, optional*) – Path to a genes annotation file
- **gene\_names\_file** (*str, optional*) – Path to a list of genes to include in the model (optional)

**set\_file\_properties** (*extract\_metadata\_from\_expression\_matrix=None, expression\_matrix\_metadata=None, expression\_matrix\_columns\_are\_genes=None, gene\_list\_index=None, meta\_data\_handler=None*)

Set properties associated with the input data files

#### Parameters

- **extract\_metadata\_from\_expression\_matrix** (*bool, optional*) – A boolean flag that should be set to True if there is non-expression data in the expression matrix. If True, *expression\_matrix\_metadata* must be provided. Defaults to False.
- **expression\_matrix\_metadata** (*list(str), optional*) – A list of columns which, if provided, will be removed from the expression matrix file and kept as metadata. Defaults to None.
- **expression\_matrix\_columns\_are\_genes** (*bool, optional*) – A boolean flag indicating the orientation of the expression matrix. False reads expression matrix [genes (rows) x samples (columns)]. True reads expression matrix [samples (rows) x genes (columns)]. Defaults to False.

- **gene\_list\_index** (*str*, *optional*) – The column name in the gene metadata file which corresponds to the gene labels in the expression and prior data files. Must be provided if *gene\_metadata\_file* was provided to *set\_file\_paths()*. Defaults to None.
- **metadata\_handler** (*str*) – A string which identifies the specific metadata parsing method to use. Options include “branching” or “nonbranching”. Defaults to “branching”.

**set\_network\_data\_flags** (*use\_no\_prior=None*, *use\_no\_gold\_standard=None*)

Set flags to skip using existing network data. Note that these flags will be ignored if network data is provided

#### Parameters

- **use\_no\_prior** (*bool*) – Flag to indicate the inferelator should be run without existing prior data. Will create a mock prior with no information. Highly inadvisable. Defaults to False
- **use\_no\_gold\_standard** (*bool*) – Flag to indicate the inferelator should be run without existing gold standard data. Will create a mock gold standard with no information. Highly inadvisable. Defaults to False

**class inferelator.workflow.WorkflowBase**

WorkflowBase handles crossvalidation, shuffling, and validating priors and gold standards

**run()**

Execute workflow, after all configuration.

**set\_crossvalidation\_parameters** (*split\_gold\_standard\_for\_crossvalidation=None*,  
*cv\_split\_ratio=None*, *cv\_split\_axis=None*)

Set parameters for crossvalidation.

#### Parameters

- **split\_gold\_standard\_for\_crossvalidation** (*bool*) – Boolean flag indicating if the gold standard should be split. Must be set to True for other crossvalidation settings to have an effect. Defaults to False.
- **cv\_split\_ratio** (*float*) – The proportion of the gold standard which should be retained for scoring. The rest will be used to train the model. Must be set between 0 and 1.
- **cv\_split\_axis** (*int*, *None*) – How to split the gold standard. If 0, split genes; this will take all the data for certain genes and keep it in the gold standard. These genes will be removed from the prior. If 1, split regulators; this will take all the data for certain regulators and keep it in the gold standard. These regulators will be removed from the prior. Splitting regulators is inadvisable. If None, the prior will be replaced with a downsampled gold standard. Setting this to 0 is generally the best choice. Defaults to None.

**static set\_output\_file\_names** (*network\_file\_name=""*, *confidence\_file\_name=""*,  
*nonzero\_coefficient\_file\_name=""*, *pdf\_curve\_file\_name=""*,  
*curve\_data\_file\_name=""*)

Set output file names. File names that end in ‘.gz’ will be gzipped.

#### Parameters

- **network\_file\_name** (*str*) – Long-format network TSV file with TF->Gene edge information. Default is “network.tsv”.
- **confidence\_file\_name** (*str*) – Genes x TFs TSV with confidence scores for each edge. Default is “combined\_confidences.tsv”
- **nonzero\_coefficient\_file\_name** (*str*) – Genes x TFs TSV with the number of non-zero model coefficients for each edge. Default is None (this file is not produced).

- **pdf\_curve\_file\_name** (*str*) – PDF file with plotted curve(s). Default is “combined\_metrics.pdf”.
- **curve\_data\_file\_name** (*str*) – TSV file with the data used to plot curves. Default is None (this file is not produced).

**set\_postprocessing\_parameters** (*gold\_standard\_filter\_method=None, metric=None*)

Set parameters for the postprocessing engine

#### Parameters

- **gold\_standard\_filter\_method** (*str*) – A flag that determines if the gold standard should be shrunk to the size of the produced model. “overlap” will only score on overlap between the gold standard and the inferred gene regulatory network. “keep\_all\_gold\_standard” will score on the entire gold standard. Defaults to “keep\_all\_gold\_standard”.
- **metric** (*str*) – The model metric to use for scoring. Supports “precision-recall”, “mcc”, “f1”, and “combined” Defaults to “combined”.

**set\_run\_parameters** (*num\_bootstraps=None, random\_seed=None, use\_mkl=None, use\_numba=None*)

Set parameters used during runtime

#### Parameters

- **num\_bootstraps** (*int*) – The number of bootstraps to run. Defaults to 2.
- **random\_seed** (*int*) – The random number seed to use. Defaults to 42.
- **use\_mkl** (*bool*) – A flag to indicate if the intel MKL library should be used for matrix multiplication, defaults to False
- **use\_numba** (*bool*) – A flag to indicate if numba should be used to accelerate the calculations. Requires numba to be installed if set. Currently only accelerates AMuSR regression, defaults to True

**set\_shuffle\_parameters** (*shuffle\_prior\_axis=None, make\_data\_noise=None, add\_prior\_noise=None*)

Set parameters for shuffling labels on a prior axis. This is useful to establish a baseline.

#### Parameters

- **shuffle\_prior\_axis** (*int, None*) – The axis for shuffling prior labels. 0 shuffles gene labels. 1 shuffles regulator labels. None means labels will not be shuffled. Defaults to None.
- **make\_data\_noise** (*bool, None*) – Replace loaded data with simulated data that is entirely random. This retains type; integer data remains integer, float remains float. Gene distributions should be centered around the mean of gene expression in the original data, but is otherwise random.
- **add\_prior\_noise** (*numeric, None*) – Add random edges to the prior data. This is a numeric value between 0 and 1 such that 0 adds no edges, 1 sets every edge in the prior to True, 0.1 sets 10% of the edges in the prior to True, and so on. Note that this will binarize the prior if it is not already binary.

## 1.3 Transcription Factor Activity (TFA) Workflow

Implementation for the Transcription Factor Activity (TFA) based Inferelator workflow.

This workflow also has a design driver which will incorporate timecourse data.

This is the standard workflow for most applications.

**class** inferelator.tfa\_workflow.TFAWorkflow

Bases: inferelator.workflows.workflow\_base.WorkflowBase

TFAWorkflow runs the timecourse driver and the TFA driver prior to regression.

**run** ()

Execute workflow, after all configuration.

**set\_design\_settings** (timecourse\_response\_driver=None, delTmin=None, delTmax=None, tau=None)

Set the parameters used in the timecourse design-response driver.

#### Parameters

- **timecourse\_response\_driver** (*bool*) – A flag to indicate that the timecourse calculations should be performed. If set False, no other timecourse settings will have any effect. Defaults to True.
- **delTmin** (*int, float*) – The minimum allowed time difference between timepoints to model as a time series. Provide in the same units as the metadata time column (usually minutes). Defaults to 0.
- **delTmax** (*int, float*) – The maximum allowed time difference between timepoints to model as a time series. Provide in the same units as the metadata time column (usually minutes). Defaults to 120.
- **tau** (*int, float*) – The tau parameter. Provide in the same units as the metadata time column (usually minutes). Defaults to 45.

**set\_tfa** (tfa\_driver=None, tfa\_output\_file=None, tfa\_input\_file=None, tfa\_input\_file\_type=None)

Perform or skip the TFA calculations; by default the design matrix will be transcription factor activity. If this is called with *tfa\_driver = False*, the design matrix will be transcription factor expression. It is not necessary to call this function unless setting *tfa\_driver = False*.

#### Parameters

- **tfa\_driver** (*bool*) – A flag to indicate that the TFA calculations should be performed. Defaults to True
- **tfa\_output\_file** (*str, optional*) – A path to a TSV file which will be created with the calculated TFAs. Note that this file may contain TF expression if the TFA cannot be calculated for that TF. If None, no output file will be produced. Defaults to None
- **tfa\_input\_file** – A path to a TFA file which will be loaded and used in place of activity calculations. If set, all TFA-related settings will be irrelevant. TSV file MUST be Samples X TFA. If None, the inferelator will calculate TFA Defaults to None
- **tfa\_input\_file\_type** – A string which identifies file type. Accepts “tsv” and “h5ad”. If None, assume the file is a TSV Defaults to None

## 1.4 Single-Cell Workflow

Run Single Cell Network Inference. This is the same network inference with some extra preprocessing functionality.

**class** inferelator.single\_cell\_workflow.SingleCellWorkflow

Bases: inferelator.workflows.tfa\_workflow.TFAWorkflow

SingleCellWorkflow has some additional preprocessing prior to calculating TFA and running regression

**add\_preprocess\_step** (*fun*, *\*\*kwargs*)

Add a preprocessing step after count filtering but before calculating TFA or regression.

#### Parameters

- **fun** (*str*, *preprocessing.single\_cell* function) – Preprocessing function. Can be provided as a string or as a function in *preprocessing.single\_cell*.  
 "log10" will take the log10 of pseudocounts  
 "ln" will take the natural log of pseudocounts  
 "log2" will take the log2 of pseudocounts  
 "fft" will do the Freeman-Tukey transform
- **kwargs** – Additional arguments to the preprocessing function

**run** ()

Execute workflow, after all configuration.

**set\_count\_minimum** (*count\_minimum=None*)

Set the minimum count value for each gene (averaged over all samples)

**Parameters** **count\_minimum** (*float*) – The mean expression value which is required to retain a gene for modeling. Data that has already been normalized should probably be filtered during normalization, not now. Defaults to None (disabled).

## 1.5 Multi-Task AMuSR Workflow

Run Multitask Network Inference with TFA-AMuSR.

**class** inferelator.amusr\_workflow.**MultitaskLearningWorkflow**

Bases: inferelator.workflows.single\_cell\_workflow.SingleCellWorkflow

Class that implements multitask learning. Handles loading and validation of multiple data packages

**create\_task** (*task\_name=None*, *input\_dir=None*, *expression\_matrix\_file=None*,  
*meta\_data\_file=None*, *tf\_names\_file=None*, *priors\_file=None*,  
*gold\_standard\_file=None*, *gene\_names\_file=None*, *gene\_metadata\_file=None*,  
*workflow\_type='single-cell'*, *\*\*kwargs*)

Create a task object and set any arguments to this function as attributes of that task object. TaskData objects are stored internally in *\_task\_objects*.

#### Parameters

- **task\_name** (*str*) – A descriptive name for this task
- **input\_dir** (*str*) – A path containing the input files
- **expression\_matrix\_file** (*str*) – Path to the expression data
- **meta\_data\_file** (*str*, *optional*) – Path to the meta data
- **tf\_names\_file** (*str*) – Path to a list of regulator names to include in the model
- **priors\_file** (*str*) – Path to a prior data file
- **gene\_metadata\_file** (*str*, *optional*) – Path to a genes annotation file
- **gene\_names\_file** (*str*, *optional*) – Path to a list of genes to include in the model (optional)

- **workflow\_type** (*str*, *inferelator.BaseWorkflow* subclass) – The type of workflow for data preprocessing. “tfa” uses the TFA workflow, “single-cell” uses the Single-Cell TFA workflow
- **kwargs** – Any additional arguments are assigned to the task object.

**Returns** Returns a task reference which can be additionally modified by calling any valid Workflow function to set task parameters

**Return type** TaskData instance

**set\_task\_filters** (*regulator\_expression\_filter=None*, *target\_expression\_filter=None*)

Set the filtering criteria for regulators and targets between tasks

**Parameters**

- **regulator\_expression\_filter** (*str*, *optional*) – “union” includes regulators which are present in any task, “intersection” includes regulators which are present in all tasks
- **target\_expression\_filter** (*str*, *optional*) – “union” includes targets which are present in any task, “intersection” includes targets which are present in all tasks

## 1.6 Cross-Validation Workflow Wrapper

This is a manager which will take an Inferelator workflow and repeatedly run it with different parameters. This is implemented using deep copies; it is therefore memory-intensive.

**class** `inferelator.crossvalidation_workflow.CrossValidationManager` (*workflow\_object=None*)

Bases: `object`

Crossvalidate an Inferelator Workflow

**\_\_init\_\_** (*workflow\_object=None*)

Create a new CrossValidationManager instance and give it a workflow

**Parameters** **workflow\_object** (*Workflow*) – The workflow to run crossvalidation with

**add\_gridsearch\_parameter** (*param\_name*, *param\_vector*)

Set a parameter to search through by exhaustive grid search

**Parameters**

- **param\_name** (*str*) – The workflow parameter to change for each run
- **param\_vector** (*iterable*) – An iterable with values to use for the parameter

**add\_grouping\_dropin** (*metadata\_column\_name*, *group\_size=None*, *seed=42*)

Run modeling on each group (defined by a metadata column) individually.

**Parameters**

- **metadata\_column\_name** (*str*) – Metadata column which has different values for each group
- **group\_size** (*int*, *None*) – The maximum size of each group. Groups will be downsampled to the same size if this is not set to None. Default is None.
- **seed** (*int*) – The random seed to use for the group downsampling (this is not the same as the seed passed to the workflow)

**add\_grouping\_dropout** (*metadata\_column\_name*, *group\_size=None*, *seed=42*)

Drop each group (defined by a metadata column) and run modeling on all of the other groups.

**Parameters**

- **metadata\_column\_name** (*str*) – Metadata column which has different values for each group
- **group\_size** (*int, None*) – The maximum size of each group. Groups will be down-sampled to the same size if this is not set to None. Default is None.
- **seed** (*int*) – The random seed to use for the group downsampling (this is not the same as the seed passed to the workflow)

**add\_size\_subsampling** (*size\_vector, stratified\_column\_name=None, with\_replacement=False, seed=42, size\_sample\_only=None*)

Resample expression data to a ratio of the original data.

**Parameters**

- **size\_vector** (*iterable(floats)*) – An iterable with numeric ratios for down-sampling. These values must be between 0 and 1.
- **stratified\_column\_name** (*str, None*) – Set this to stratify sampling (to maintain group size ratios). If None, do not maintain group size ratios. Default is None.
- **with\_replacement** (*bool*) – Do sampling with or without replacement. Defaults to False
- **seed** – The random seed to use when selecting observations (this is not the same as the seed passed to the workflow)
- **seed** – int





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## Model Selection & Regression Modules

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### 2.1 BBSR

**class** inferelator.regression.bbsr\_python.BBSRRegressionWorkflowMixin  
 Bayesian Best Subset Regression (BBSR)

<https://doi.org/10.15252/msb.20156236>

**set\_regression\_parameters** (*prior\_weight=None*, *no\_prior\_weight=None*,  
*bsr\_feature\_num=None*, *clr\_only=None*, *ordinary\_least\_squares\_only=None*)

Set regression parameters for BBSR

#### Parameters

- **prior\_weight** (*float*) – Weight for edges that are present in the prior network. Defaults to 1.
- **no\_prior\_weight** (*float*) – Weight for edges that are not present in the prior network. Defaults to 1.
- **bsr\_feature\_num** (*int*) – The number of features to include in best subset regression. Defaults to 10.
- **clr\_only** (*bool*) – Only use Context Likelihood of Relatedness to select features for BSR, not prior edges. Defaults to False.
- **ordinary\_least\_squares\_only** (*bool*) – Use OLS instead of Bayesian regression, for testing. Defaults to False.

### 2.2 AMuSR

**class** inferelator.regression.amusr\_regression.AMUSRRegressionWorkflowMixin  
 Multi-Task AMuSR regression

<https://doi.org/10.1371/journal.pcbi.1006591>

**set\_regression\_parameters** (*prior\_weight=None, lambda\_Bs=None, lambda\_Ss=None, heuristic\_Cs=None, tol=None, relative\_tol=None*)

Set regression parameters for AmUSR.

#### Parameters

- **prior\_weight** (*numeric*) – Weight for edges that are present in the prior network. Non-prior edges have a weight of 1. Set this to 1 to weight prior and non-prior edges equally, Defaults to 1.
- **lambda\_Bs** (*list(floats) or np.ndarray(floats)*) – Lambda\_B values to search during model selection. If not set, lambda\_B will be chosen using the heuristic  $\lambda_b = c * \sqrt{d \log p / n}$  from Castro 2019 Defaults to not set. Must be provided if lambda\_S is set.
- **lambda\_Ss** (*list(floats) or np.ndarray(floats)*) – Lambda\_S values to search during model selection. If not set, lambda\_S will be chosen using the heuristic  $0.5 < \lambda_s / \lambda_b < 1$  from Castro 2019 Defaults to not set.
- **heuristic\_Cs** (*list(floats) or np.ndarray(floats)*) – c values to search during model selection. Values of c to calculate  $\lambda_b = c * \sqrt{d \log p / n}$ , Defaults to  $\text{np.logspace}(\text{np.log10}(0.01), \text{np.log10}(10), 20)[::-1]$ . Does not have an effect if lambda\_B is provided.
- **tol** (*float*) – Convergence tolerance for amusr regression
- **relative\_tol** (*float*) – Relative convergence tolerance for amusr regression

## 2.3 Scikit-Learn

**class** inferelator.regression.sklearn\_regression.**SKLearnWorkflowMixin** (*\*args, \*\*kwargs*)

Use any scikit-learn regression module

**set\_regression\_parameters** (*model=None, add\_random\_state=None, \*\*kwargs*)

Set parameters to use a sklearn model for regression

#### Parameters

- **model** (*BaseEstimator subclass*) – A scikit-learn model class
- **add\_random\_state** (*bool*) – Flag to include workflow random seed as “random\_state” in the model
- **kwargs** (*any*) – Any arguments which should be passed to the scikit-learn model class instantiation

## 2.4 Elastic-Net

**class** inferelator.regression.elasticnet\_python.**ElasticNetWorkflowMixin** (*\*args, \*\*kwargs*)

Set default parameters to run scikit-learn ElasticNetCV

**set\_regression\_parameters** (*model=None, add\_random\_state=None, \*\*kwargs*)

Set parameters to use a sklearn model for regression

#### Parameters

- **model** (*BaseEstimator subclass*) – A scikit-learn model class
- **add\_random\_state** (*bool*) – Flag to include workflow random seed as “random\_state” in the model
- **kwargs** (*any*) – Any arguments which should be passed to the scikit-learn model class instantiation

## 2.5 StARS-Lasso

**class** inferelator.regression.stability\_selection.StARSWorkflowMixin(\*args, \*\*kwargs)

Stability Approach to Regularization Selection (StARS)-LASSO. StARS-Ridge is implemented on an experimental basis.

<https://arxiv.org/abs/1006.3316> <https://doi.org/10.1016/j.immuni.2019.06.001>

**set\_regression\_parameters** (*alphas=None, num\_subsamples=None, method=None, \*\*kwargs*)  
Set regression parameters for StARS-LASSO

### Parameters

- **alphas** (*list(float)*) – A list of alpha (L1 term) values to search. Defaults to logspace between 0. and 10.
- **num\_subsamples** (*int*) – The number of groups to break data into. Defaults to 20.
- **method** (*str*) – The model to use. Can choose from ‘lasso’ or ‘ridge’. Defaults to ‘lasso’. If ‘ridge’ is set, `ridge_threshold` should also be passed. Any value below `ridge_threshold` will be set to 0.
- **kwargs** (*any*) – Any additional arguments will be passed to the LASSO or Ridge scikit-learn object at instantiation



### 3.1 Network File

```
network_file_name = "network.tsv"
```

The `network.tsv` is a long-format TSV file containing Regulator -> Target edges. This TSV file is sorted by the confidence score of the regulator (TF) -> target (gene) edge, from largest to smallest.:

target	regulator	combined_confidences	gold_standard	precision	
↪ recall	MCC	F1			
BSU24750	BSU04730	0.999986	1	1	
↪ 0.00165	0.04057	0.003295			
BSU13020	BSU04730	0.999984			
BSU09690	BSU04730	0.99998			
BSU06590	BSU04730	0.999978			
BSU18510	BSU04730	0.999976			
BSU25800	BSU25810	0.999975			

If the gene and TF are in the gold standard, the gold standard for this edge is reported (1 if present, 0 if not present), and the model performance is calculated. The Precision, Recall, MCC, and F1 scores are calculated assuming that all edges above a row (with greater confidence scores) are predicted TF -> Gene interactions, and all values below are predicted to not be TF -> Gene interactions. Rows which do not contain any gold standard (either 1 or 0) indicate that the regulator or the target are not in the Genes x TFs gold standard matrix. These rows will not be scored.

Also included is a column indicating if the network edge was in the prior (1, 0, or not present if the gene or TF were not present in the prior network). The `beta.sign.sum` column is the number of times the model coefficient occurred and the sign (positive model coefficients will be reported as a positive value, and negative model coefficients will be reported as a negative value). The `var.exp.median` column reports the median amount of variance in the gene explained by the regulator.

## 3.2 InferelatorResults

```
class inferelator.postprocessing.InferelatorResults (network_data,      betas_stack,  
                                                    combined_confidences,    met-  
                                                    ric_object,      betas_sign=None,  
                                                    betas=None)
```

For network analysis, the results produced in the `output_dir` are sufficient. Model development and comparisons may require to values that are not written to files. An `InferelatorResults` object is returned by the `workflow.run()` methods (A list of `InferelatorResults` objects is returned by the `CrossValidationManager.run()` method).

This object allows access to most of the internal values created by the inferelator.

**name**

Results name, usually set to task name. Defaults to None.

**network**

Network dataframe, usually written to `network.tsv.gz`

**betas\_sign**

The aggregate sign of non-zero betas. This is a dataframe which is Genes x TFs

**betas\_stack**

Count of non-zero betas. This is a dataframe which is Genes x TFs

**combined\_confidences**

Confidence scores for tf-gene network edges. This is a dataframe which is Genes x TFs

**tasks**

Task result objects if there were multiple tasks. None if there were not. This is a dict, keyed by task ID

## 4.1 Input Data

All data provided to the inferelator should be in TSV format.

The inferelator package **requires** two data structures to function:

- A gene expression matrix which contains some expression data for  $G$  genes and  $N$  samples. Any unit is generally acceptable provided all samples are the same unit and are reasonably normalized together.
- A text list of  $K$  genes which should be modeled as regulators (like Transcription Factors)

The performance with no additional data is extremely poor, however. In addition to the two required data elements, there is other data which can be provided.

The most important of these additional elements is some known knowledge about regulatory connections.

- A prior knowledge connectivity matrix  $[G \times K]$  which links the genes  $G$  to the regulators  $K$ . This matrix should have a zero where a gene is not regulated by a regulator. It should have a non-zero value where a gene is known to be regulated by a regulator. This can be as simple as a boolean matrix, but sign and magnitude will affect calculation of regulator activity.
- A gold standard connectivity matrix  $[G \times K]$  which links the genes  $G$  to the regulators  $K$ . This matrix should have a zero where a gene is not regulated by a regulator. It should have a non-zero value where a gene is known to be regulated by a regulator. It will be interpreted as a boolean matrix, so sign and magnitude of non-zeros is not considered.

Also important is sample metadata. This is necessary if there is a time element to the samples, or if there is some grouping criteria. If time series data is included, there are two supported formats for this data. If time series data is not included, any metadata structure is valid.

The first format is **branching** and has 5 columns:

```
isTs | is1stLast | prevCol | del.t | condName
=====
TRUE | f          | NA    | NA  | A-1
```

(continues on next page)

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TRUE	m	A-1	15	A-2
TRUE	l	A-2	15	A-3

- **isTs** is TRUE or FALSE and indicates if this sample is in a time series.
- **is1stLast** is **f** if this sample is the first sample in a time series. It is **m** if this sample is a middle sample in a time series. It is **l** if this sample is the last sample in a time series. It is **NA** if this sample is not in a time series
- **prevCol** is the name of the sample which comes before this sample
- **del.t** is the time elapsed since the sample which comes before this sample
- **condName** is the name of this sample. It must match the sample name in the expression data.

The second format is **nonbranching** and has 3 columns:

```
condName | strain | time
=====
A-1      | A      | 0
A-2      | A      | 15
A-3      | A      | 30
```

- **condName** is the name of this sample. It must match the sample name in the expression data.
- **strain** is the name of the sample group.
- **time** is the absolute time elapsed during this sample group's experiment.

Finally, gene metadata can also be provided. This is currently used to restrict modeling to just some genes.

## 4.2 Workflow setup

The inferelator is implemented on a workflow model. The first step is to create a workflow object. At this stage, the type of regression model and workflow must be chosen:

```
from inferelator import inferelator_workflow

worker = inferelator_workflow(regression="bbsr", workflow="tfa")
```

- Valid options for regression include “bbsr”, “elastic-net”, and “amusr”.
- Valid options for workflow include “tfa”, “single-cell”, and “multitask”.

The next step is to set the location of input data files:

```
worker.set_file_paths(input_dir=".",
                      output_dir="./output_inferelator",
                      expression_matrix_file="expression.tsv",
                      tf_names_file="regulators.tsv",
                      meta_data_file="meta_data.tsv",
                      priors_file="priors.tsv",
                      gold_standard_file="gold_standard.tsv")
```

The input directory will be added to all file locations which are not absolute paths. The output directory will be created if it does not exist.

Finally, run parameters should be set:



```
worker.set_run_parameters(num_bootstraps=5, random_seed=42)
```

This worker can now be run with:

```
network_result = worker.run()
```

## 4.3 Multitask Workflows

The inferelator supports inferring networks from multiple separate “tasks” at the same time. Several modeling options exist, but all must use the multitask workflow:

```
worker = inferelator_workflow(regression="amusr", workflow="multitask")
```

- **amusr** regression is a multitask learning model that shares information during regression.
- **bbsr-by-task** regression learns separate networks using the BBSR model, and then aggregates them into a joint network.
- **elasticnet-by-task** regression learns separate networks using the Elastic Net model, and then aggregates them into a joint network.

After creating a workflow, only the input, output and gold standard file location should be provided directly:

```
worker.set_file_paths(input_dir=".", output_dir="./output_network", gold_standard_
↪file="gold_standard.tsv.gz")
```

Other information should be provided to each separate task. These can be created by calling the `.create_task()` function. This function returns a task reference which can be used to set additional task properties:

```
task_1 = worker.create_task(task_name="Bsubtilis_1",
                             input_dir=".",
                             tf_names_file='tf_names.tsv',
                             meta_data_file='GSE67023_meta_data.tsv',
                             priors_file='gold_standard.tsv.gz',
                             workflow_type="tfa")
task_1.set_expression_file(tsv='GSE67023_expression.tsv.gz')

task_2 = worker.create_task(task_name="Bsubtilis_2",
                             input_dir=".",
                             tf_names_file='tf_names.tsv',
                             meta_data_file='meta_data.tsv',
                             priors_file='gold_standard.tsv.gz',
                             workflow_type="tfa")
task_2.set_expression_file(tsv='expression.tsv.gz')
```

Additional parameters can be set on the main workflow. Task references made with `.create_task()` are automatically included when the workflow is started. The workflow can then be started with `.run()`:

```
worker.set_run_parameters(num_bootstraps=5, random_seed=42)
worker.run()
```

## 4.4 Parallelization

The inferelator supports three major parallelization options. These can be set using a controller class. Calling the multiprocessing environment should be protected with the `if __name__ == '__main__':` pragma. This is necessary to prevent a specific error in creating new processes that occurs when `os.fork()` is unavailable. Multiprocessing options should be set prior to creating and running workflows. It is not necessary to set multiprocessing more than once per session:

```
from inferelator import MPControl

if __name__ == '__main__':
    MPControl.set_multiprocess_engine("multiprocessing")
    MPControl.client.processes = 12
    MPControl.connect()
```

- **multiprocessing** engine uses the pathos implementation of python's multiprocessing. It creates multiple processes on one computer.
- **local** engine uses no multiprocessing and runs from a single process. In some cases, python libraries (like numpy) may use multiple threads within this process.
- **dask-cluster** engine uses the dask scheduler-worker library in combination with the dask\_jobqueue cluster-management library to manage processes through a job scheduler. Currently, only SLURM is supported. Correctly configuring this for your cluster may be a challenge.

## CHAPTER 5

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### Examples

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Example scripts are currently available on [GitHub](#).



## References

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### 7.1 Inferelator v0.6.1 *January 3, 2023*

#### New Functionality:

- Extended support for mRNA velocity & decay calculations
- Added new experimental TFA modules

#### Code Refactoring:

- Workflow, ResultProcessor, and InferelatorData restructured for readability and clearer commenting

#### Bug Fixes:

- Slicing individual gene data returns numpy vector instead of anndata view
- Corrected several deprecated pandas calls to eliminate FutureWarnings

### 7.2 Inferelator v0.6.0 *September 14, 2022*

#### New Functionality:

- Support for grouping arbitrary genes from multiple tasks into learning groups
- Workflow to learn homology groups together
- Workflow to explicitly incorporate velocity and decay into learning
- Added support for batching parallelization calls to reduce overhead when data is relatively small

#### Code Refactoring:

- Refactored multi-task learning to parameterize tfbs and genes for each task
- Refactored parallelization around joblib & dask
- Removed pathos and replaced with joblib

- Optimized StARS-LASSO by replacing standalone LASSO with `lasso_path`

Bug Fixes:

- Fixed several messages to be more informative
- `use_no_prior` is appropriately applied in multitask learning

## **7.3 Inferelator v0.5.8 *February 23, 2022***

Bug Fixes:

- Corrected combining multi-task gene and tf labels

## **7.4 Inferelator v0.5.7 *September 29, 2021***

New Functionality:

- Added support for numba acceleration of AMuSR with `.set_run_parameters(use_numba=True)` (PR #46)

Code Refactoring:

- Updated example scripts
- Removed deprecated KVS multiprocessing and associated code

Bug Fixes:

- Gene labels are included as the first column of the produced confidences TSV file by default
- Matplotlib backend selection checks for non-interactive mode

## **7.5 Inferelator v0.5.6 *August 16, 2021***

New Functionality:

- Added code to randomly generate noise in prior with `.set_shuffle_parameters(add_prior_noise=None)`
- Added in-workflow benchmarks for CellOracle and pySCENIC

Code Refactoring:

- Minor changes to matplotlib interface
- Improved testing for multitask workflows
- Improved error messaging around prior and gold standard
- Switch from Travis.ci to GitHub Actions for continuous integration

## **7.6 Inferelator v0.5.5 *April 29, 2021***

New Functionality:

- Added `.set_regression_parameters(tol=None)` to parameterize tolerances in AMuSR regression



Code Refactoring:

- Profiled and optimized AMuSR code

## 7.7 Inferelator v0.5.4 *April 23, 2021*

Bug Fixes:

- Fixed bug in multitask prior processing
- Fixed bug in dask cluster setup
- Suppressed stdout warning when output network MCC is not finite

## 7.8 Inferelator v0.5.3 *March 22, 2021*

New Functionality:

- Added the ability to control threads-per-process when using dask

Bug Fixes:

- Fixed bug in result dataframe that failed to create columns in older versions of pandas

## 7.9 Inferelator v0.5.2 *January 29, 2021*

New Functionality:

- Added flag `.set_shuffle_parameters(make_data_noise=True)` to model on randomly generated noise
- Output TSV files are gzipped by default
- Added `.set_output_file_names()` as interface to change output file names
- Added `.set_regression_parameters(lambda_Bs=None, lambda_Ss=None, heuristic-Cs=None)` for AMuSR regression

Bug Fixes:

- Fixed bug(s) with dask cluster scaling
- Fixed float precision bug in mutual information

Code Refactoring:

- Added additional tests
- Refactored AMuSR code

## 7.10 Inferelator v0.5.1 *November 22, 2020*

Bug Fixes:

- Fixed bug that prevented PDF summary figure generation

## **7.11 Inferelator v0.5.0 *November 14, 2020***

### New Functionality:

- Changed output to include additional performance metrics (Matthews Correlation Coefficient and F1)

### Bug Fixes:

- Fixed several bugs around data loading
- Fixed several float tolerance bugs

### Code Refactoring:

- Added additional tests
- Improved dask cluster configurations
- Improved documentation

## **7.12 Inferelator v0.4.1 *August 4, 2020***

### New Functionality:

- Added a regression module based on stability selection
- Added a regression module that can apply any scikit-learn regression model

### Bug Fixes:

- Fixed row labels in matrix outputs

### Code Refactoring:

- Added additional tests

## **7.13 Inferelator v0.4.0 *April 7, 2020***

### New Functionality:

- Support for sparse data structures
- Support for h5 and mtx input files
- Added several flags that can change behavior of BBSR (clr\_only, ols\_only)

### Bug Fixes:

- Changed behavior of precision-recall to average the precision of ties instead of randomly ordering

### Code Refactoring:

- Refactored the core data structures from pandas to AnnData backed by numpy or scipy arrays
- Data matrices are loaded and maintained as OBS x VAR throughout the workflow. Data files which are in GENE x SAMPLE orientation can be loaded if `.set_file_properties(expression_matrix_columns_are_genes=False)` is set.
- Use `sparse_dot_mkl` with the intel Math Kernel Library to handle sparse (dot) dense multiplication
- Improved memory usage

- Added unit tests for dask-related functionality
- Changed a number of error messages to improve clarity

## 7.14 Inferelator v0.3.2 *December 19, 2019*

### New Functionality:

- Improved error messages associated with misaligned data structures
- Added example script and data for the multitask workflows

### Bug Fixes:

- Corrected several bugs when using the CrossValidationManager on multitask workflows

### Code Refactoring:

- This is the final release which will be fully py2.7 compatible
- Additional unit testing

## 7.15 Inferelator v0.3.1 *December 10, 2019*

### New Functionality:

- Created a CrossValidationManager which handles parameter searches on workflows. Replaces the single\_cell\_cv\_workflow which did not generalize well.
- Workflow parameters are now set through functional setters like set\_file\_paths(), instead of through setting (cryptic) instance variables
- Calculated transcription factor activities can be saved to a file prior to inference. This is set with *workflow.set\_tfa(tfa\_output\_file = "Filename.tsv")*

### Bug Fixes:

- Many

### Code Refactoring:

- Rebuilt the multitask workflow with TaskData objects instead managing data in many lists of things.

## 7.16 Inferelator v0.3.0 *July 30, 2019*

### New Functionality:

- Created a MultiprocessingManger for abstract control of multiprocessing.
- Implemented a scheduler-worker model through the dask package for cluster computing.
- Implemented a map model through the pathos implementation of multiprocessing for local computing.
- Example scripts and datasets are now provided

### Bug Fixes:

- Many

### Code Refactoring:

- Rebuilt the core workflow
- Workflow assembly by inheritance is managed with a factory function
- Refactored regression to act as a mapped function for easier multiprocessing

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