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ReciPies: A Lightweight Data Transformation Pipeline for Reproducible ML

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Summary

Machine Learning (ML) workflows live or die by their data-preprocessing steps. In Python, these steps are often scattered across ad-hoc scripts or opaque scikit-learn snippets that are hard to read, audit, or reuse. `ReciPies` provides a concise, human-readable, and reproducible way to declare, execute, and share preprocessing pipelines following configuration-as-code principles. It lowers the cognitive load of feature engineering, improves reproducibility, and makes methodological choices explicit for researchers, engineering teams, and peer reviewers.

Statement of need

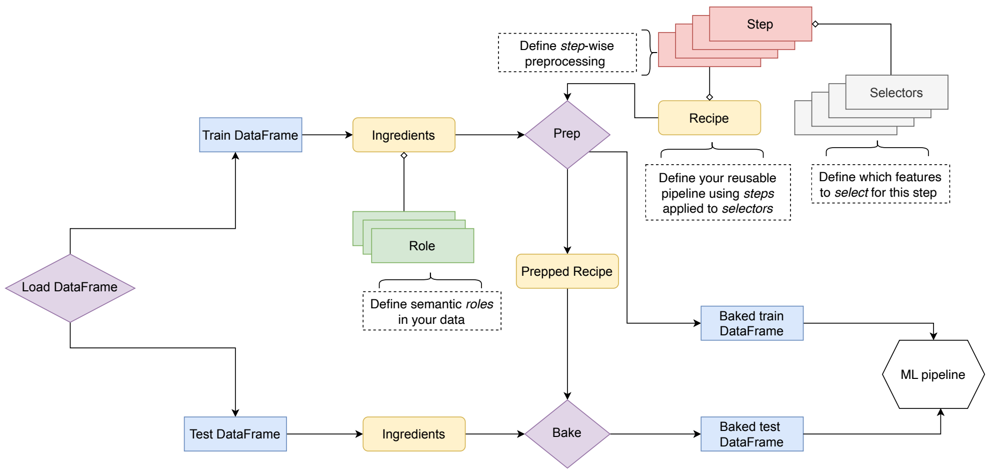
Transparent and reproducible preprocessing remains a weak link in many scientific ML studies. The consequences are (1) confounded research results (Gundersen & Kjensmo, 2018), (2) complicated peer review (Semmelrock et al., 2025), and (3) poor reuse (Samuel et al., 2021). Researchers and engineers working with longitudinal regulated data (e.g., in energy production, health, finance, or environmental monitoring) in particular need pipelines they can audit, serialize, and hand to collaborators without reverse-engineering a tangle of imperative code. The current lack of reproducibility has been documented extensively in the literature (Gundersen & Kjensmo, 2018; Johnson et al., 2017; Kelly et al., 2019; Raff, 2019; Semmelrock et al., 2025); moreover, scientific venues have begun to address this issue (Various, 2024).

Related work

Scikit-learn provides `Pipeline` and `ColumnTransformer`, along with a rich estimator ecosystem (Pedregosa et al., 2011), but lacks role-based variable grammar, limited human readability, and awkward serialization. Feature-engine (Galli, 2021), pyjanitor (J. et al., 2019), or scikit-lego (Warmerdam et al., 2025) add helpful transformers and data-cleaning verbs. However, none provide a unified, role-centric abstraction with backend flexibility. The R `recipes` package established the prep/bake pattern and a clean grammar for preprocessing (Kuhn et al., 2024). `ReciPies` brings these ideas to Python, extends them with backend-agnostic execution on Pandas and Polars, and emphasizes configuration-as-code artifacts suitable for a wide range of machine learning pipelines.

Design and implementation

`ReciPies` adopts a tidy, stepwise *recipe* interface that emphasizes semantic roles over column names and a strict separation of fitting from application. Transformations are declared on roles such as predictor, outcome, identifier, or timestamp. Recipes are prepped on training data and baked on new data to prevent leakage. Each step is inspectable, versionable, and serializable to JSON or YAML for provenance and review. Steps are composable with explicit state and deterministic behavior given fixed inputs and seeds. `RecIPies` supports both Pandas (McKinney, 2010), which is widely adopted in the ML community, and the more recent Polars (Vink et al., 2024), which offers increased performance.



Step
Define *step*-wise preprocessing
Selectors
Train DataFrame
Ingredients
Prep
Recipe
Define your reusable pipeline using *steps* applied to *selectors*
Define which features to *select* for this step
Role
Define semantic *roles* in your data
Prepped Recipe
Load DataFrame
Baked train DataFrame
ML pipeline
Test DataFrame
Ingredients
Bake
Baked test DataFrame

A typical workflow 1) loads a Pandas or Polars training `DataFrame`, 2) wraps it as an `Ingredients` object that records role metadata, 3) defines a `Recipe` from `Steps` operating on columns selected based on roles by `Selectors`, 4) preps the recipe on the training split to estimate parameters, and 5) bakes it on the held-out split to apply those parameters without leakage. The baked outputs feed downstream modeling and evaluation. Figure 1 gives an overview of this workflow.

```
import polars as pl
from sklearn.model_selection import train_test_split
from sklearn.impute import MissingIndicator
from recipies import Ingredients, Recipe
from recipies.selector import has_role
from recipies.step import StepImputeFill, StepScale, StepSklearn

# Load and split Physionet Computing in Cardiology Challenge 2019 dataset
df = pl.read_csv("Physionet_CiCC_2019.csv", sep="|")
df_train, df_test = train_test_split(df, test_size=0.2, random_state=42)

# Define ingredients (training set + roles)
roles = {"outcomes": ["SepsisLabel"], "predictors": ["Age", "HR", "Temp"], "groups": ["PatientID"],
"sequences": ["ICULOS"]}
ing = Ingredients(df_train, roles=roles)

# Define the recipe for processing the ingredients (e.g., scaling and imputation)
rec = Recipe(ing)
rec.add_step(StepScale())
rec.add_step(StepSklearn(MissingIndicator(features="all"), sel=has_role("predictor")))
rec.add_step(StepImputeFill(strategy="forward"), sel=has_role("predictor"))

# Prepare (=fit) recipe on training data and apply the same recipe to the test set
df_train = rec.prep()
df_test = rec.bake(df_test)
```

Figure 2 demonstrates usage on the PhysioNet Computing in Cardiology 2019 dataset (Reyna et al., 2020), including role assignment, temporal imputation, and normalization. The prepped recipe serializes to JSON or YAML, and reloading the artifact reproduces the transforms across supported platforms.

Complete code and interactive notebooks are available in the project documentation. `RecIPies` also provides a benchmarking suite comparing the performance of different preprocessing steps on (generated) data. `RecIPies` is already used as the bedrock of reproducible pipelines in Yet Another ICU Benchmark (Van de Water et al., 2024) The adaptable, configurable code modules that make extensive use of `RecıPies` can be found here; this demonstrates that `RecıPies` can be used for arbitrary research domains. Our work shows that there is no need to sacrifice readability for performance, nor flexibility for simplicity. We encourage the development of domain-specific step libraries and integration patterns that can benefit the broader ecosystem.

Future steps

Our first step is to expand the library of Polars-native steps to fully leverage its columnar execution model, particularly for time-series operations and large-scale aggregations, where Polars shows significant performance advantages. Second, we aim to integrate with ML versioning systems to streamline the transition from research to production.

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