NANYANG
TECHNOLOGICAL
UNIVERSITY
SINGAPORE

School of Computer
Science and Engineering
College of Engineering

EXPLORATION OF EXPLAINABLE ARTIFICIAL INTELLIGENCE METHODS

ON CHROMATIN INTERACTIONS NEURAL NETWORK

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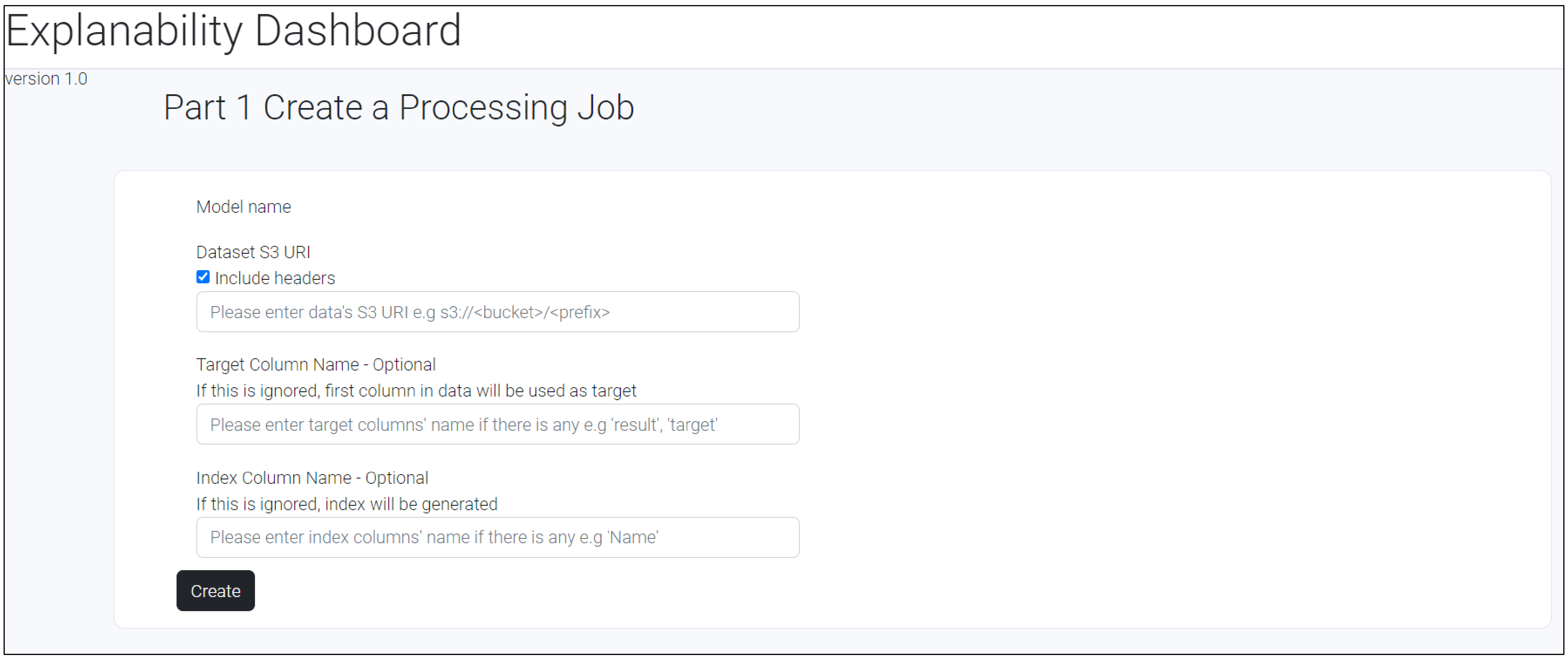

Explanability Dashboard

version 1.0

Part 1 Create a Processing Job

Model name

Dataset S3 URI

☑ Include headers

Please enter data's S3 URI e.g s3://<bucket>/<prefix>

Target Column Name - Optional

If this is ignored, first column in data will be used as target

Please enter target columns' name if there is any e.g 'result', 'target'

Index Column Name - Optional

If this is ignored, index will be generated

Please enter index columns' name if there is any e.g 'Name'

Project Objectives:

- Investigate the utilization of Explainable Artificial Intelligence (XAI) approaches to enhance the interpretability of domain-specific neural networks analyzing Hi-C data and chromatin interactions in Genome Biology.
- Examine the integration of XAI methods into the analytic pipeline to provide clear and comprehensible explanations for the decisions made by neural networks.
- Address the challenge of obscure and hard-to-interpret outcomes produced by sophisticated machine learning models in Genome Biology.
- Enable clearer comprehension and more effective utilization of knowledge obtained from neural networks specialized in analyzing chromatin interactions.

The dashboard interface provides convenient access to key functionalities, including Feature Importance, Classification Stats, Individual Predictions, and Model Performance Metrics. Additionally, it incorporates SHAP values to transparently illustrate how the model makes predictions at the instance level.