

# Single-cell Morphology Quality Control (coSMicQC)

Dave Bunten<sup>1\*</sup>, Jenna Tomkinson<sup>1\*</sup>, Vincent Rubinetti<sup>1</sup>, Gregory Way<sup>1</sup>

<sup>1</sup>Department of Biomedical Informatics, University of Colorado Anschutz Medical Campus  
\*These authors contributed equally to this work.



Department of Biomedical Informatics  
SCHOOL OF MEDICINE  
UNIVERSITY OF COLORADO **ANSCHUTZ MEDICAL CAMPUS**

## I. Erroneous outliers and analysis

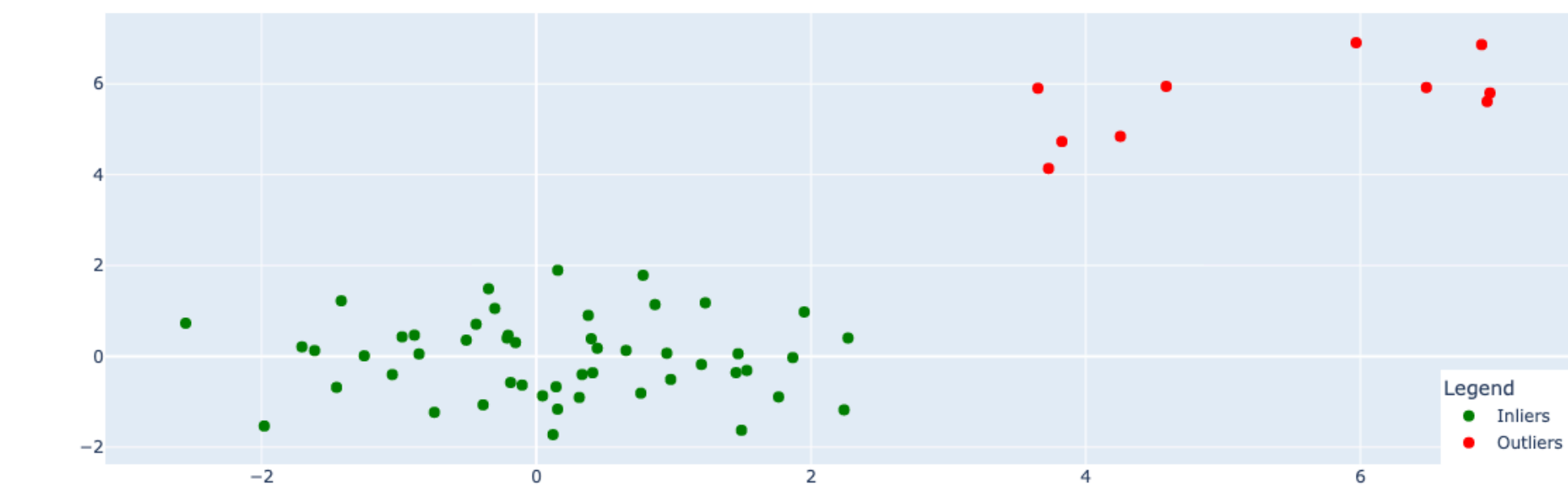


Figure 1: Erroneous outlier anomalies can measure outside our expectations and impact analysis.

Single-cell morphology data from high-throughput microscopy provide critical insights into disease mechanisms and therapeutic efficacy. However, **segmentation errors** during image analysis such as misidentifying cell compartments or artifacts as cells can lead to inaccurate single-cell measurements and **erroneous anomalies** within the data.

Researchers often resort to **error-prone, bespoke filtering methods** or aggregate data into bulk profiles to avoid discrepancies caused by anomaly outliers. These techniques fail to perform **quality control** on the data, often compromising the quality of single-cell profiles and impeding the potential for meaningful discoveries.

## II. Single-cell quality control package

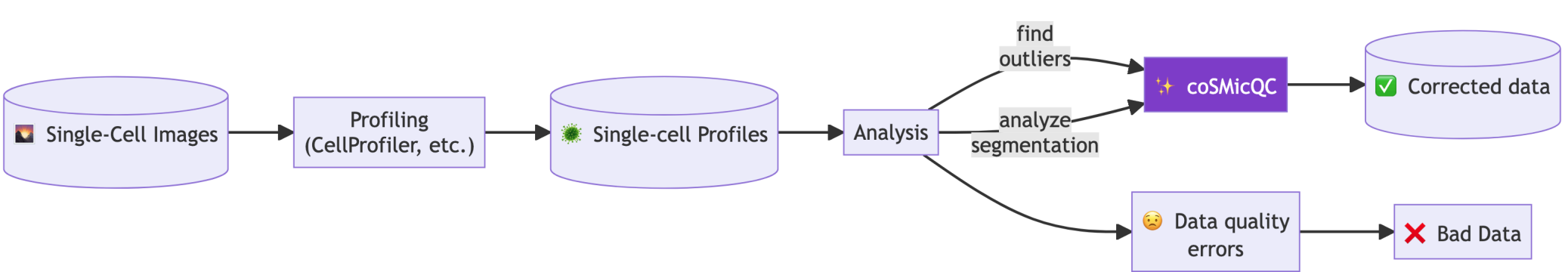


Figure 2: coSMicQC enables high-quality data outcomes by checking for outliers.

To address these challenges, we introduce **coSMicQC (Single-cell Morphology Quality Control)**, an open source Python package designed to enhance the accuracy of single-cell morphology analysis. **coSMicQC** offers default and customizable thresholds for quality control, integrating seamlessly into both command line and Python API workflows.

**coSMicQC** features interactive visualizations that help users identify outlier distributions, and it introduces the **CytoDataFrame** — a novel data format that links single-cell measurements with their corresponding images and segmentation masks in real-time, enriching data analysis and interpretation.

## III. Getting started with coSMicQC

### ☆ 1) Installation

```
# pip install from pypi
pip install coSMicQC

# install directly from source
pip install git+https://github.com/WayScience/coSMicQC.git
```

coSMicQC may be installed from PyPI or source.

### ☆ 2) Finding outliers

```
import cosmicqc

# load a parquet file with single-cell
# profile data and find outliers
scdf = cosmicqc.analyze.find_outliers(
    df="single-cell-profiles.parquet",
    metadata_columns=[
        "Metadata_ImageNumber",
        "Image_Metadata_Plate_x"
    ],
    feature_thresholds={
        "Nuclei_AreaShape_Area": -1
    },
)
```

Number of outliers: 328			
Outliers Range:			
Nuclei_AreaShape_Area Min: 734.0			
Nuclei_AreaShape_Area Max: 1904.0			
	Nuclei_AreaShape_Area	Metadata_ImageNumber	Image_Metadata_Plate_x
23	921.0	2	Plate_2
28	845.0	2	Plate_2
29	1024.0	2	Plate_2
32	787.0	2	Plate_2
37	1347.0	2	Plate_2
...	...	...	...

Figure 3: Reports in coSMicQC provide quality control feedback for analysis.

The find\_outliers function in **coSMicQC** uses single-cell feature thresholds to provide a report on how many outliers were detected. We use **z-scores** to help define thresholds used throughout coSMicQC. find\_outliers may be used through Python or CLI (see below).

```
# CLI interface for coSMicQC find_outliers
$ cosmicqc find_outliers \
  --df single-cell-profiles.parquet \
  --metadata_columns \[Metadata_ImageNumber\] \
  --feature_thresholds
  '{"Nuclei_AreaShape_Area": -1}'

Number of outliers: 328
Outliers Range:
Nuclei_AreaShape_Area Min: 734.0
Nuclei_AreaShape_Area Max: 1904.0
...
```

### ☆ 3) Visualizing outlier distributions

```
import cosmicqc

# label outliers within the profiles
scdf = cosmicqc.analyze.label_outliers(
    df="single-cell-profiles.parquet",
    include_threshold_scores=True,
    # show outlier histogram plots
).show_report()
```

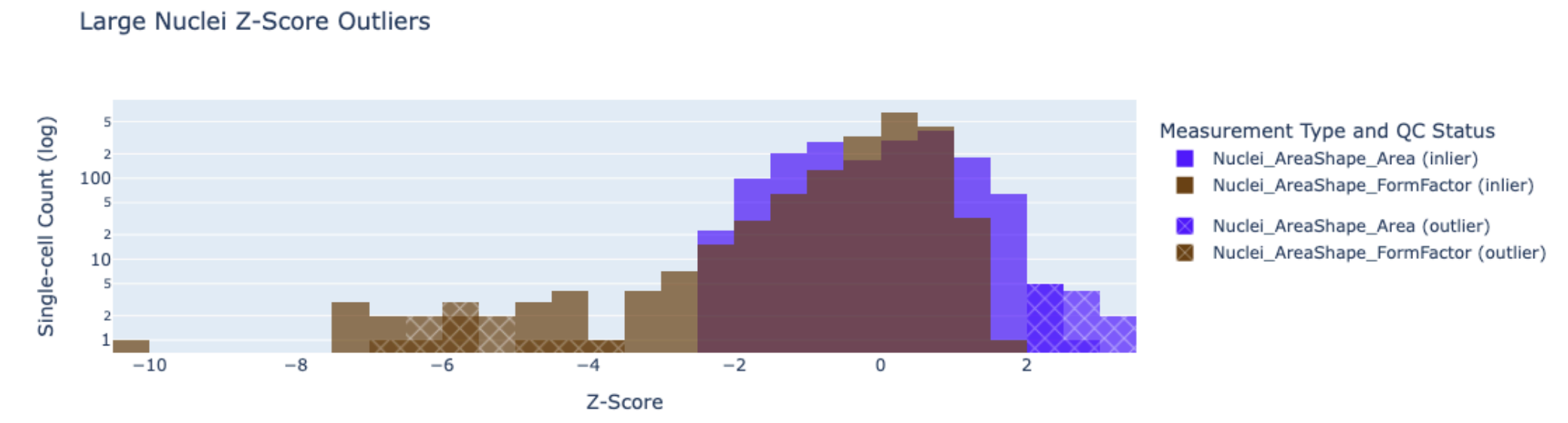


Figure 4: Histograms from coSMicQC help scientists identify where outliers occur in the distribution.

Deep erroneous anomaly analysis is enabled within **coSMicQC** through the **label\_outliers** function, which appends z-score data for features, and the **CytoDataFrame.show\_report** method to visualize where outliers are detected within the dataset.

### ☆ 4) Understanding outlier segmentation issues

```
import cosmicqc

# passing image and mask dirs to display
images
cosmicqc.CytoDataFrame(
    data="single-cell-profiles.parquet",
    data_context_dir="./image_directory/",
    data_mask_context_dir="./
mask_directory/",
)
```

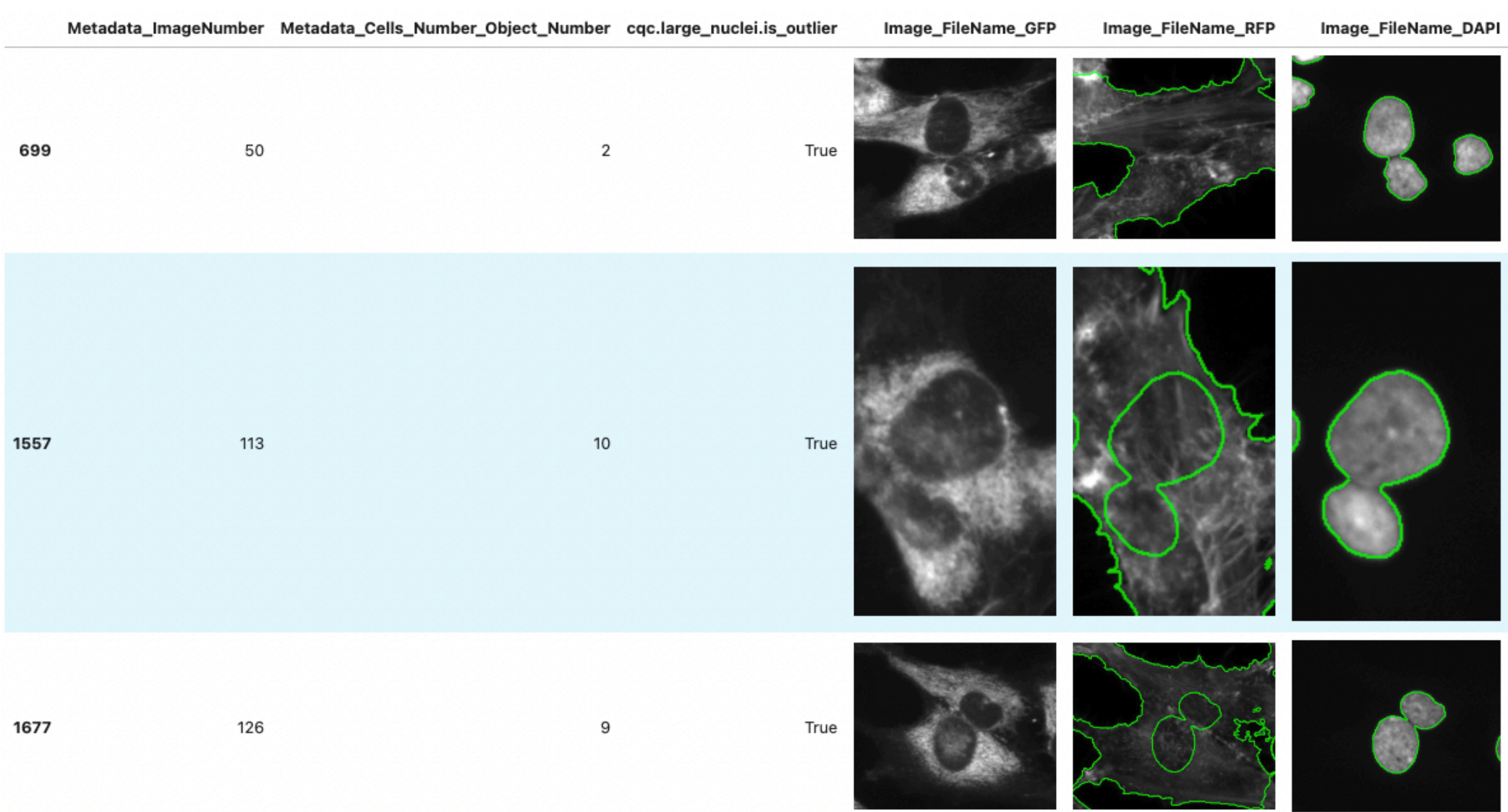


Figure 5: Displaying outlier and image data increases analysis iteration within familiar interfaces.

**CytoDataFrames** returned by all **coSMicQC** operations enable researchers to analyze outlier status alongside single-cell images directly in a Jupyter environment.

## IV. Real-world applications

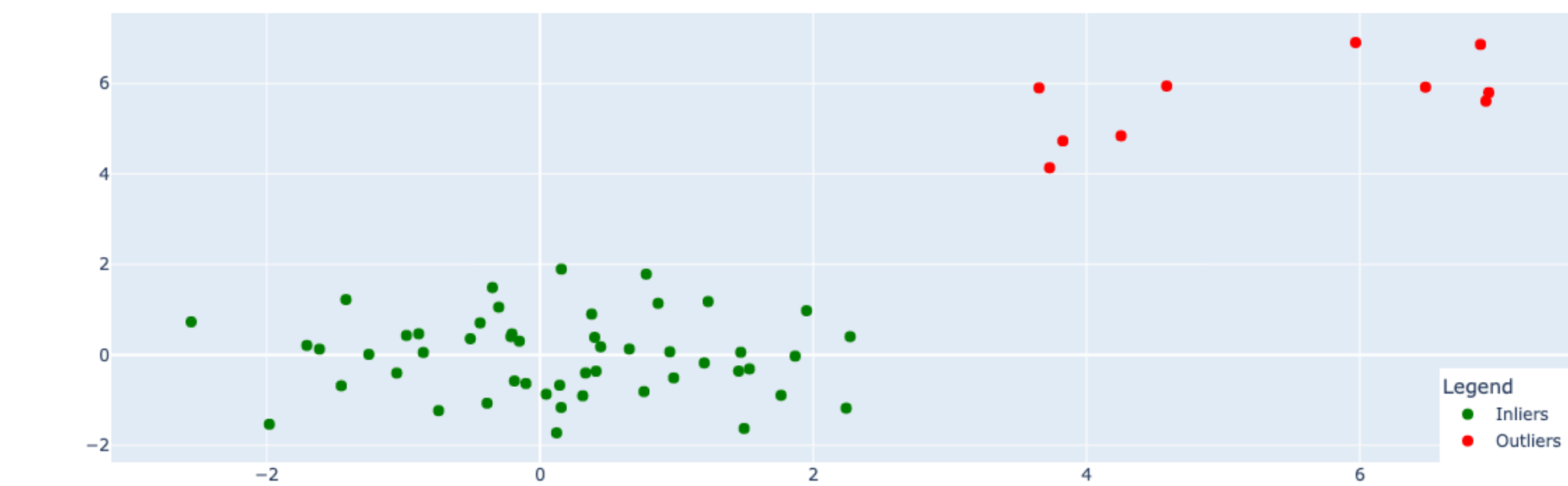


Figure 6: Etiam viverra sollicitudin velit.  
Lorem ipsum dolor sit amet, consectetur adipiscing elit. In vel augue ante. Duis placerat ex id turpis consequat, at aliquet arcu vehicula.

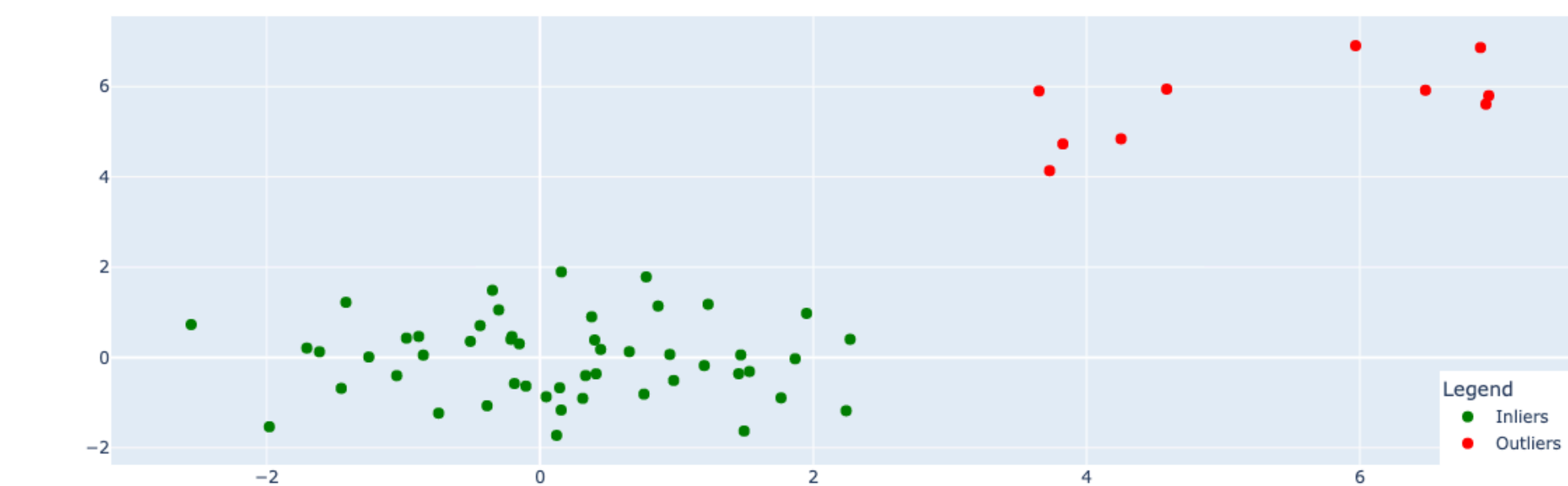


Figure 7: Ut ut metus at diam hendrerit dictum.

Donec bibendum ex vitae egestas ornare. Cras ut vulputate diam. Nullam feugiat feugiat purus, eu various metus maximus sit amet.

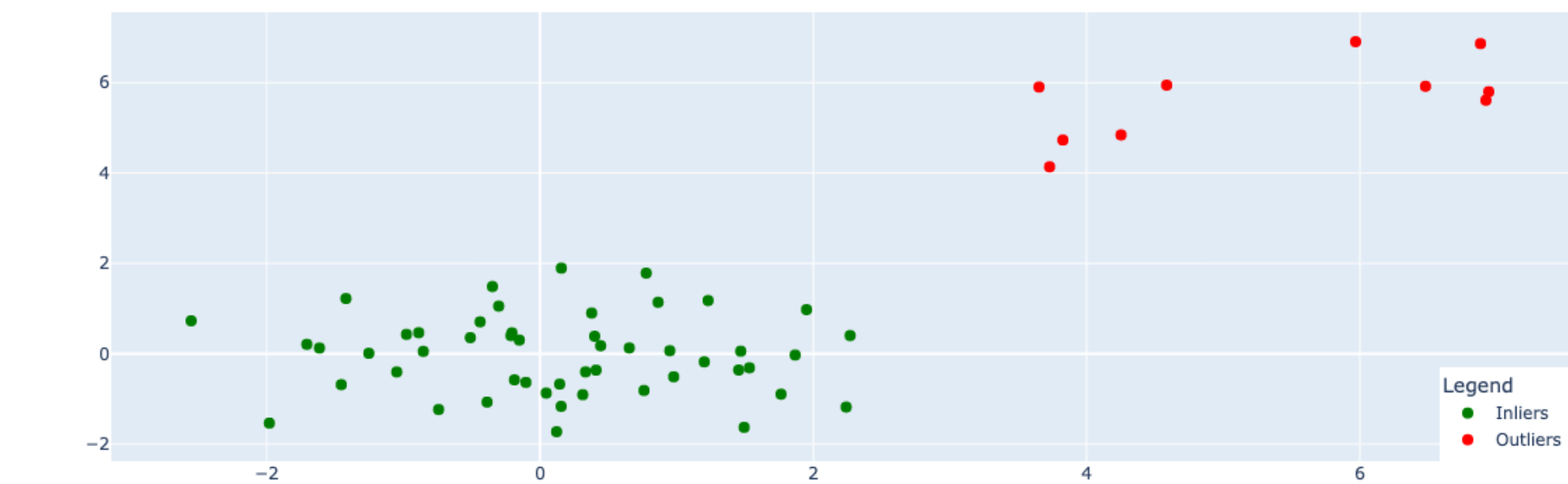


Figure 8: Praesent eu sem id nibh viverra finibus.

Fusce ac mi eu augue suscipit sodales. Morbi quis gravida dui. Name tellus elit, ullamcorper ut ipsum ut, eleifend facilisis dui.

## V. Acknowledgements

Special thanks goes to the following for their help in contributing to the **coSMicQC** inspiration, development, or related work.

- **CU Anschutz**: Timothy A. McKinsey, Josh Travers
- **iNFixion**: Michelle Mattson-Hoss, Herb Sarnoff