

## PANORAMA 360: Performance Data Capture and Analysis for End-to-End Scientific Workflows

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#### PANORAMA 360

#### Overview of the Project Description

The Panorama 360 aims to further the understanding of the behavior of scientific workflows as they are executing in heterogeneous environments. Panorama 360 collects and correlates workflow performance data into a comprehensive view, that can characterize the **end-to-end** workflow performance on today's systems and drive the design of the future generation systems.

The Panorama 360 architecture collects data from these individual data sources: the **Pegasus WMS**, the **Globus Online** service, the TCP STatistics and Analysis Tool (Tstat) and the **DARSHAN** HPC I/O Characterization Tool

Our approach for correlating the real time application and infrastructure monitoring data can be used to verify application behavior, perform anomaly detection and diagnosis, and support adaptivity during workflow execution, in an **online** manner. This can lead to improved performance and stability of scientific workflows and benefit the DOE-relevant applications.

Ultimately, by having all these data and analysis tools in our disposal, we envision the creation of a workflow performance data repository and a collection of tools that will be publicly available and can drive science forward.

#### IMPACT ON DOE SCIENCE Nanodiamond and MCViNE workflows

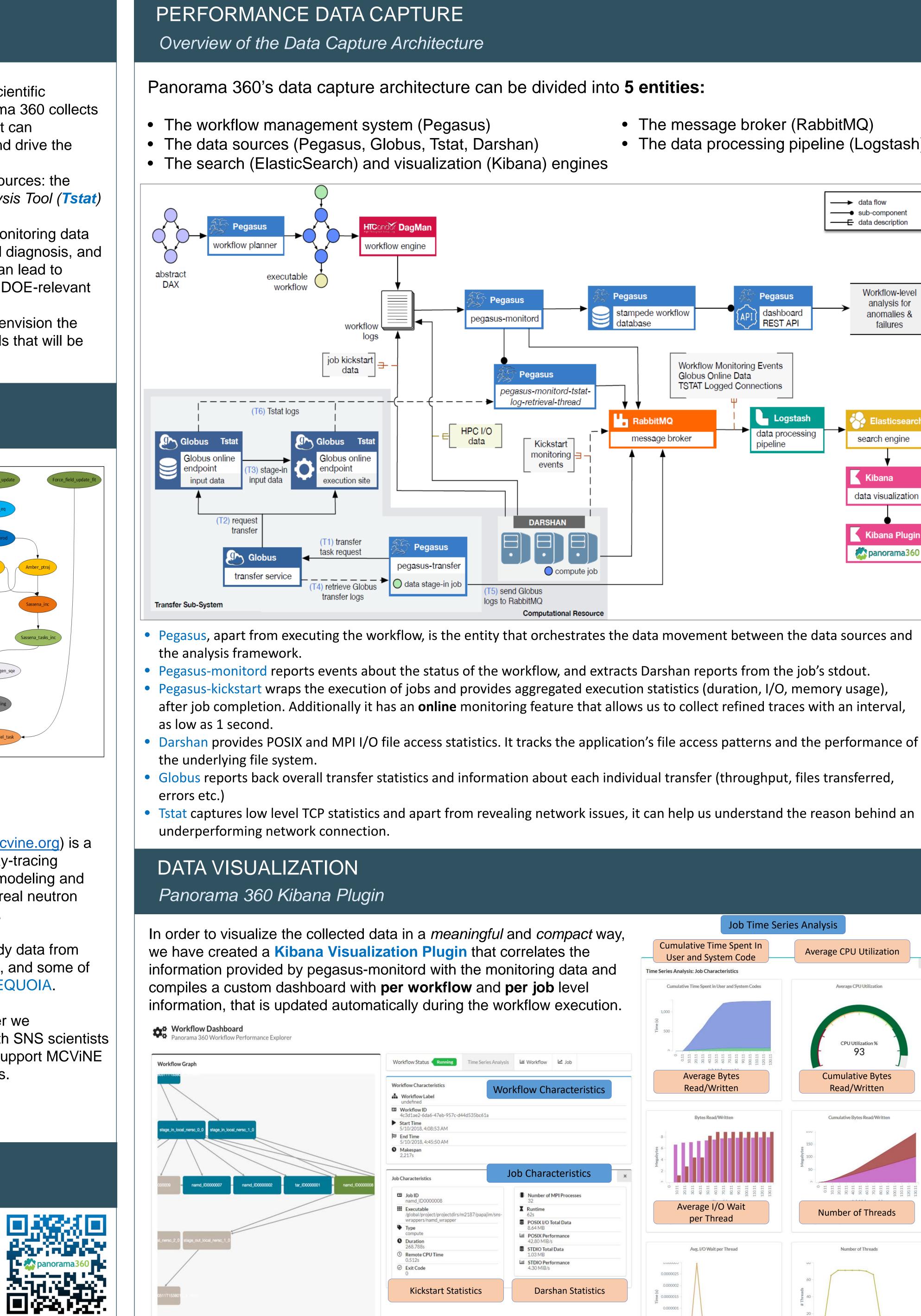
• We have extended the SNS-Nanodiamond workflow with (a) DAKOTA parameter sweep, and (b) feedback loop capability, using **Dakota** (https://dakota.sandia.gov). Dakota based on an internal model generates the Simulation Parameters and triggers a *Pegasus* analysis driver that initiates a new workflow. • Dakota can instantiate multiple Sassena\_tasks\_gen\_sqe simulation workflows in parallel and by using the **Pegasus Ensemble Manager** we can have more control over their execution. sampleassembly.tar.gz beam.tar.gz MCVINE (http://www.mcvine.org) is a Monte Carlo neutron ray-tracing program for computer modeling and simulations that mirror real neutron /beam sampleassembly scattering experiments. scatter.pml multi-scatter.pml MCViNE is used to study data from many SNS instruments, and some of Multi-scatter them are ARCS and SEQUOIA. scattered-neutrons multi-scattered-neutrons During the past summer we collaborated closely with SNS scientists MCViNE-multi-scatter MCViNE-scatter and explored ways to support MCViNE workflows with Pegasus. ms.nxs no ms.nxs

## LEARN MORE

https://panorama360.github.io Website GitHub Repository https://github.com/Panorama360

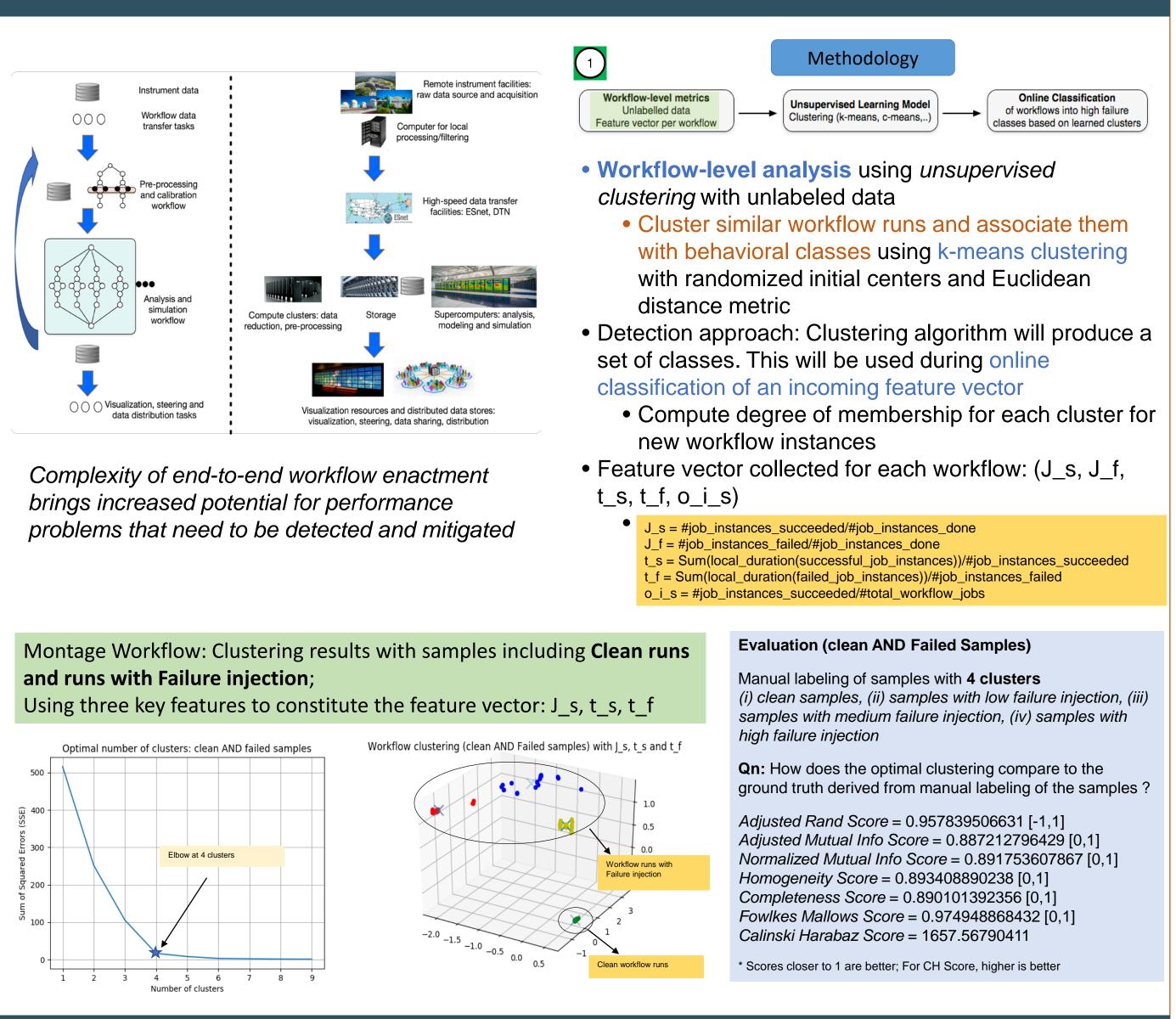


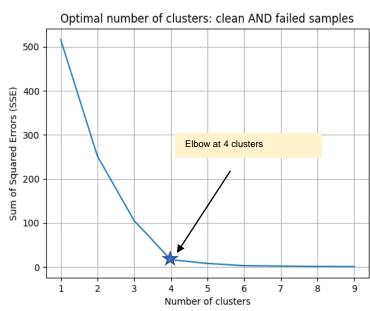
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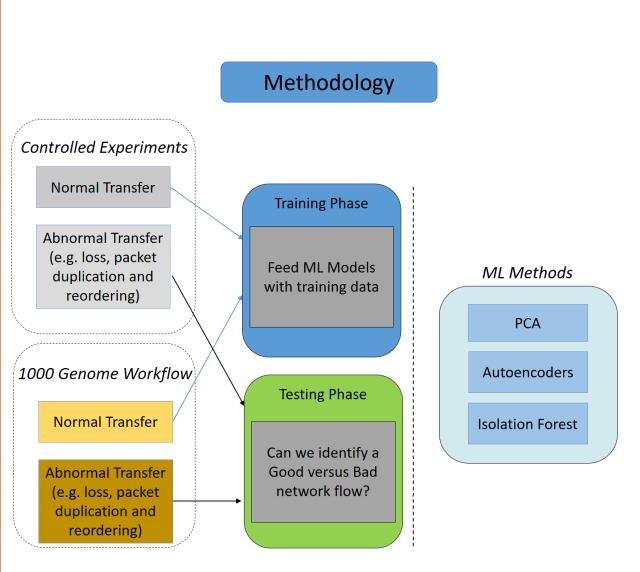
#### • The message broker (RabbitMQ) • The data processing pipeline (Logstash) data flow sub-component data description Workflow-level Pegasus analysis for stampede workflow dashboard anomalies 8 REST API failures Workflow Monitoring Events Globus Online Data **TSTAT Logged Connections** RabbitMO Elasticsearc data processing message broker search engine pipeline Kibana data visualization Kibana Plugin 🛣 panorama 360 Job Time Series Analysis Cumulative Time Spent In Average CPU Utilization User and System Code Time Series Analysis: Job Characteristics Average CPU Utilization Cumulative Time Spent in User and System Codes PU Utilization % 93 0.11 10.11 20.11 20.11 40.11 50.11 70.11 80.11 80.11 90.11 100.11 **Cumulative Bytes** Average Bytes Read/Written Read/Written Cumulative Bytes Read/Written **Bytes Read/Writte** 10.11 20.11 30.11 40.11 50.11 70.11 80.11 90.11 110.11 110.11 0111 1011 2011 2011 4011 4011 5011 8011 9011 10011 11011 Average I/O Wait Number of Threads per Thread Avg. I/O Wait per Thread Number of Threads 0.0000025 -0.000002 g 0.0000015 -0.000001 0 0.111 10.11 20.111 20.111 50.111 60.111 70.111 80.111 80.111 110.0111 110.0111 110.0111 0.11 10.11 20.11 30.11 40.11 50.11 50.11 90.11 110011 110011 110011 110011 Job Makespan (s Job Makespan (

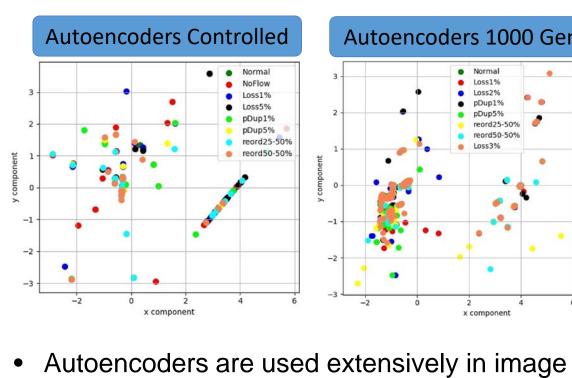
### **PERFORMANCE ANOMALY DETECTION** Workflow Performance





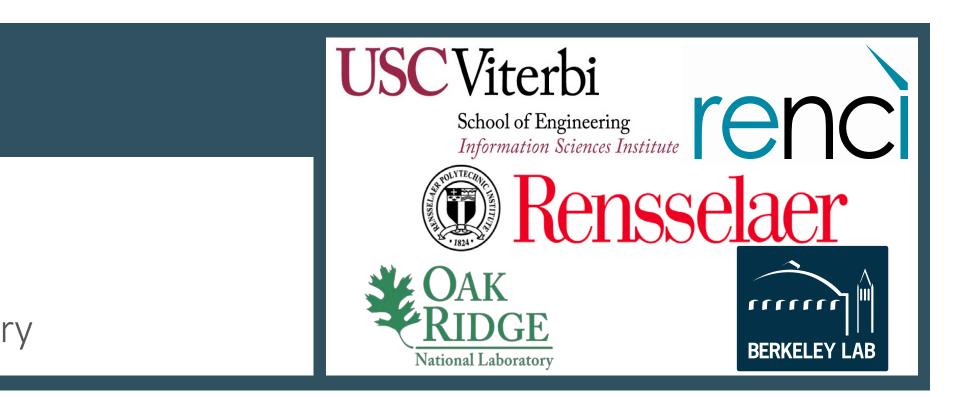
#### PERFORMANCE ANOMALY DETECTION Infrastructure - Network Performance



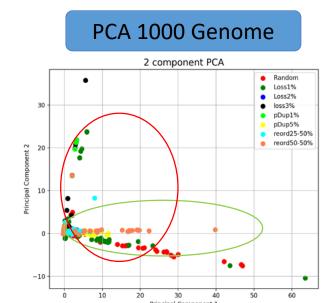


- analysis
- In our case, no clusters were found From literature, autoencoders don't perform well for text or csv inputs

No.	Experiment type (runs for 1 hour)	Tstat Sample	No.	Experiment type	Tstat Sample
1	Random Traffic (iperf sends traffic at random)	152	1	Workflow runs	1475
2	No flow	120	2	1% Loss	1563
3	1% Loss	120	3	2% Loss	1636
4	5% Loss	120	4	3% Loss	1948
5	1% Packet Duplication	60	5	1% Packet Duplication	1574
6	5% Packet Duplication	60	6	5% Packet Duplication	1527
7	25% - 50% Packet reordering	50	7	25% - 50% Packet reordering	1491
8	50% - 50% Packet reordering	60	8	50% - 50% Packet reordering	1592

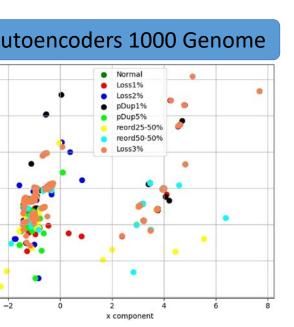


# PCA Controlled 4 6 8 10 12 Principal Component 1



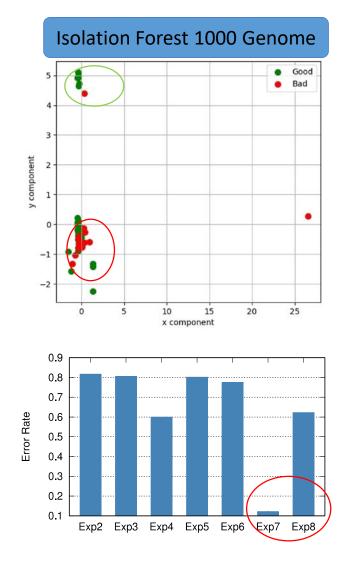
• In controlled experiments there are clear normal/abnormal clusters

- None found in 1000 Genome workflow runs • Found most influential variables (Reducing 150 to 26) • RTT, RTO, window details, segment size
- In 1000 Genome workflow, RTT was much higher due to the change in topology, and that was most likely the cause of no clusters



ents

solation Forest Controll GoodBad • • 10 15 20 25



- Isolation Forest identified good and bad flows more successfully than the other classifiers
- But it has high error rates !!!
- In the case of the workflow, the error rate for Exp8 improves significantly