Comparative Evaluation of Big-Data Systems on Scientific Image Analytics Workloads

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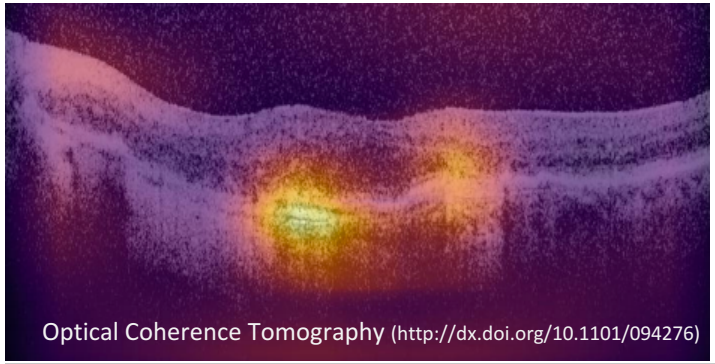
OF COMPUTER SCIENCE & ENGINEERING

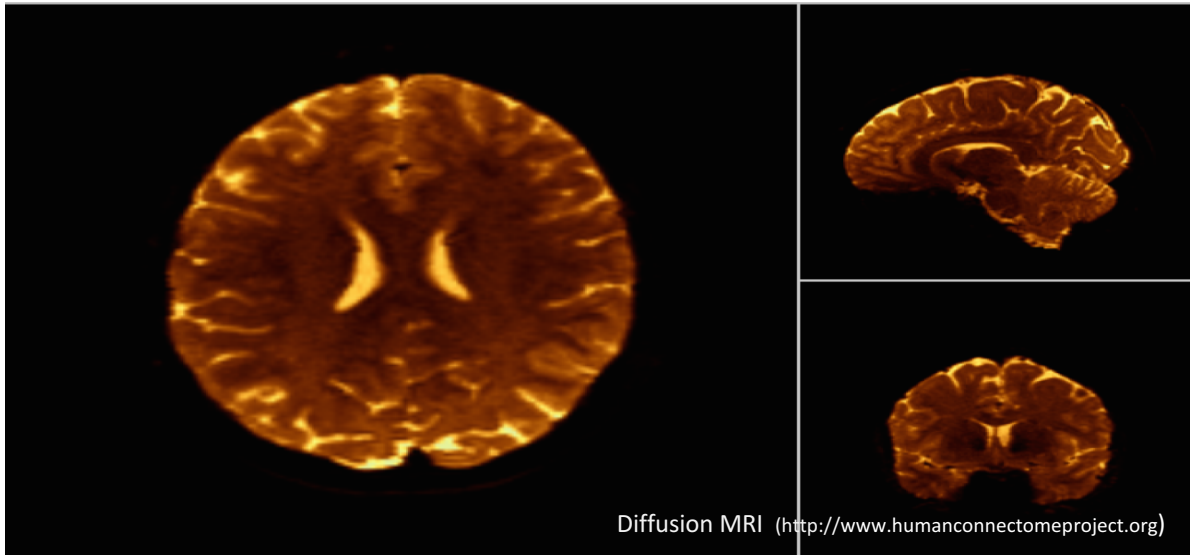
eScience Institute
ADVANCING DATA-INTENSIVE DISCOVERY IN ALL FIELDS

Scientific Images

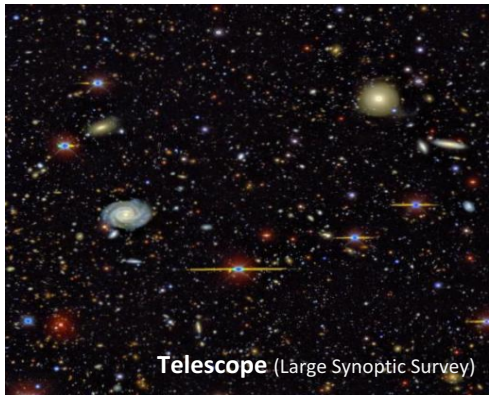
Telescope (Large Synoptic Survey)



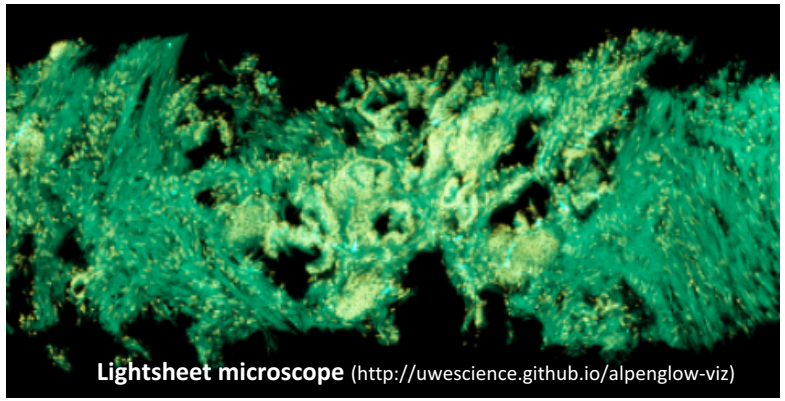
Optical Coherence Tomography (http://dx.doi.org/10.1101/094276)



Diffusion MRI (http://www.humanconnectomeproject.org)



Telescope (Large Synoptic Survey)

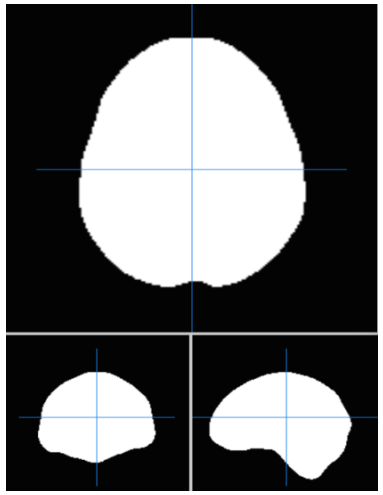


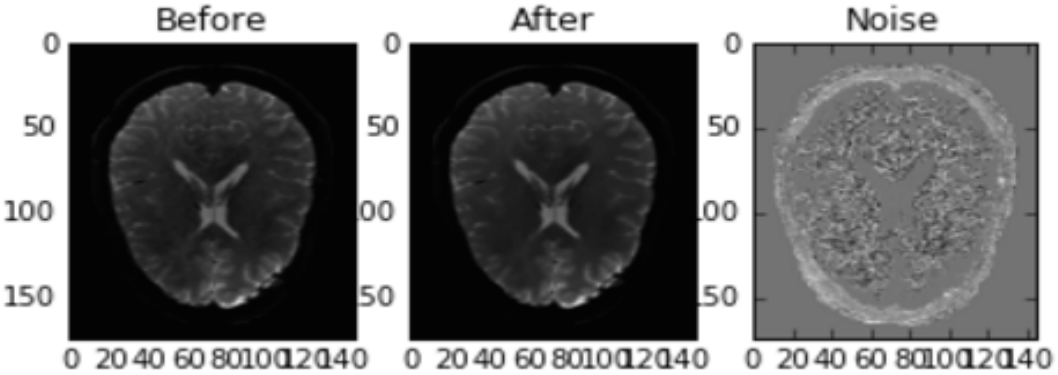
Lightsheet microscope (http://uwescience.github.io/alpenglow-viz)

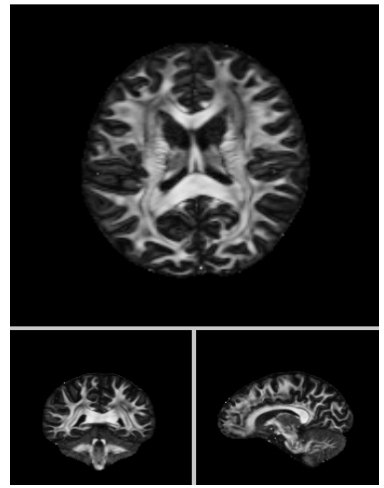
http://www.humanconnectomeproject.org

Neuroscience: Use case

1. Mask-creation
2. Denoising
3. Model fitting







Scientific Image Analysis Today

- Domain specific libraries (Python, Matlab, etc.).
- Driver code is Python e.g. Jupyter notebook.
- Which runs on a laptop.

How do we scale the computation?

Experiments and Analyses

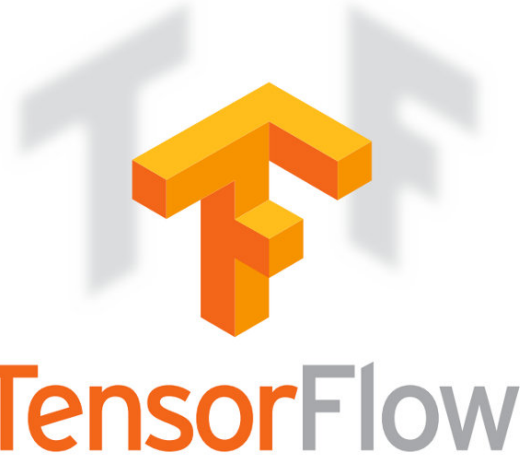
How well do existing systems support scientific image analytics?

Outline

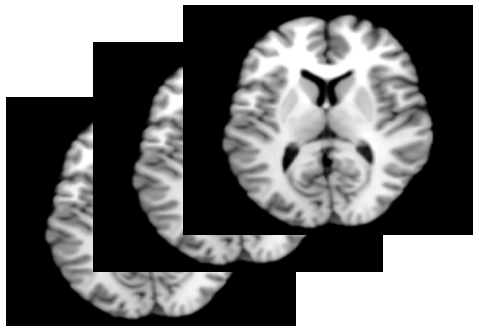
- Systems
- Use case
- Implementation
- Evaluation & Results
- Areas of research
- Conclusion

Systems

- **Dask**: Parallel Python library
- **Myria**: Shared-nothing, relational DBMS
- **SciDB**: Multidimensional array DBMS
- **Spark**: In-memory big data system
- **TensorFlow**: Machine learning library

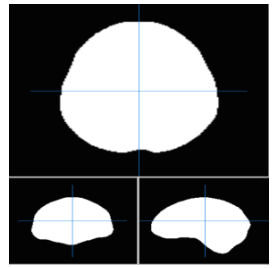


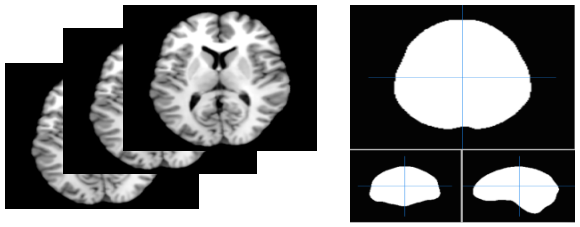
Neuroscience: Query Plan



MASK-CREATION

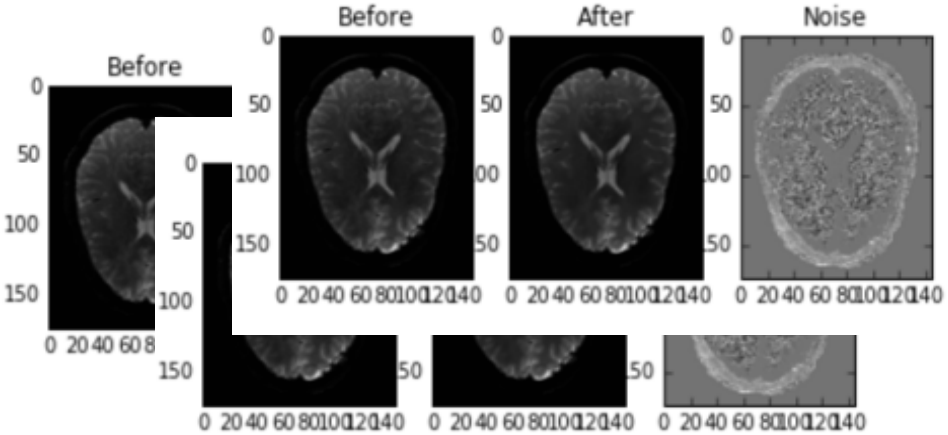
$$\sigma_{\text{imageid}} \rightarrow \Upsilon_{\text{subject}} \rightarrow G_{\text{Avg}} \rightarrow \text{UDF}_{\text{Median\_OTSU}}$$

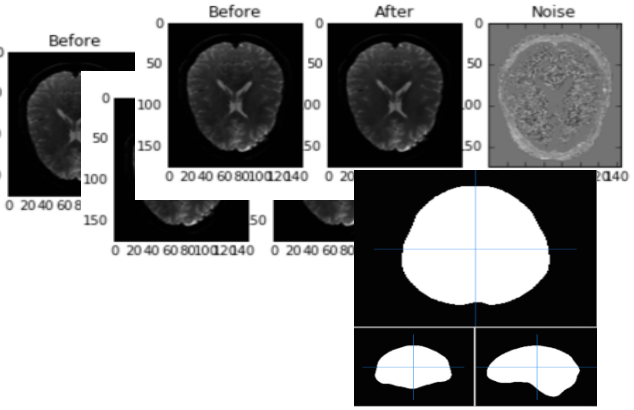




DENOISING

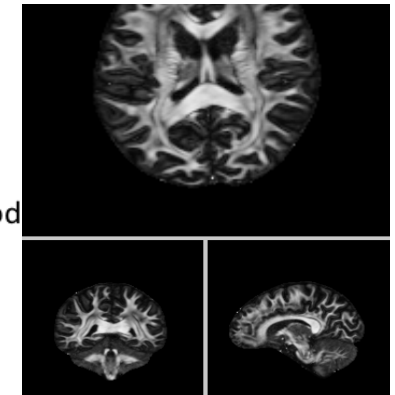
$$\bowtie_{\text{subject}} \rightarrow \text{UDF}_{\text{Denoise}}$$





MODEL FITTING

$$\text{Flatmap}_{\text{image->voxel}} \rightarrow \bowtie_{\text{subject}} \rightarrow \Upsilon_{\text{voxel, subject}} \rightarrow \text{UDA}_{\text{TensorMod}}$$



Complex User Defined Functions

```
    if len(input_volume.shape) == 4:
        if vol_idx is not None:
            b0vol = np.mean(input_volume[..., tuple(vol_idx)], axis=3)
        else:
            b0vol = input_volume[..., 0].copy()
    else:
        b0vol = input_volume.copy()
    # Make a mask using a multiple pass median filter and histogram
    # thresholding.
    mask = multi_median(b0vol, median_radius, numpass)
    thresh = otsu(mask)
    mask = mask > thresh

    if dilate is not None:
        cross = generate_binary_structure(3, 1)
        mask = binary_dilation(mask, cross, iterations=dilate)

    # Auto crop the volumes using the mask as input_volume for bounding box
    # computing.
    if autocrop:
        mins, maxs = bounding_box(mask)
        mask = crop(mask, mins, maxs)
        croppedvolume = crop(input_volume, mins, maxs)
        maskedvolume = applymask(croppedvolume, mask)
    else:
        maskedvolume = applymask(input_volume, mask)
    return maskedvolume, mask
```

[Diffusion MR Imaging in Python http://dipy.org]

"A threshold selection method from gray-level histograms", Nobuyuki Otsu IEEE Transactions on Systems, Man, and Cybernetics ,Jan. 1979

Implementation

- **Dask**: Task graph with Python data structures and functions.
- **Myria**: MyriaL and user-defined Python functions.
- **SciDB**:
  - *Implementation 1: Pure AQL .*
  - *Implementation 2:* AQL and Python function using *stream().*
- **Spark**: PySpark with Python lambdas.
- **TensorFlow**: Compute graph in Python with *tensors*.

Evaluation

- Qualitative
  - Can existing pipelines run on the systems?
  - How much effort is required to implement scientific pipelines?
  - How much technical expertise is required to optimize the system?
- Quantitative
  - How do systems scale with increasing data size?
  - What is the speed-up with cluster size increase?
  - Do systems show similar per-step performance?
  - System Tuning

Can we implement & execute end-to-end pipelines?

With great difficulty!

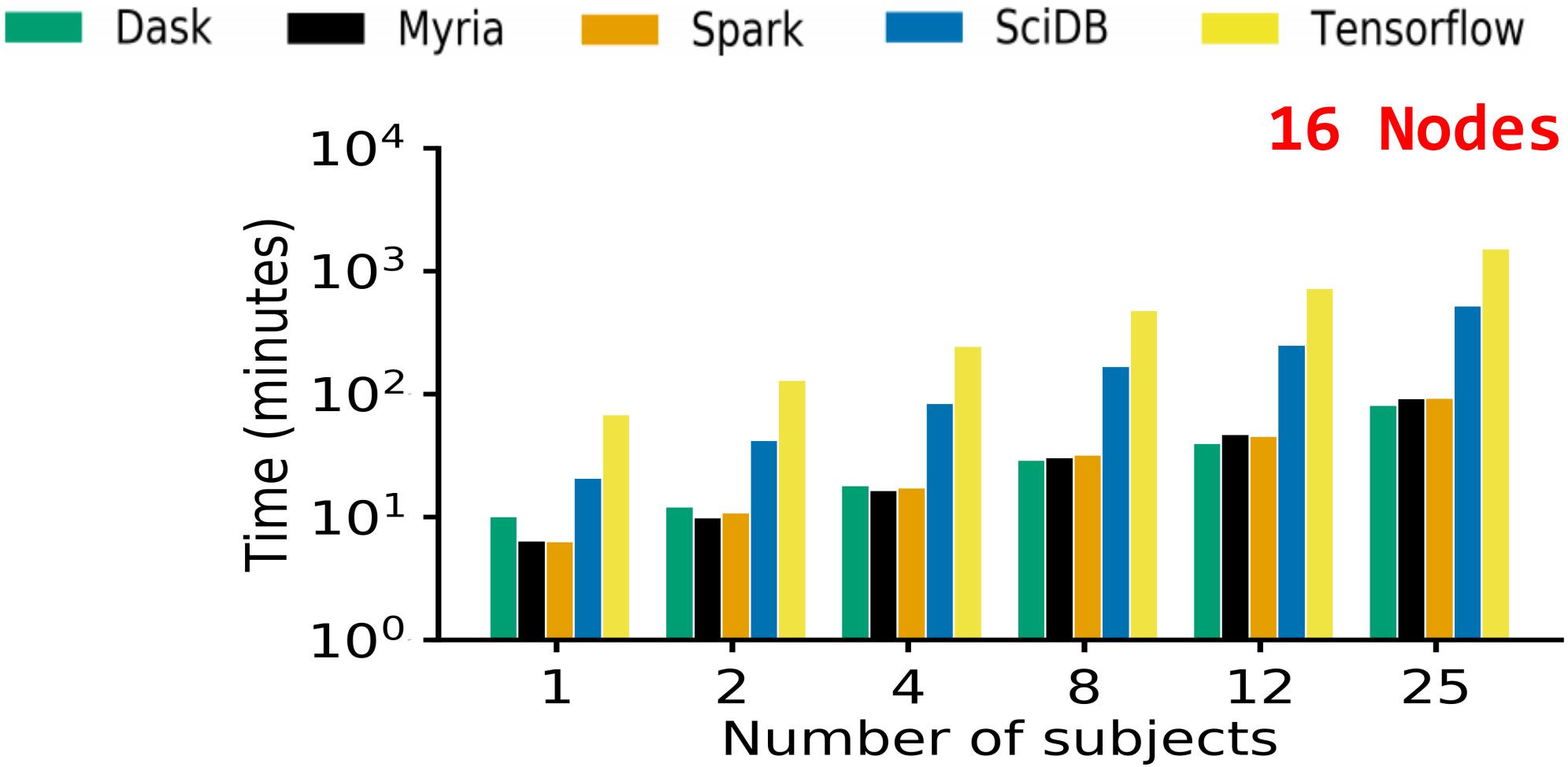
Qualitative Evaluation

How much effort is required to implement scientific pipelines?

	Dask	Myria	SciDB	Spark	TensorFlow
Reuse and (total) code*	20 (120)	16 (75)	16 (315)	17 (114)	0 (500+)
Streamlined installation	✓	✓	✗	✓	–
Flexible data formats	✓	–	✗	–	✗
Debuggability	✗	✓	–	✓	✓

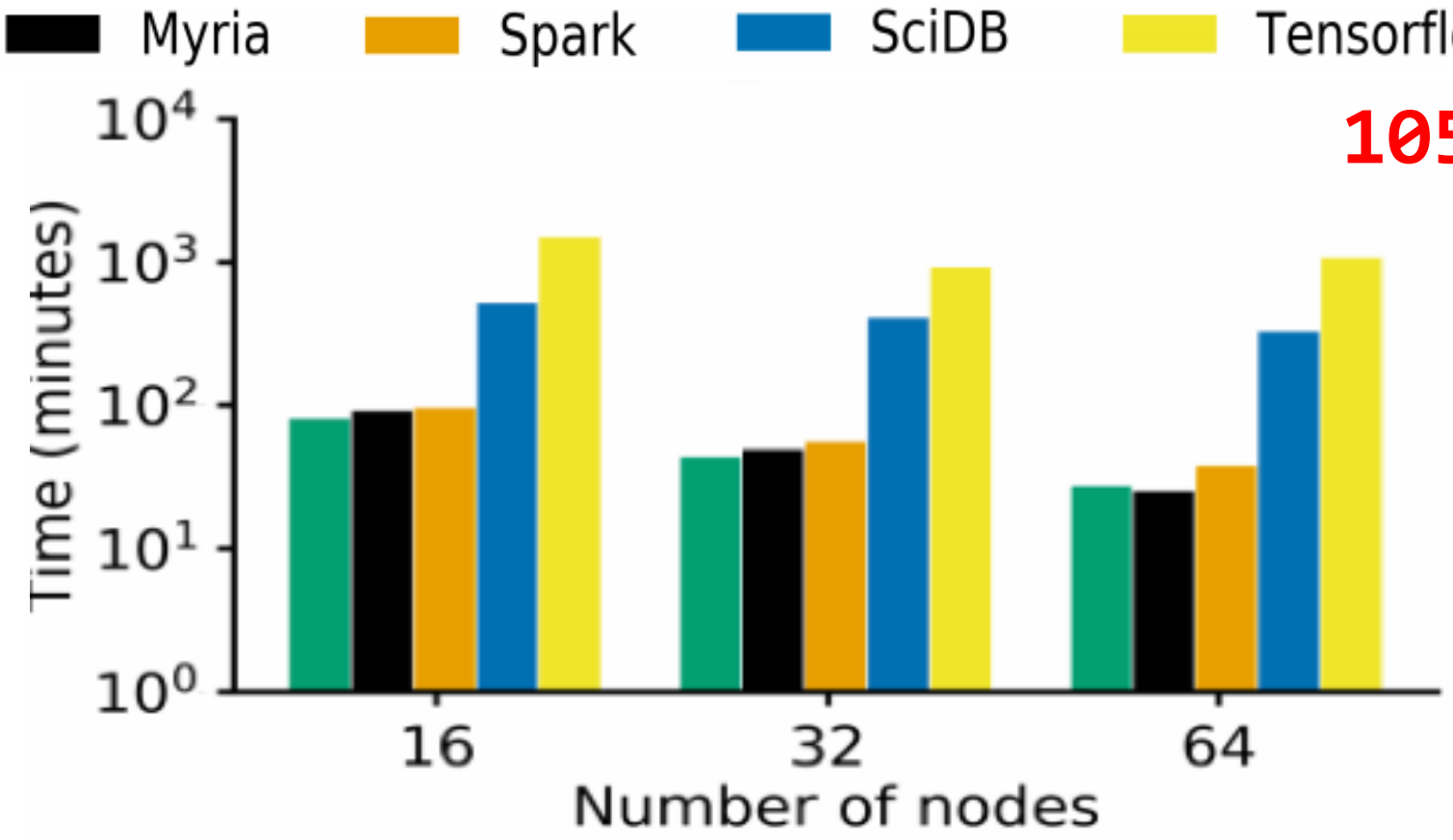
*Reference implementation for neuroscience use case was 26 lines of Python driver code calling into DiPy library.

End-to-end runtime



Subjects	1	2	4	8	12	25
Input	4.2GB	8.4GB	16.8GB	33.6GB	50.4GB	105GB

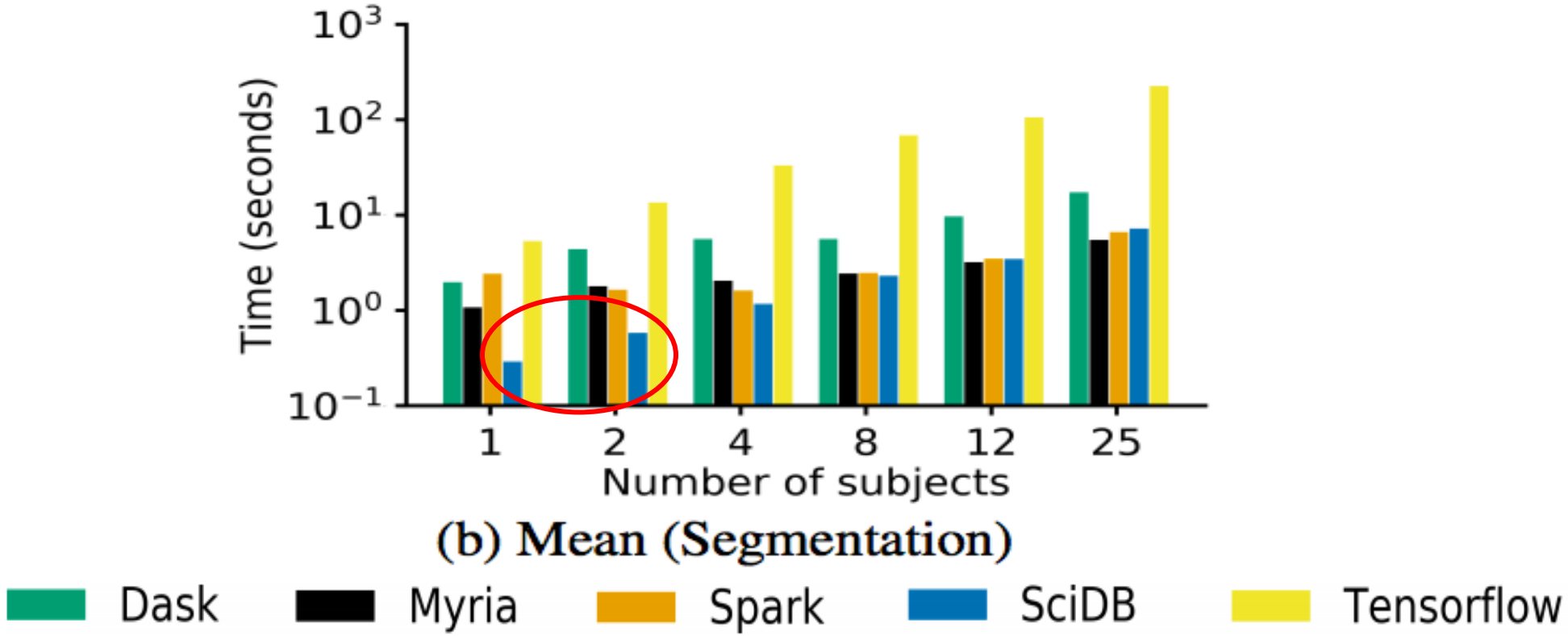
End-to-end: Speed-up



(d) Neuroscience: End-to-end runtime with varying cluster size

Re-write vs. Re-use

Re-write takes more time, but might be more efficient!



System Tuning

- None of the systems perform well with default settings
- All require manual tuning
- Two areas that require tuning in all systems:
  - Degree of parallelism
  - Memory management

Results Summary

	Dask	Myria	SciDB	Spark	TensorFlow
Code reuse, reference impl. (26)	20 (120)	16 (75)	16 (315)	17 (114)	0 (500+)
Streamlined installation	✓	✓	✗	✓	–
Flexible data formats	✓	–	✗	–	✗
Debbugability	✗	✓	–	✓	✓
Out of box performance	✗	✗	✗	✗	✗

Areas of Research

- Need to efficiently support pipelines with UDFs
- Large tuple sizes
- Memory management
- Self-tuning & robust systems

Conclusion

- Scientific image analytics is increasingly important
- Big Data systems are still too difficult to use and …
  - need to provide streamlined installation
  - need improvement in overall robustness and usability
  - out of box settings are the only ones that matter

Thank You!

TensorFlow: Sven Dorkenwald

SciDB: Dongfang Zhao

Dask: Alvin Cheung & Parmita Mehta

Myria: Parmita Mehta

Spark: Parmita Mehta & Tomer Kaftan

Neuroscience Domain Expert: Ariel Rokem

Astronomy Domain Expert: Jake VanderPlaas, Andrew Connolly, Yusra Alsayyad