

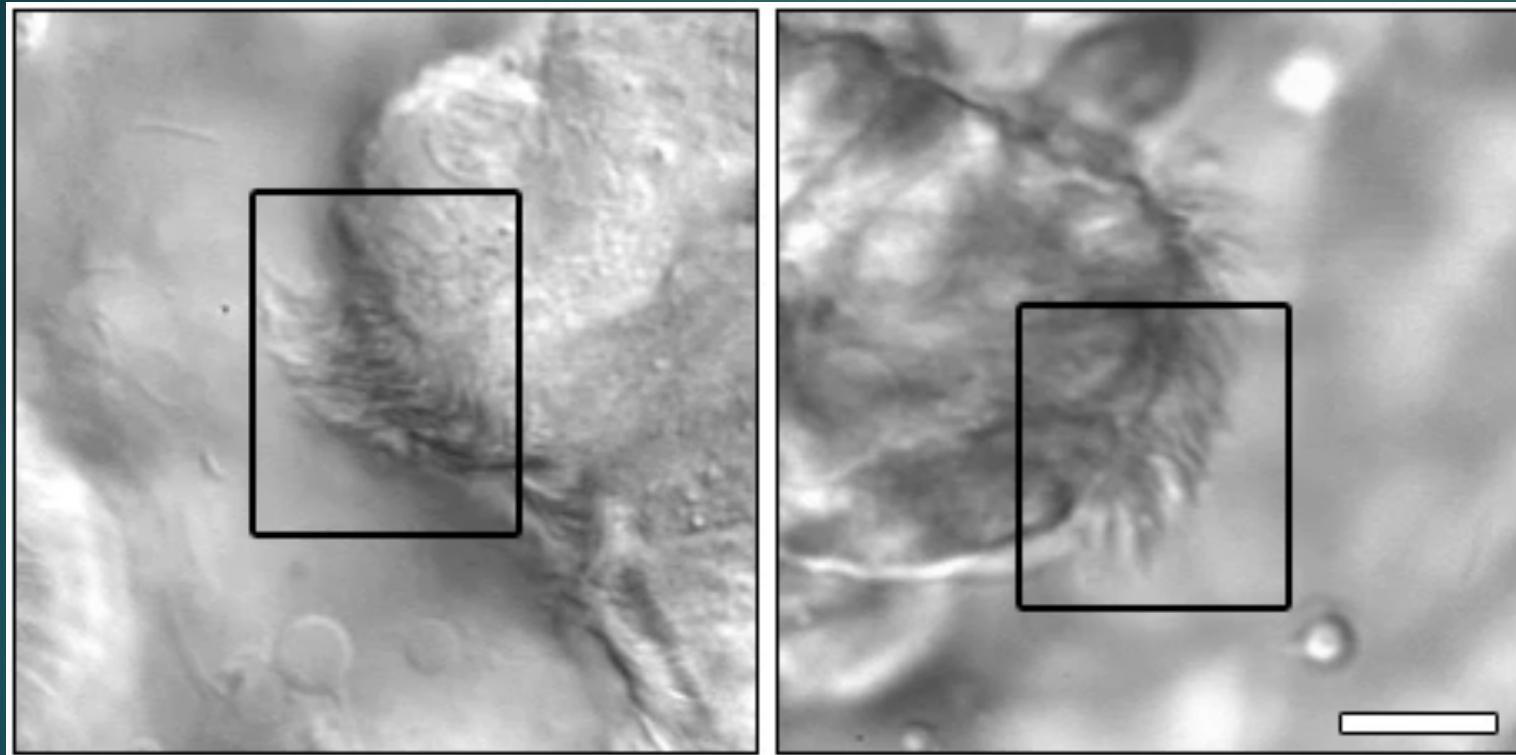
Python For Public Health: Building Statistical Models Of Ciliary Motion

Shannon Quinn
University of Georgia

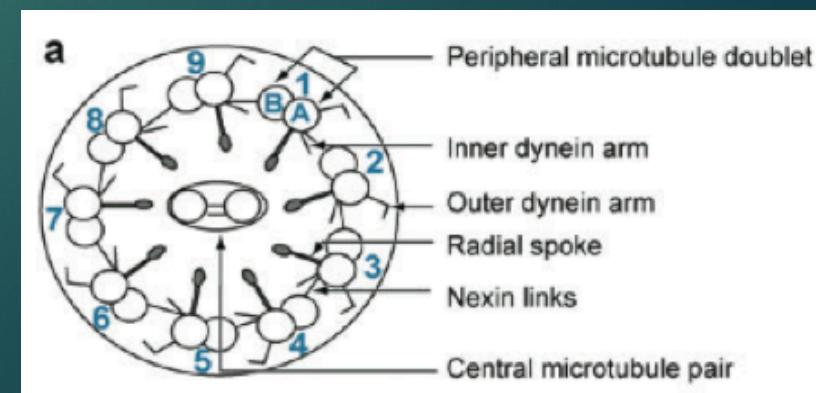
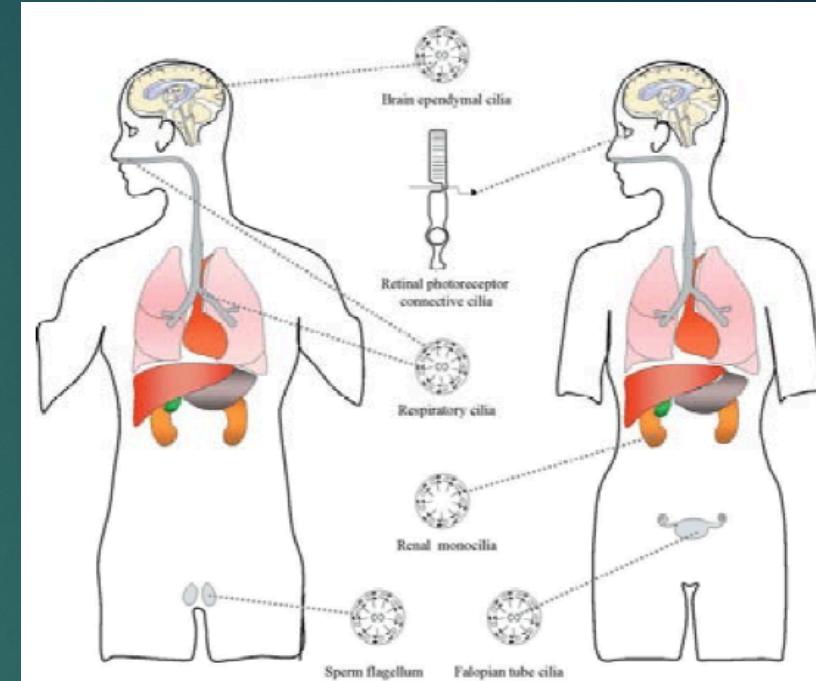
PyCon 2016

Part I: Cilia and their pathologies

What are cilia?

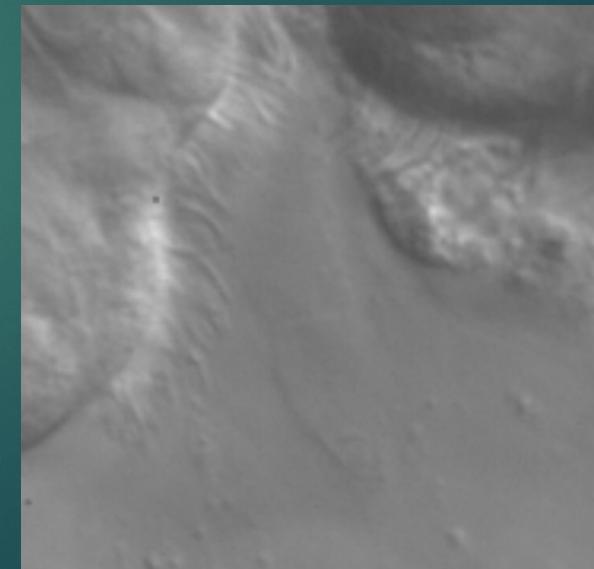
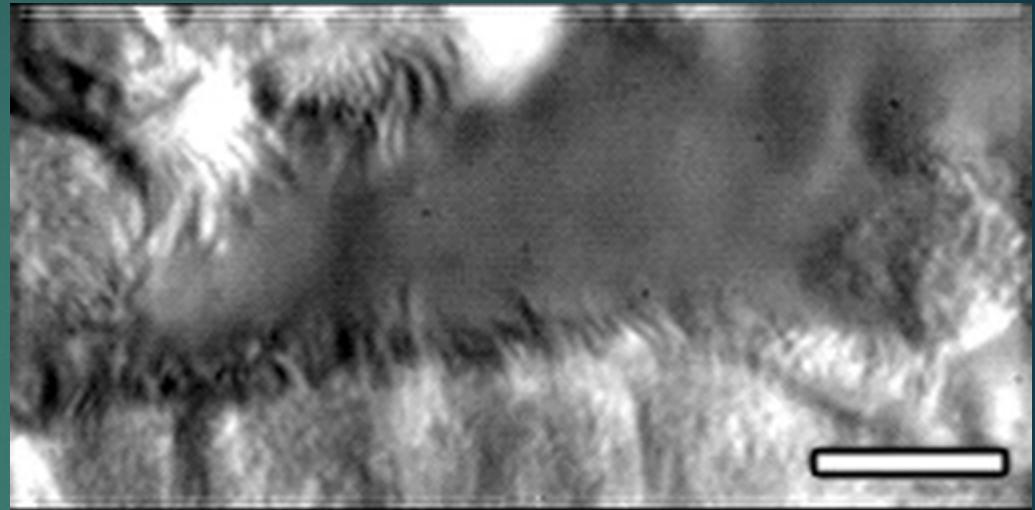


Scale bars: 10µm

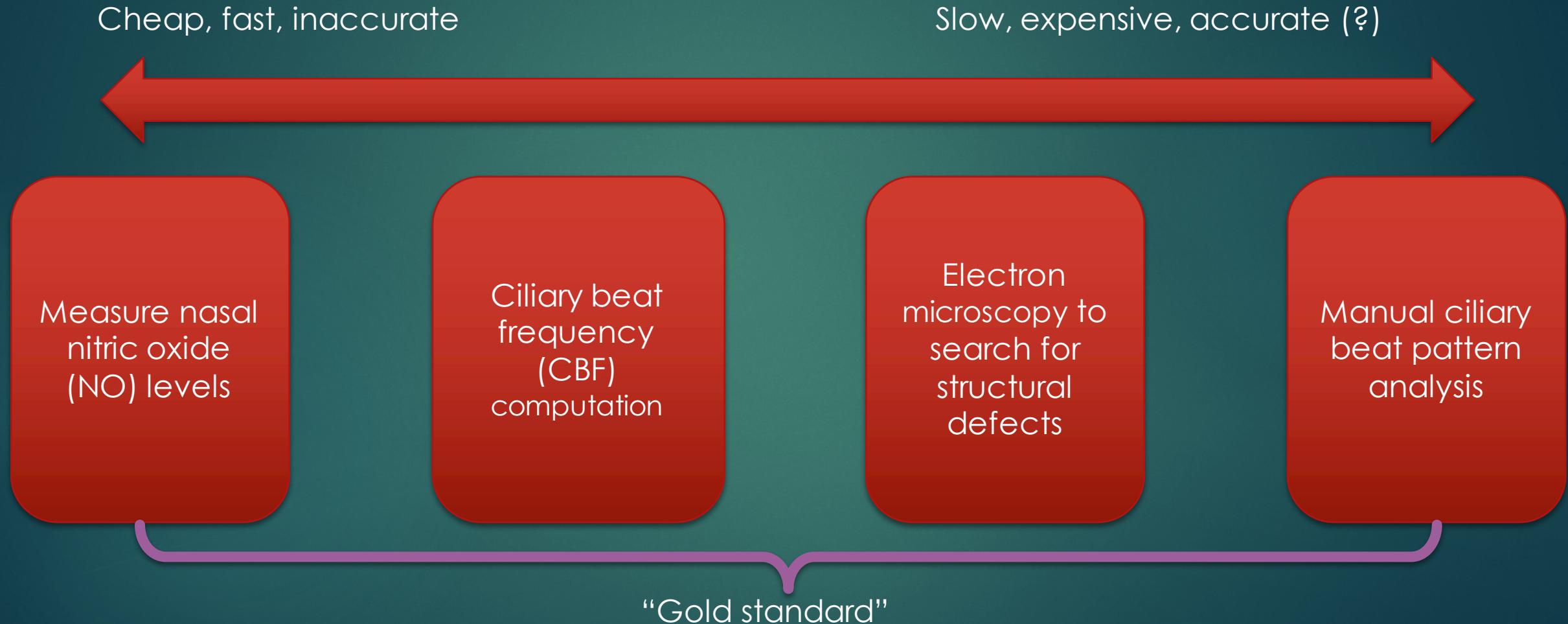


Why do we care about cilia?

- ▶ Clinical
 - ▶ Ciliopathies
 - ▶ Association with congenital heart disease
- ▶ Developmental
 - ▶ Nodal flow
 - ▶ Left-right asymmetry

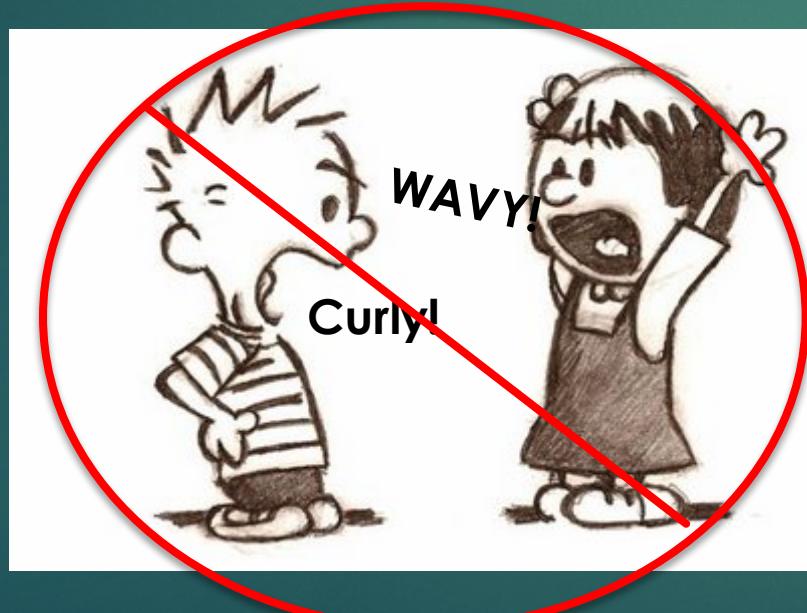


How do we diagnose ciliopathies?



What is our goal?

- ▶ *Input:* high-speed video of ciliary biopsy
- ▶ *Output:* quantitative properties of observed motion



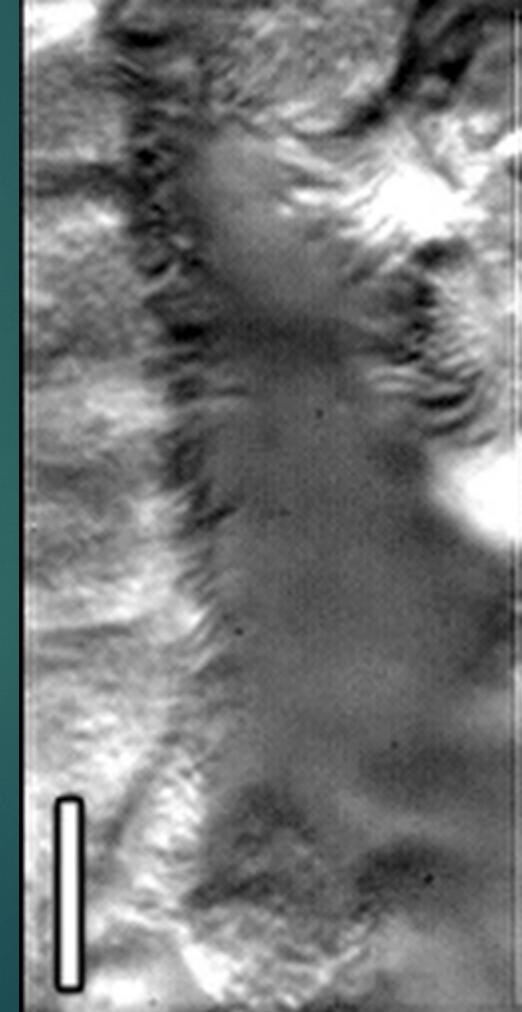
7.4



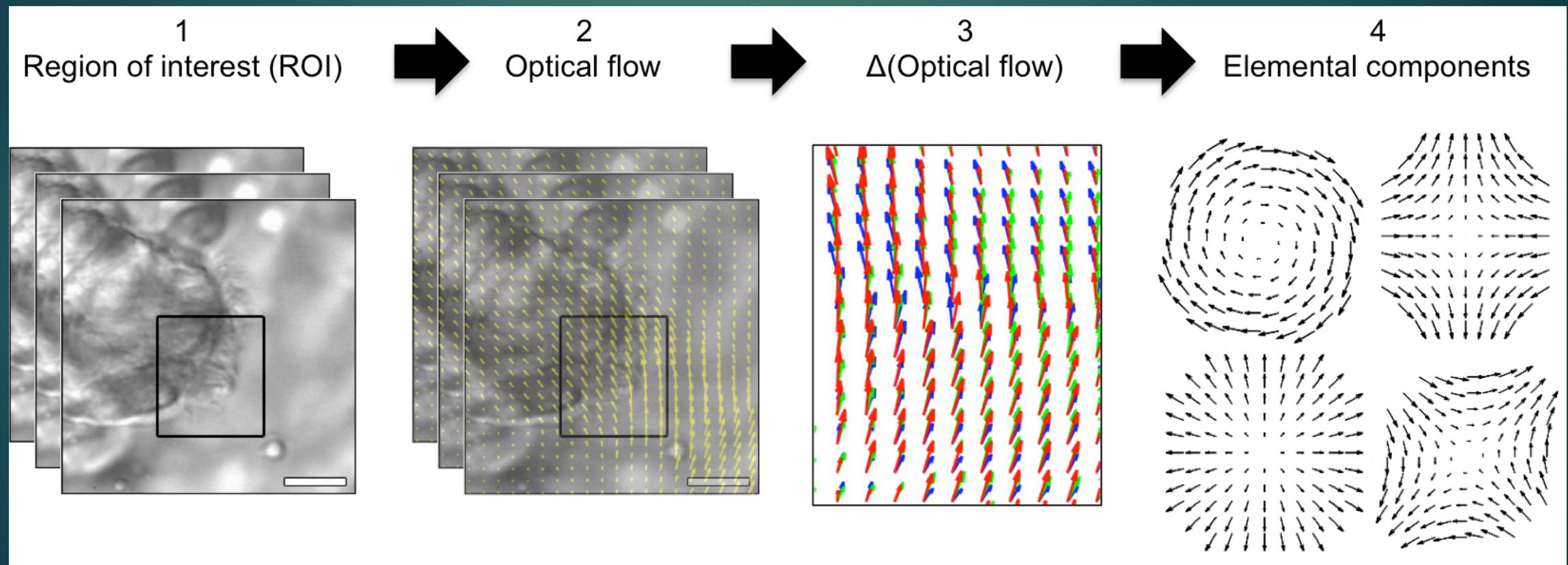
Part II: Quantitative features of ciliary motion



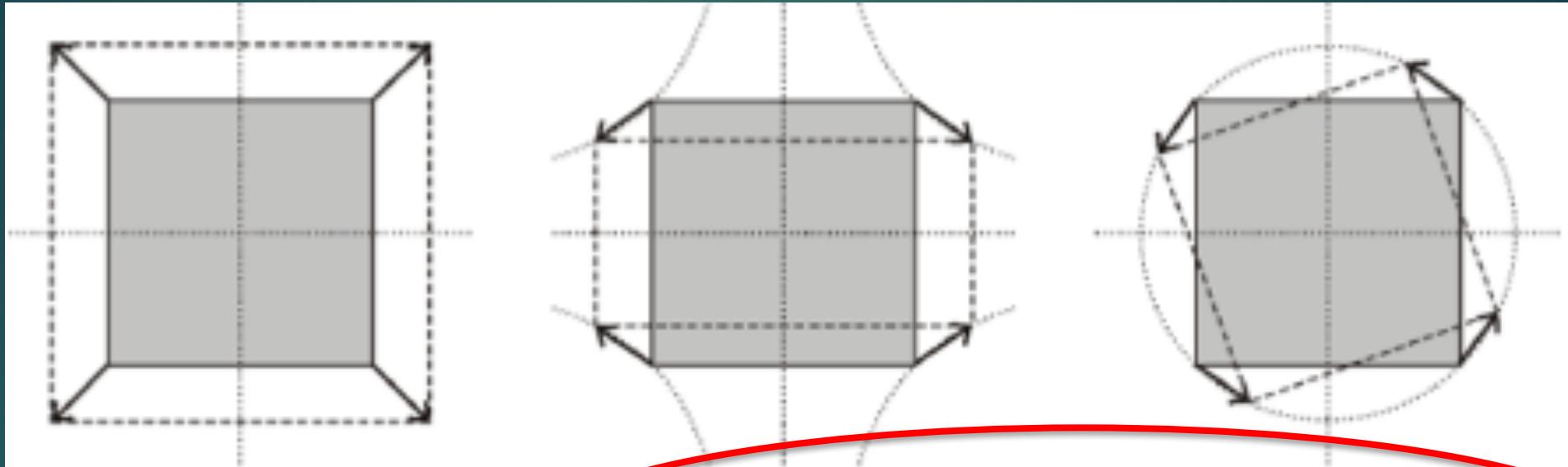
Strategy for quantifying motion



From videos to features



Features describing motion



Scaling (zoom)

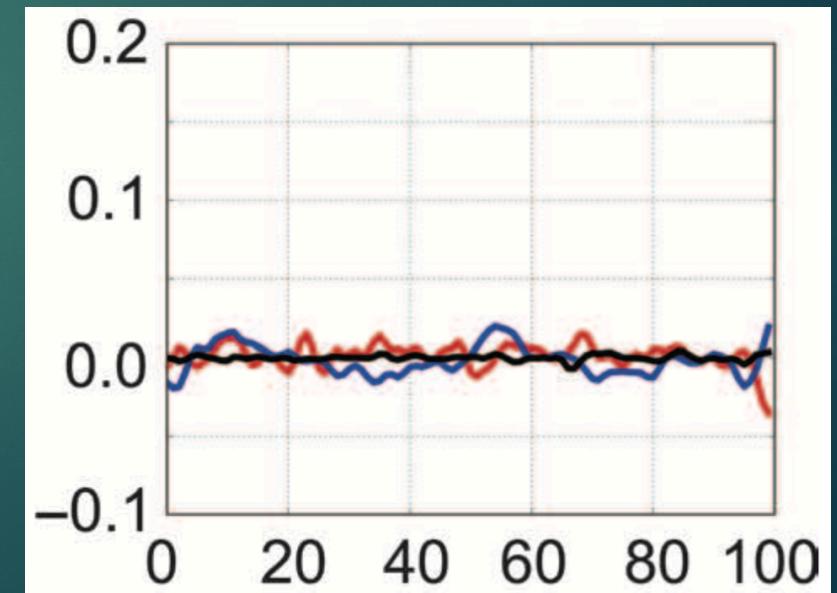
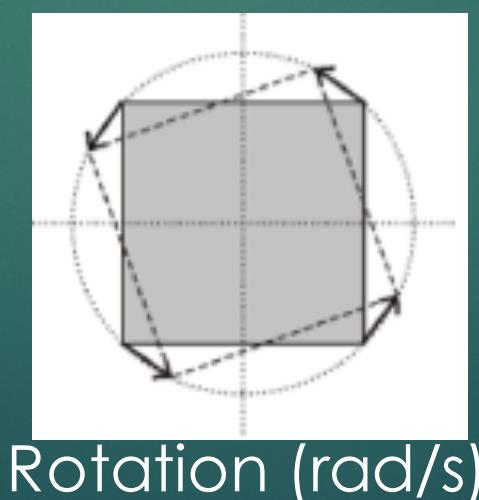
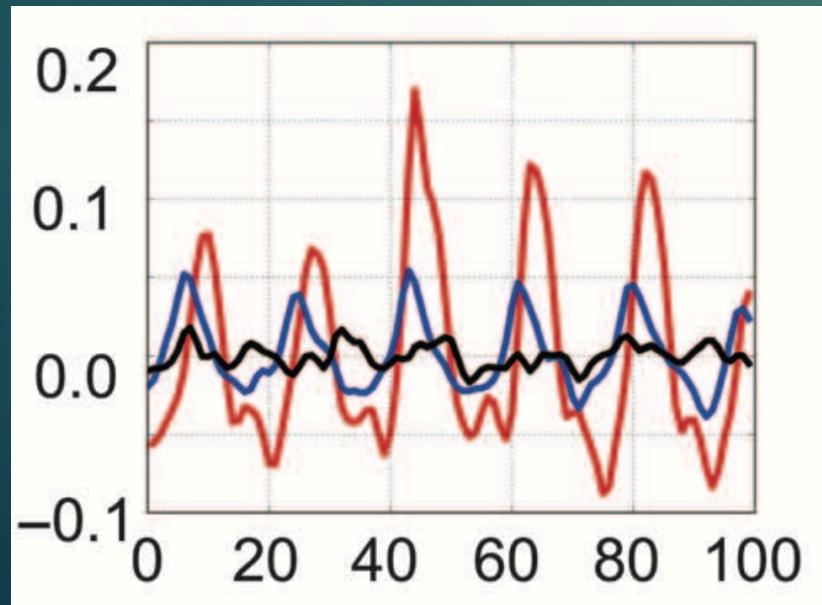
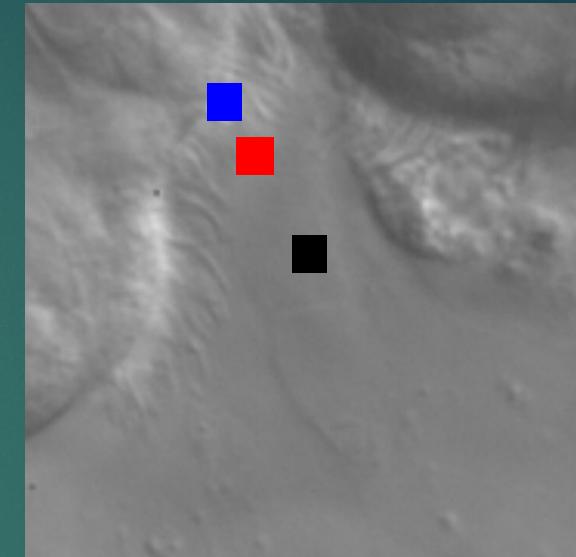
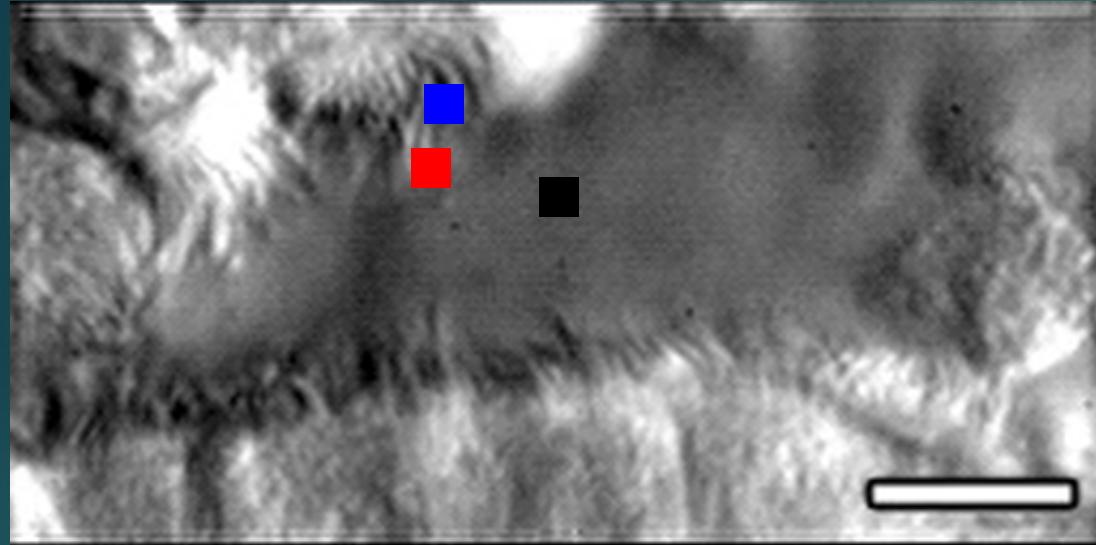
Deformation
(biaxial shear)

Rotation (curl)

Not useful in
2D

"Novel use of differential image velocity invariants to categorize ciliary motion defects." Quinn SP, Francis R, Lo C, Chennubhotla CS. *Proceedings of the Biomedical Science and Engineering Conference (BSEC) 2011*.

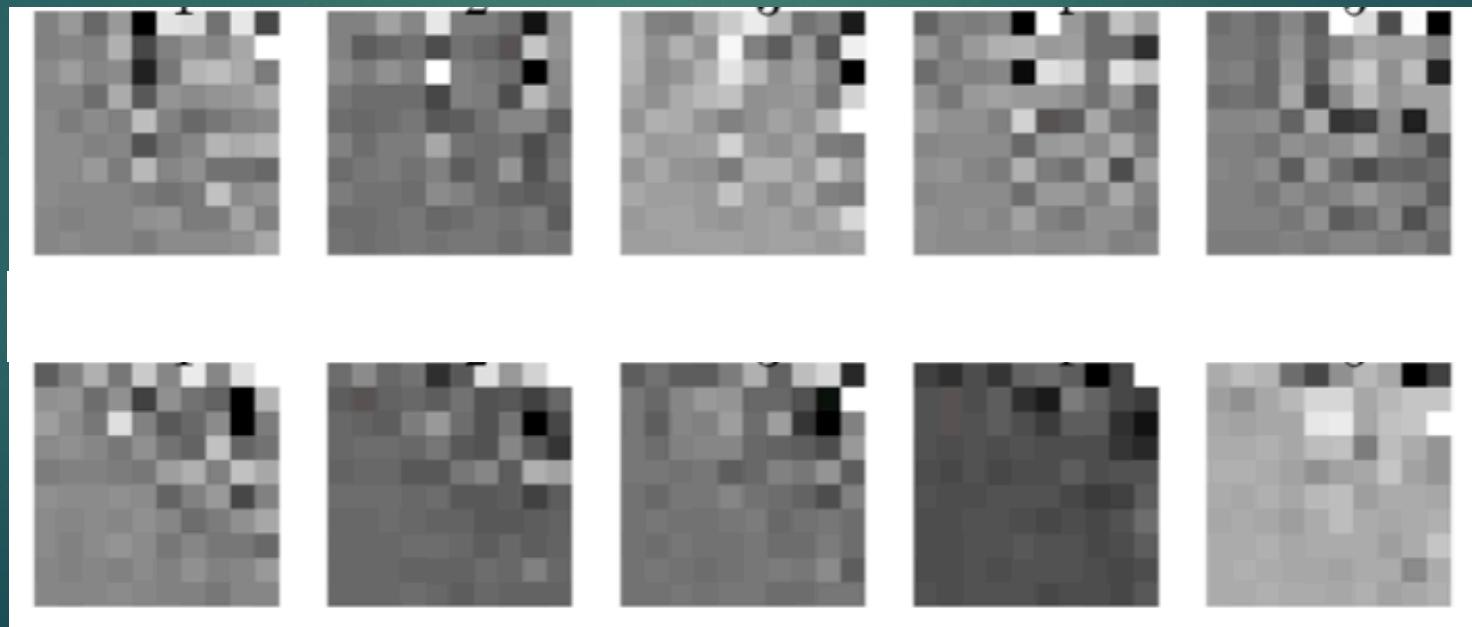
What do these features look like?



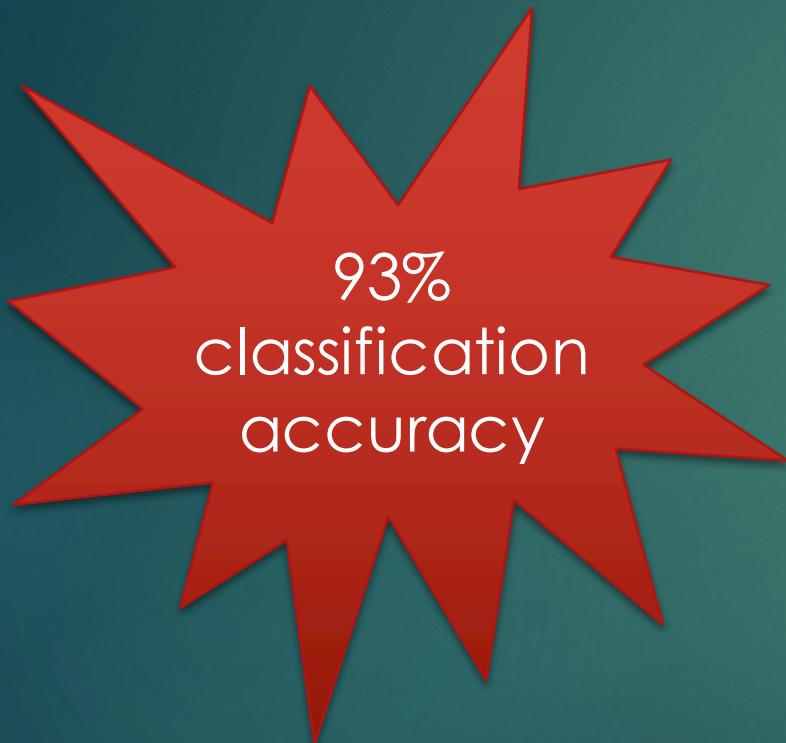
How do we represent these features?

Feature vectors!

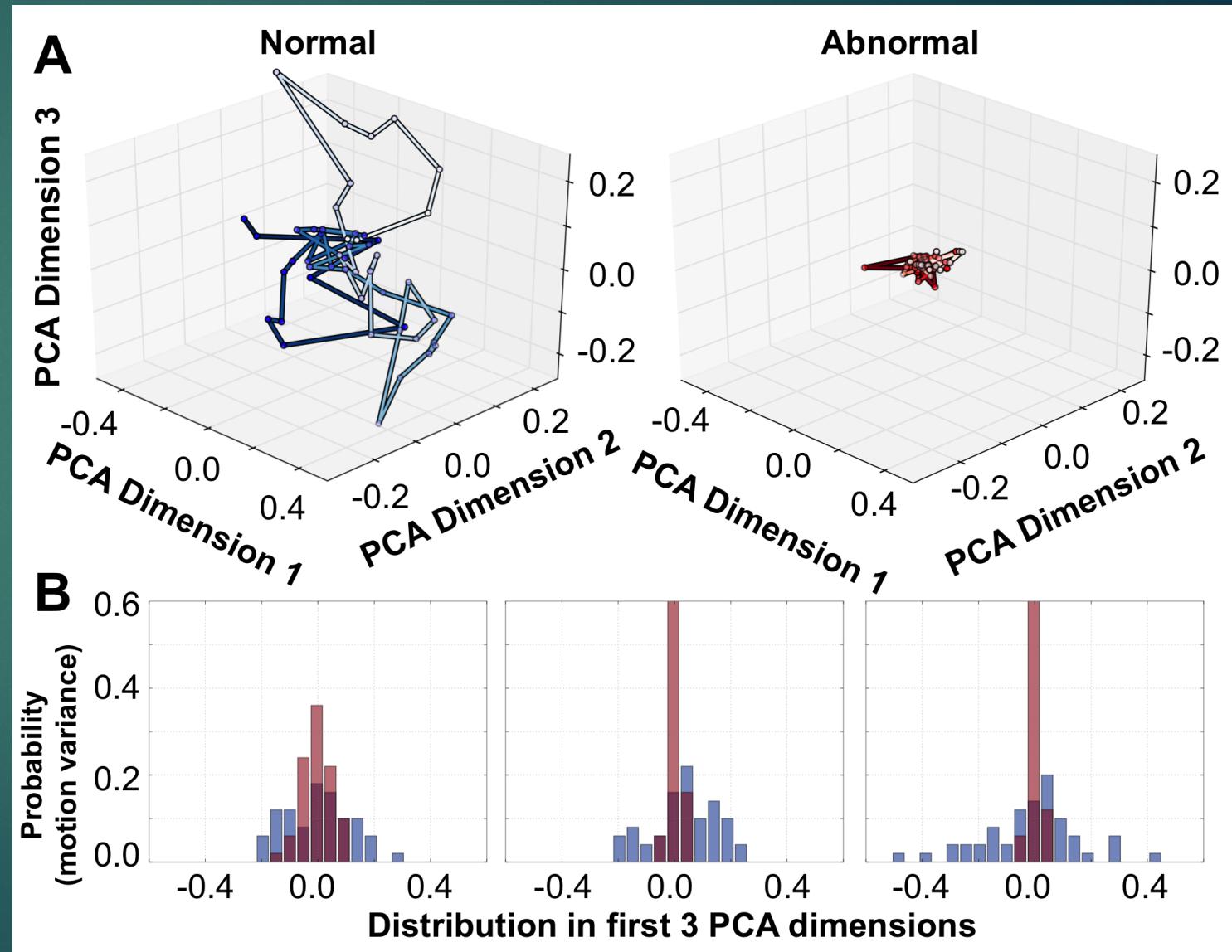
$$\vec{y}_t = C\vec{x}_t$$
$$\vec{x}_t = A_1\vec{x}_{t-1} + A_2\vec{x}_{t-2} + \dots + A_d\vec{x}_{t-d}$$



What can we do with these features?



Automated identification of abnormal respiratory ciliary motion in nasal biopsies. Quinn SP, Zahid M, Durkin J, Francis R, Lo C, Chennubhotla CS. *Science Translational Medicine* 2015.



Part III: The Python ecosystem

Collecting data from collaborators

1. Upload to django website
2. Annotate manually
3. Save annotations in database using SQLAlchemy

django
SQLAlchemy

1

Logout

← Go annotate videos Overview Contact

Cilia Video Uploader

Version 0.1

Here you can upload videos of ciliary motion, or delete videos you no longer want considered.

1. Drag & drop videos from your desktop to this webpage. Alternatively, click the "Add files..." button and select a video.
2. Repeat this process until you have selected all videos you wish to upload.
3. Click the blue "Start upload" button. Go grab some coffee!

If anything goes wrong, please send us a description of the problem, how to reproduce it, and a screenshot to [spq1 at pitt dot edu](mailto:spq1@pitt.edu).

+ Add files... Start upload Cancel upload Delete

1001-13.avi Processing... Start Cancel

Usage notes

- Uploaded videos are restricted to **.avi** format.
- The maximum file size for an uploaded video is **2 GB**.
- Check [this list of supported browsers](#) to see if yours will work with this site.
- Capture framersates are assumed to be **200 fps**.
- Uploaded files will not be deleted until the user specifies.

3

Logout

← List of videos Overview Contact

Annotating 9028-4avi

Version 0.1

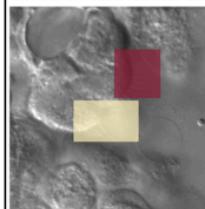
Using this interface, you can annotate your video by adding new ROIs, removing previous ROIs, or resizing current ROIs. Once you click "Save", the ROIs will be committed to the database. Any changes you make must be "Save"ed again to take effect.

If anything goes wrong, please send us a description of the problem, how to reproduce it, and a screenshot to [spq1 at pitt dot edu](mailto:spq1@pitt.edu).

Add a region of interest

ROI Position (X, Y) ROI Dimensions (W, H) Delete ROI

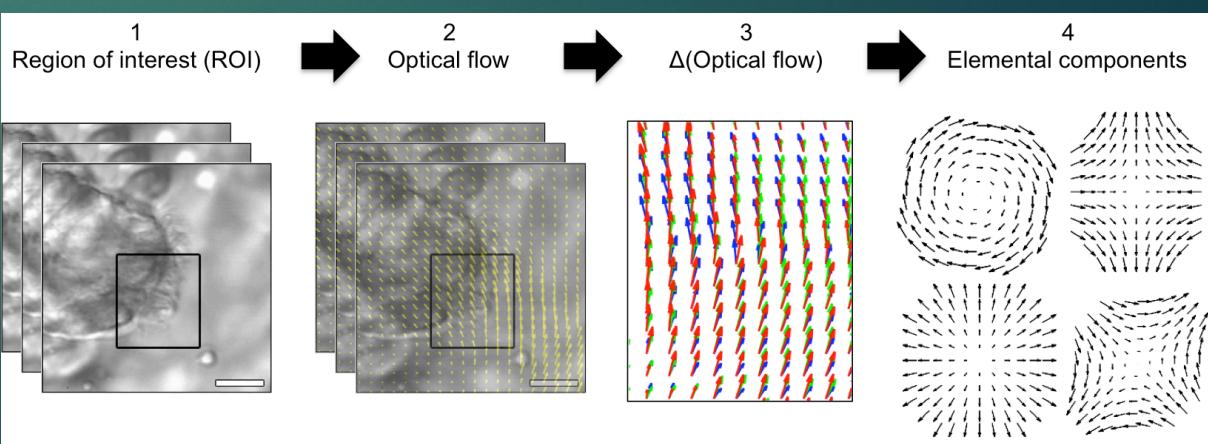
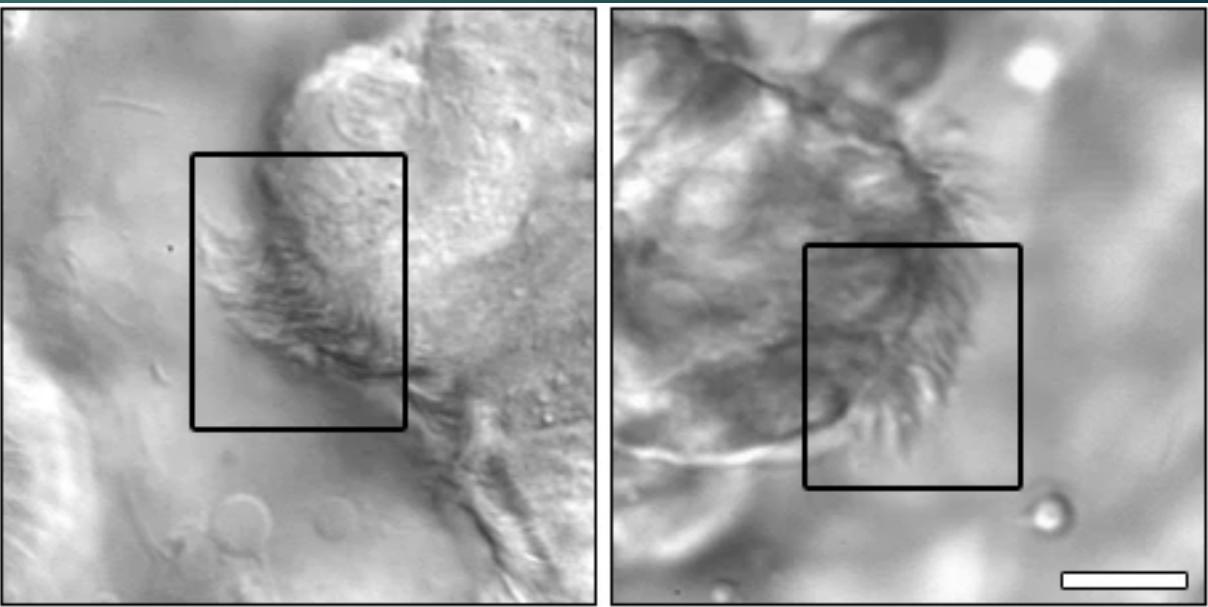
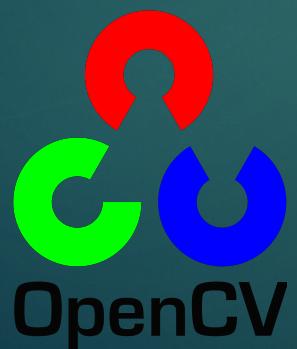
129, 53	57, 60	Delete ROI
79, 116	80, 51	Delete ROI



Save ROIs!

Processing raw video data

1. Videos in AVI format
2. Convert to NumPy arrays with OpenCV
3. Compute optical flow with OpenCV
4. Compute rotation with SciPy signal processing filters



Derivation of time series models

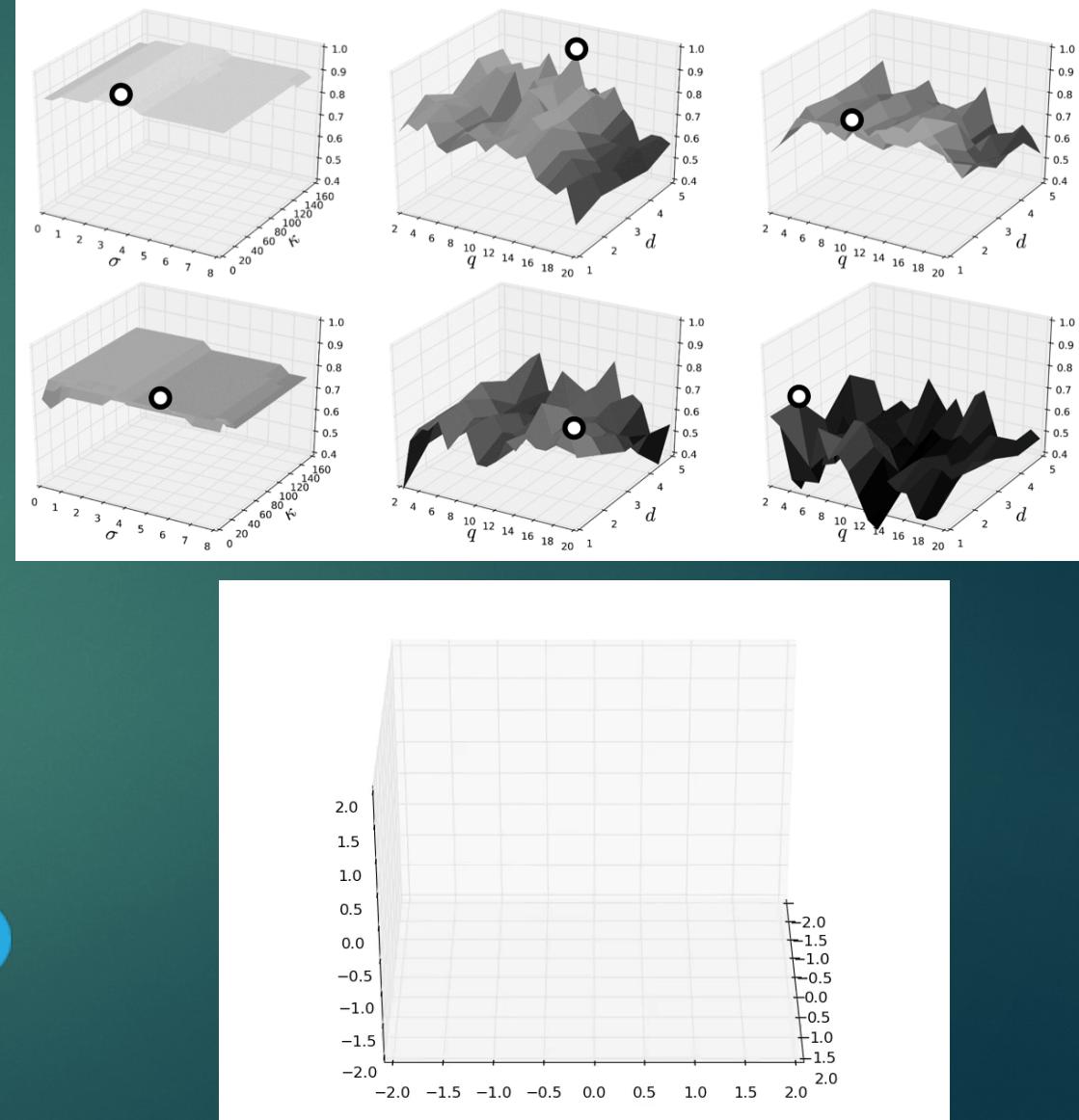
- ▶ ...custom code!
- ▶ scipy.linalg

```
U, S, Vt = sla.svd(raw_data, full_matrices = False)
C = U[:, :q]
Sh = np.diag(S)[:q, :q]
Vth = Vt[:q, :]
X = np.dot(Sh, Vth)
return [X, C]
```

$$-(F_1 \ F_2 \ \dots \ F_M) = X_{M+1}^\tau \begin{bmatrix} X_M^{\tau-1} \\ \vdots \\ X_2^{\tau-M+1} \\ X_1^{\tau-M} \end{bmatrix}^\diamond$$

Classification pipeline

- ▶ Cross-validation for model fitting and testing using scikit-learn
- ▶ joblib / PySpark for parameter scanning
- ▶ matplotlib + seaborn / bokeh for visualization





(BONUS ROUND)

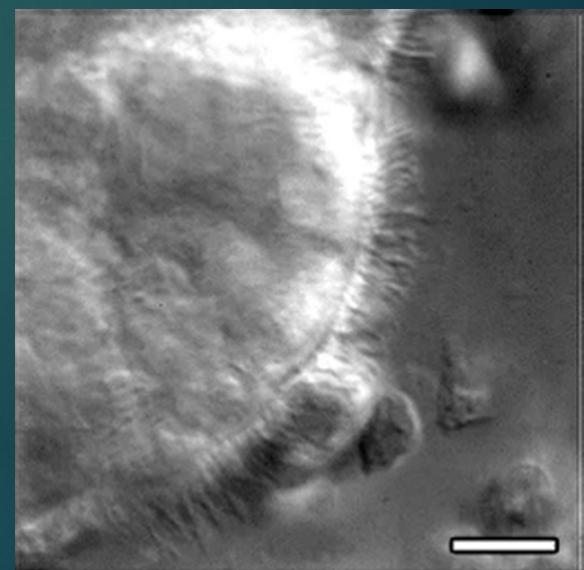
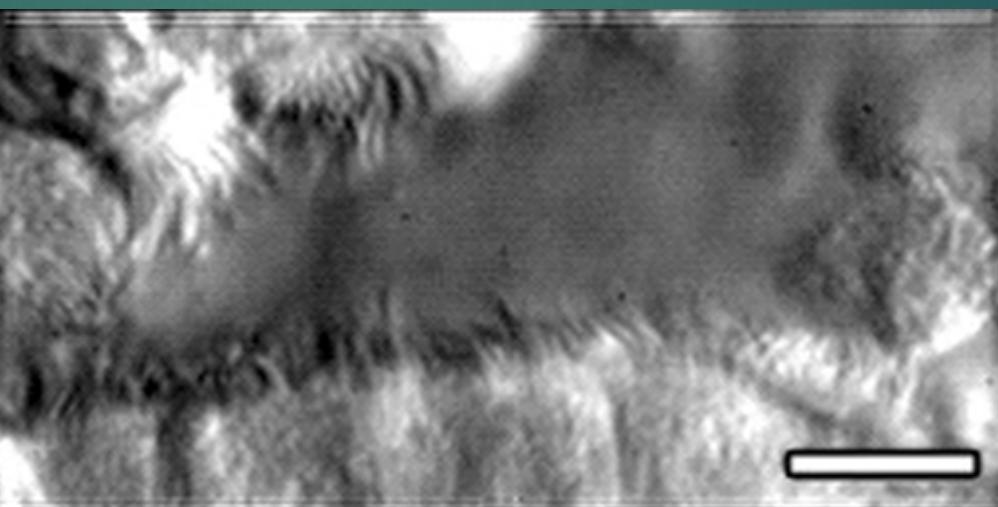
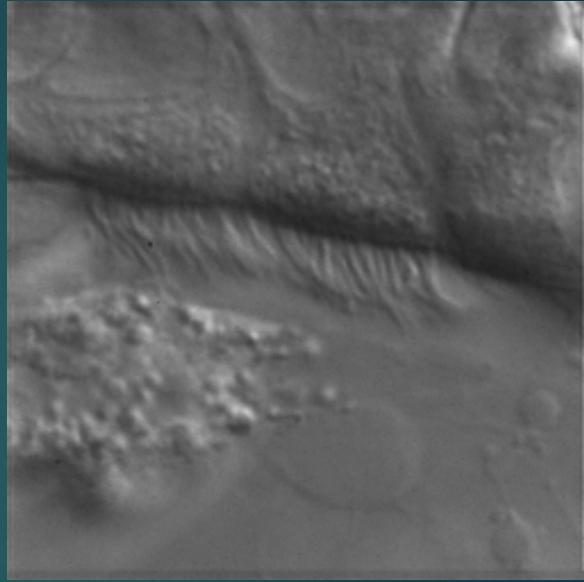
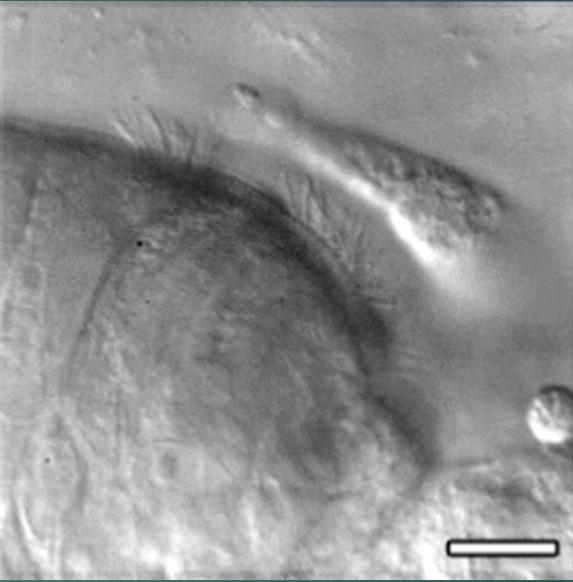
Part IV: Conclusions and future
directions

Conclusions

- ▶ 93% classification: methods are sound
 - ▶ Dynamic texture representation is accurate
- ▶ Blackbox tool for clinicians
 - ▶ Web front-end + Python middleware + Spark back-end
- ▶ Upload video -> Get analysis
 - ▶ Assist experts with diagnostics
- ▶ Expert input
 - ▶ Phenotype annotations, regions of interest

Future directions

- ▶ Normal / Abnormal is an oversimplification...
- ▶ Unsupervised motion clustering pipeline
- ▶ Associate specific motion phenotypes with clinical conditions



Thank you!

- ▶ spq@uga.edu
- ▶ @SpectralFilter
- ▶ <https://magsol.github.io/>

