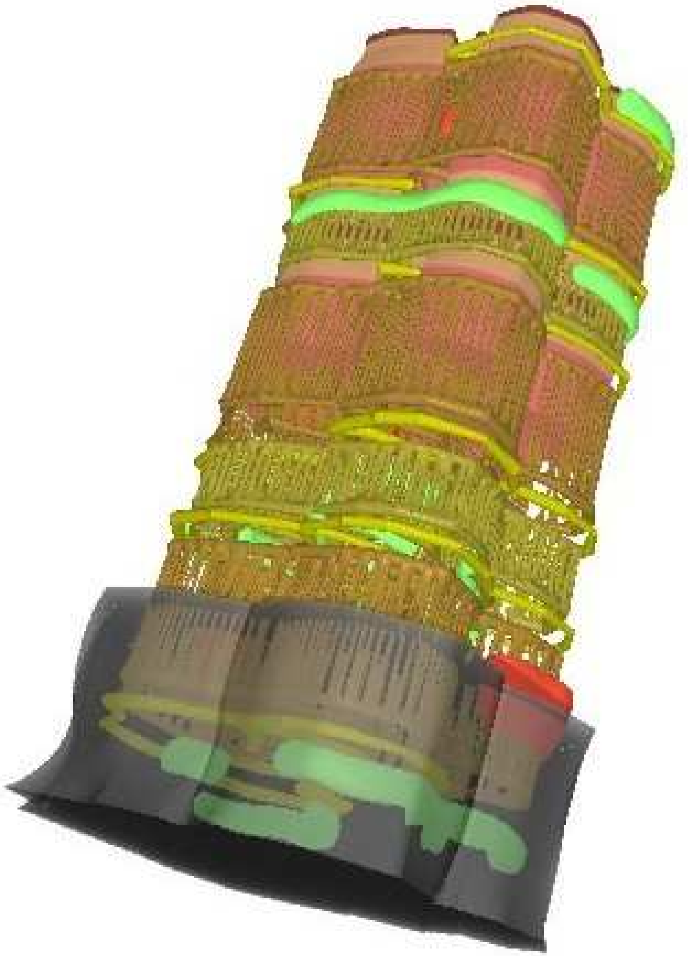
GeomCell, towards modeling the muscle cell dynamic geometry

Michal Remiš

Faculty of Mathematics, Physics and Informatics, Comenius University, Bratislava, Slovakia

Geometrical Modeling of Living Cells



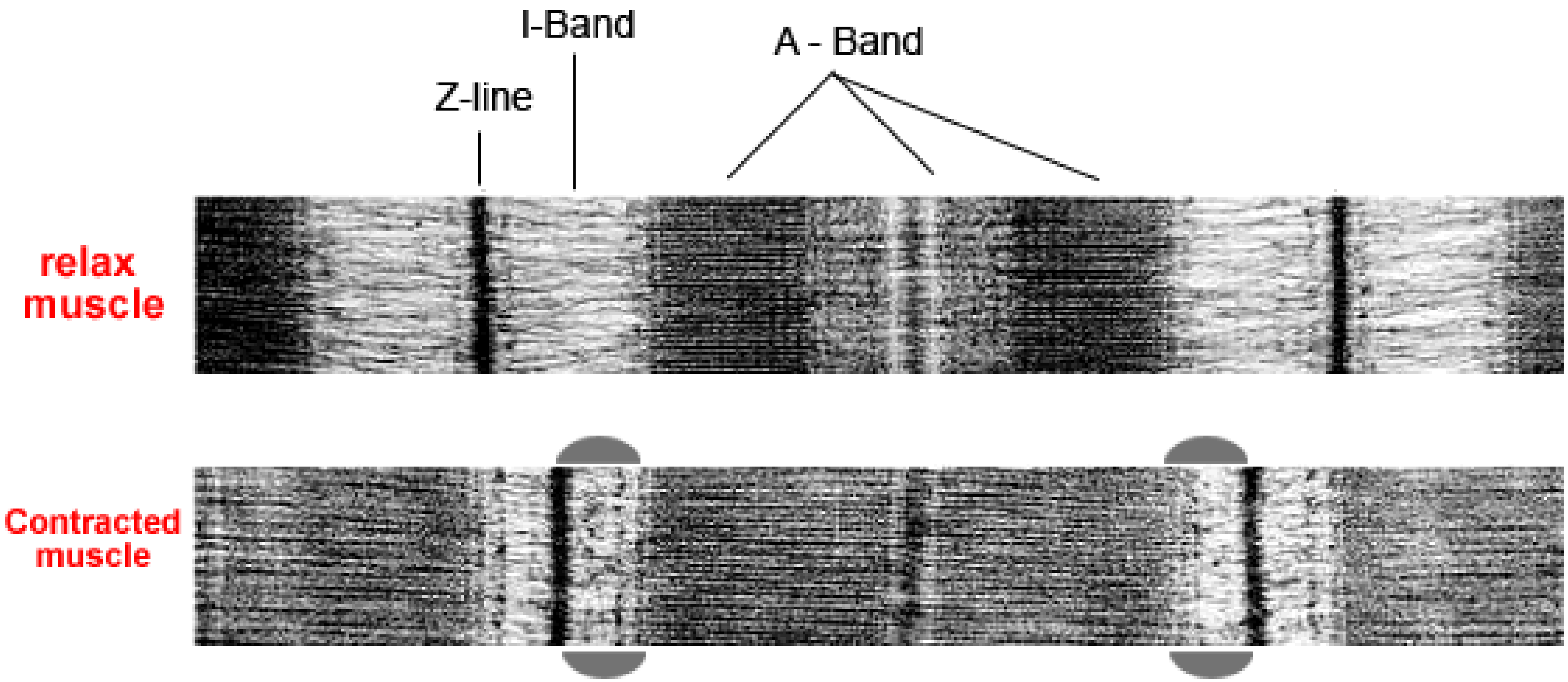
- RNDr. Július Parulek, PhD.
- XISL – open source library for implicit surfaces representation
- Particular organelles were defined
- Cell models may be generated by distribution of organelles
- Model fulfils important stereological properties

Towards dynamics

CellDyn - framework over XISL library for simulation of cell dynamics

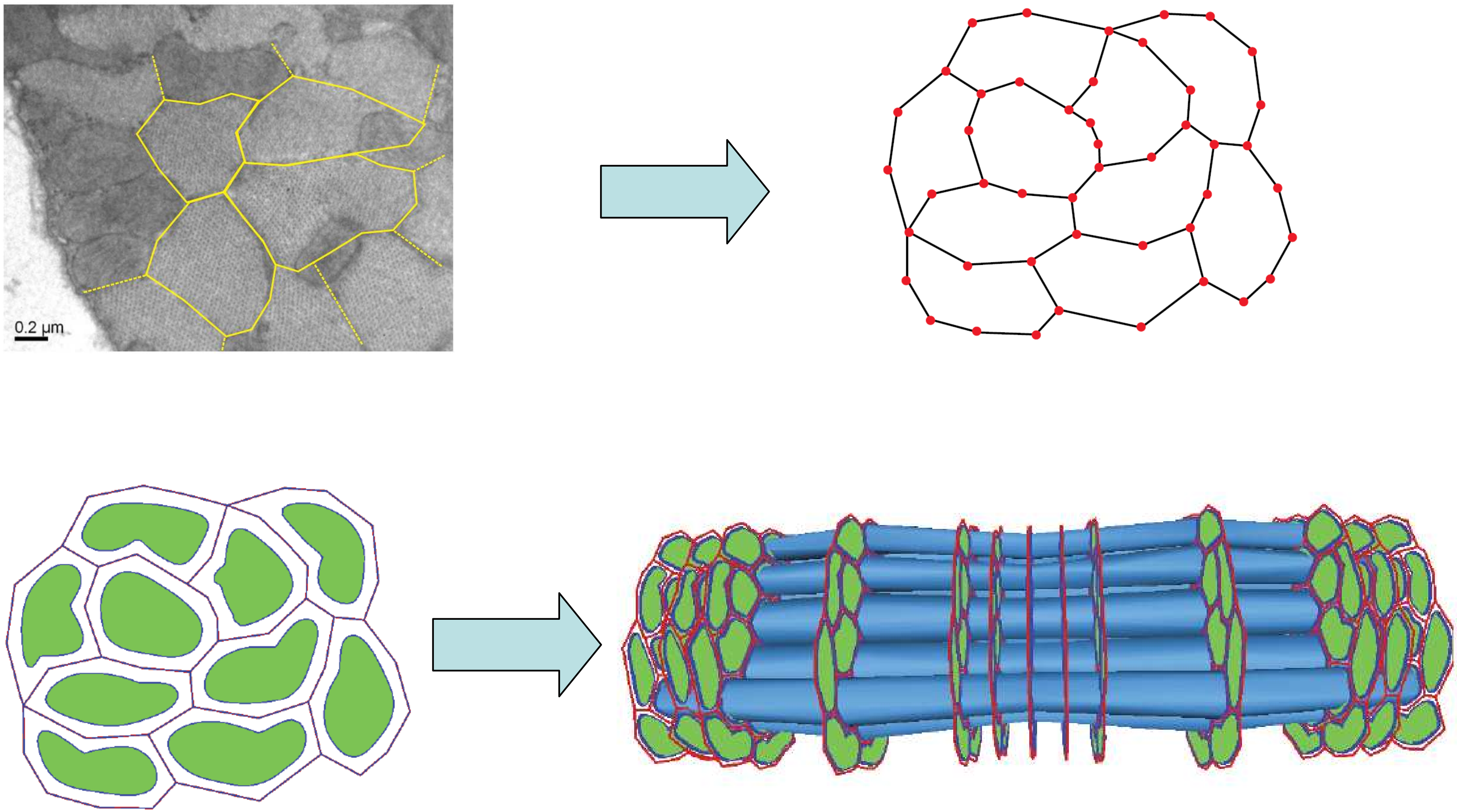
- Understand organelle as biological object rather then just a implicit function
- Modifies implicit organelle properties to reach desired effect
- We still load data from generated models to coincide with reality

Myofibril contraction



- Myofibril is divided in Z-line, I-Band and A-Band sectors
- During contraction myofibril sectors behave differently
- In CellDyn we try to simulate this process

GeomCell myofibril modelling principles

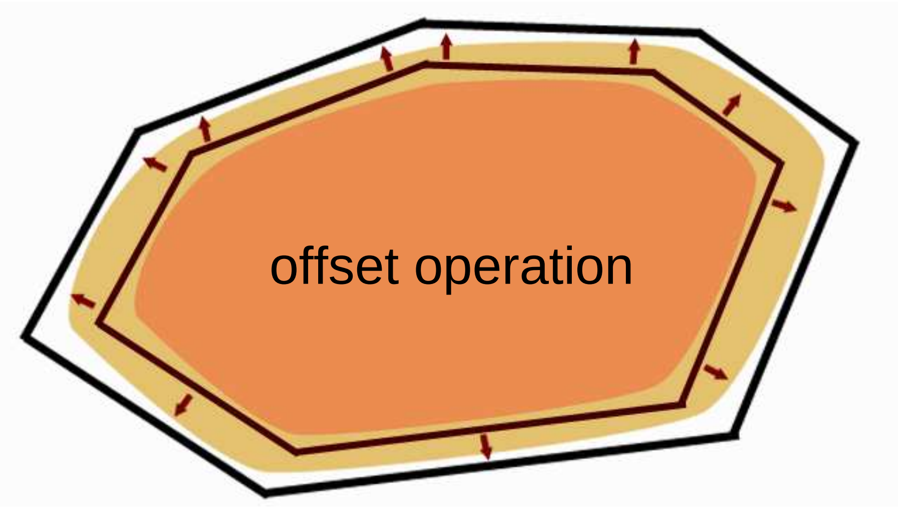


CellDyn myofibril contraction

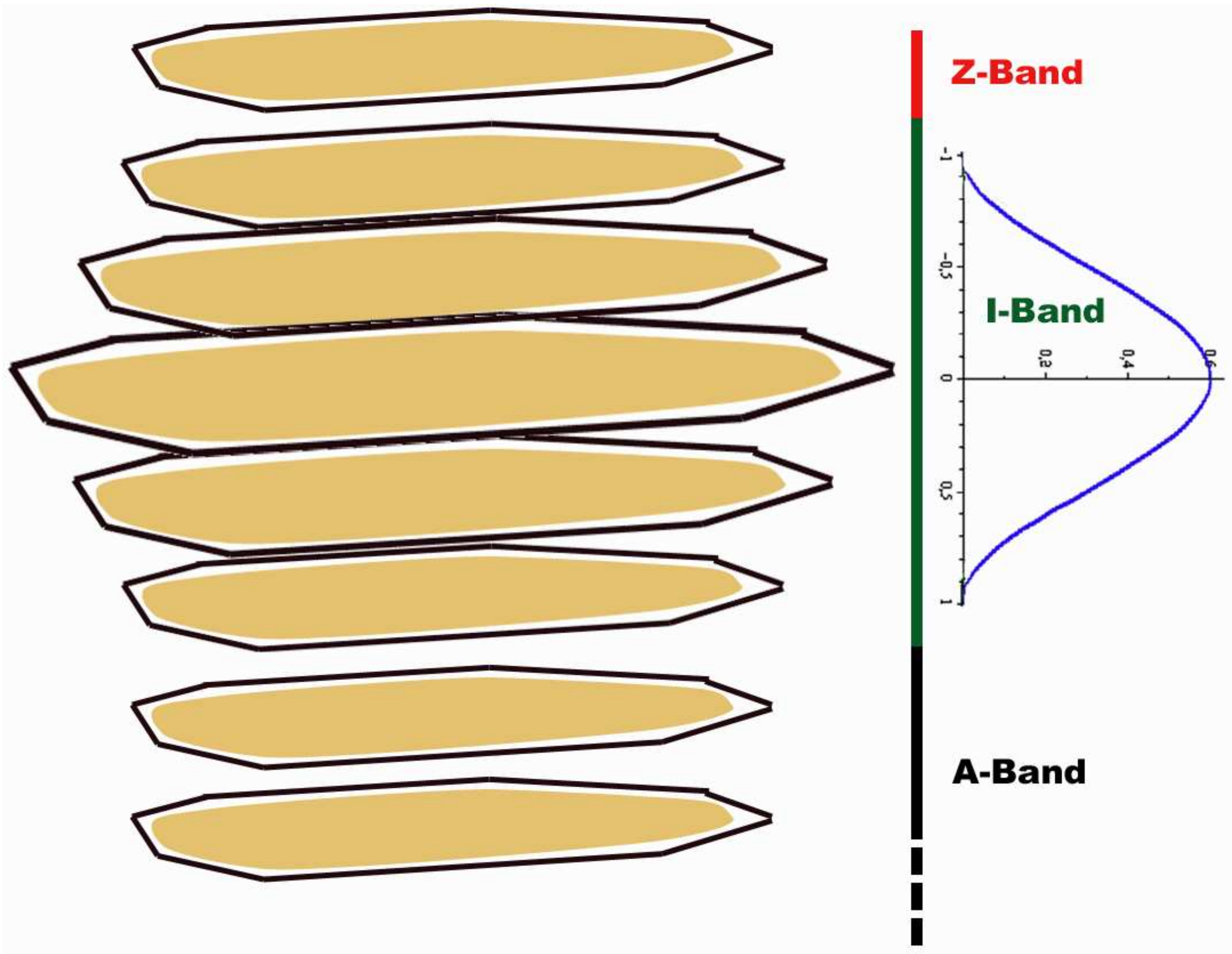
• single myofibrils are extracted from GeomCell generated model and imported into CellDyn

• myofibril sections are determined and polygon skeleton is assigned

• offset operation is attached to every skeleton polygon



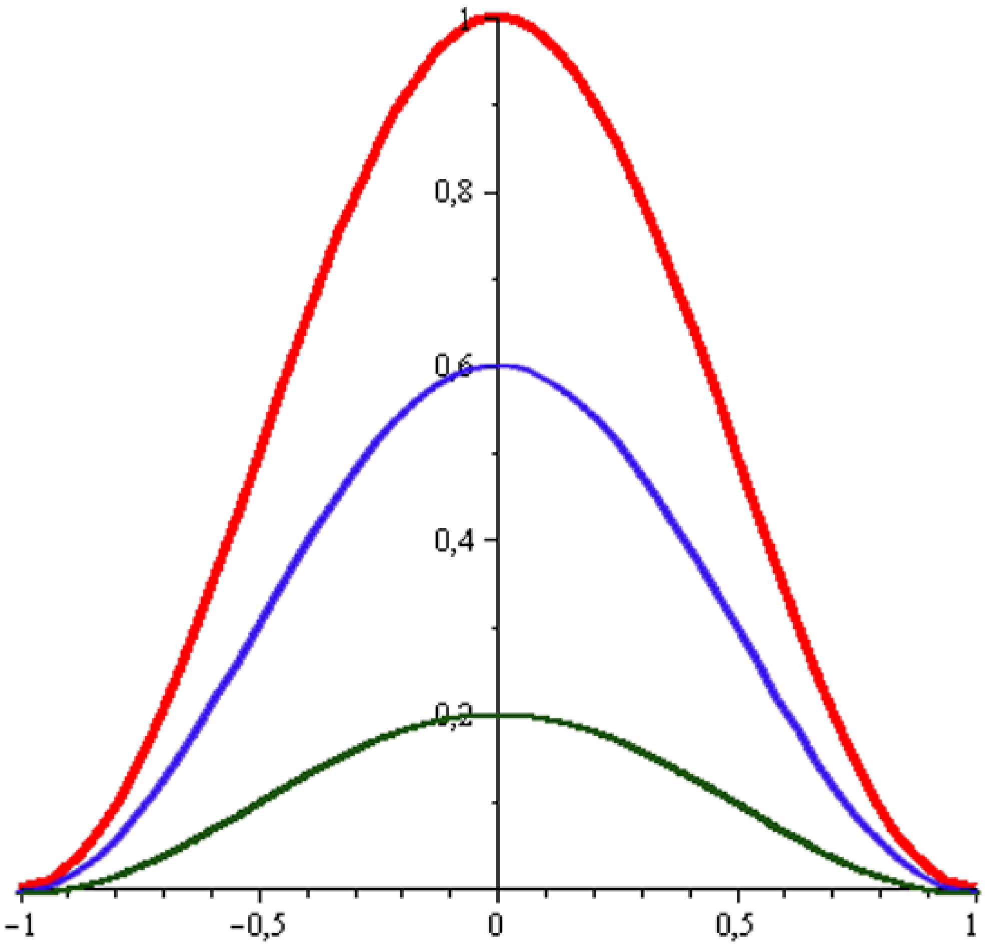
CellDyn contraction dynamics



Every myofibril sector behave differently

- **A-Band** remains unchanged
- **I-Band** is shortened and bulged. Bulge si achieved by adjusting offset operation over polygons. Shape of bulge is determined by a function.
- **Z-Band** remains unchanged but follows I-Band region

Bulging I-Band



$$h := x \rightarrow 1 - \frac{4}{9}x^6 + \frac{17}{9}x^4 - \frac{22}{9}x^2$$

x determines longitudal position inside I-Band

- Shape and Size of bulge is controlled by function
- We use gaussian like polynomial function.
- Size of bulge is achieved by scaling of the function
- On the left you may see shape of bulge for different desired size *d* (amount of contraction)

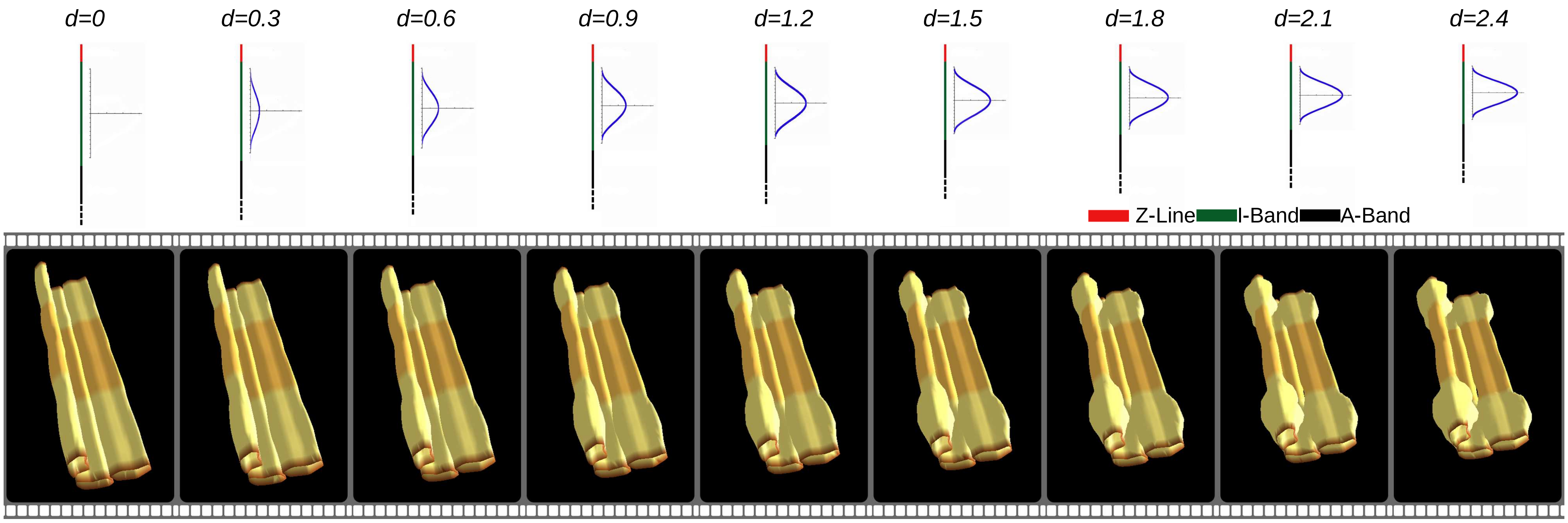
d = 0.2

d = 0.6

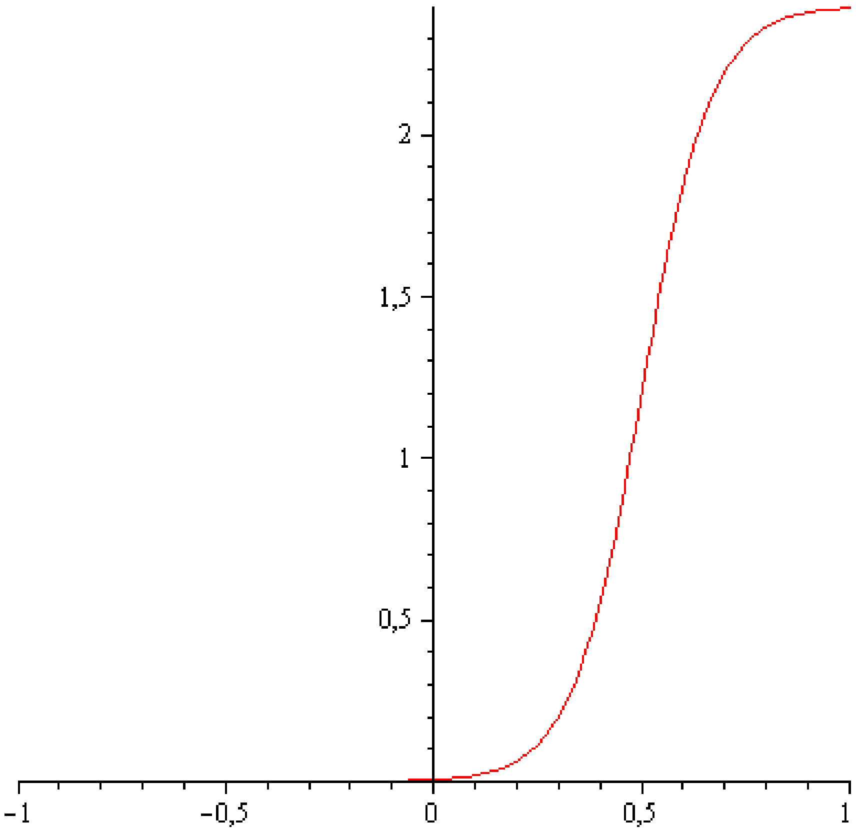
d = 1

Going dynamic

By varying contraction amount over time we achieve myofibril contraction dynamics.



Amount of contraction changes over time

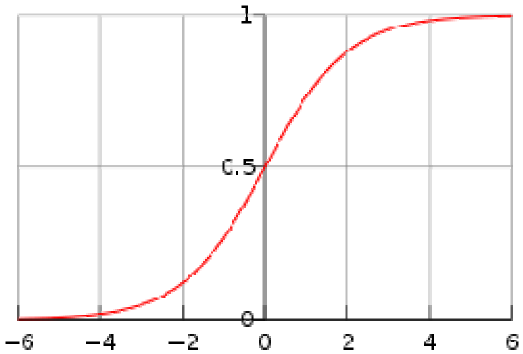


$$d := t \to \frac{2.4}{1 + e^{-12t+6}}$$

- Size of contraction over is controlled by a function.
- We have modified *logistic function* to our needs

logistic function – *sigmoid* curve widely used in range of field to model growth

$$l := x \to \frac{1}{1 - e^{-x}}$$



alltogether in action

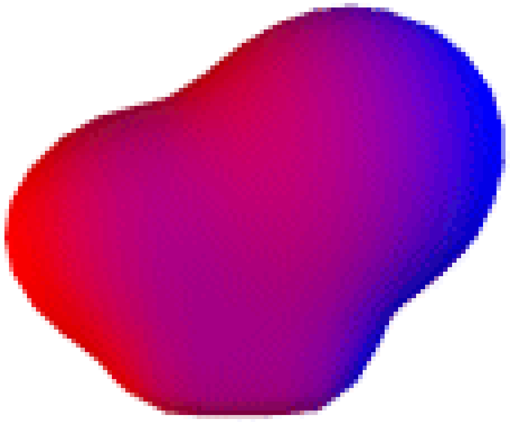
Show Video

Conclusions

- CellDyn offers trustworthy simulation of myofibril contraction dynamics
- Simulation performed on myofibril model of real cells obtained by stereology based modeling.

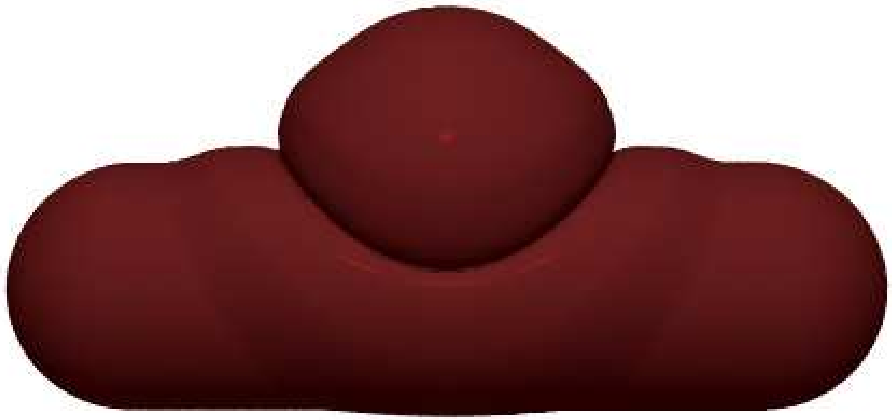
- Computationally very intensive (5s frame)
- Easy parallelisation in this step.

Future work



- Simulate myofibril interaction with mytochondrions

- Include mytochondrions into the simulation
- Point based implicit surface, points connected by spring system.



Thank you for your attention.

time for your questions.