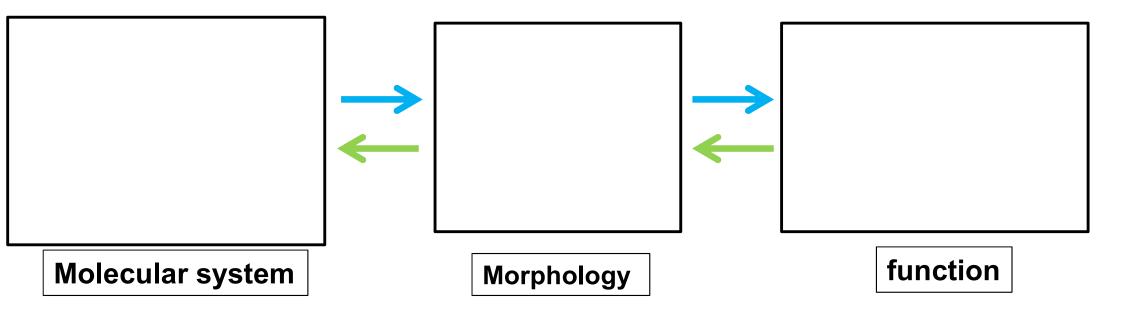
### Self-organization of Golgi apparatus

Masashi Tachikawa Theoretical Biology Laboratory, Riken

## Theoretical modeling of organelle (細胞小器官)



#### Logic to connect between scales

- How do molecular systems generate shapes?
- How do shapes generate functions?

# Golgi body

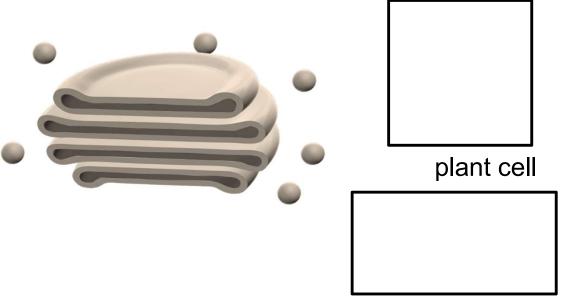
Closely stacked, flattened membrane sacs with discoid shapes (<u>cisternae, 槽</u>)

Fusion and fission of vesicles carry Golgi processes

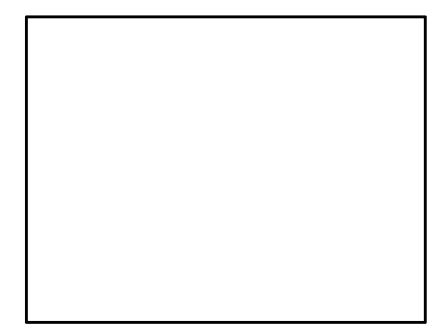
Observed with electron microscopy

#### **Function**

- hub of intra-cellular traffic of membrane and cargo(積荷) proteins
- Modify cargo proteins (<u>Glycosylation</u>)

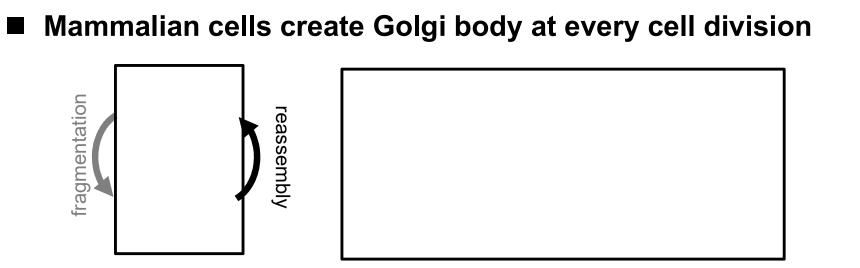


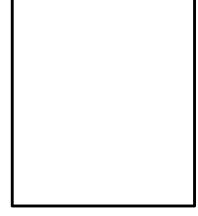
#### animal cell



### "What I cannot create, I do not understand."

Dr. Richard Feynman





Experimentalists reproduce Golgi body in test tubes

Tang et al. Nature Protocols, 2010

Golgi disassembly and reassembly assay using purified proteins

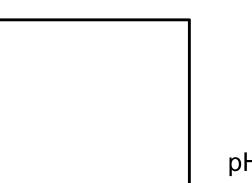
Creating Golgi body in computer (our project)

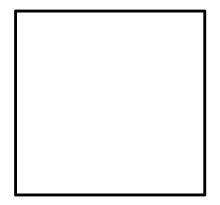
### Morphological aspects of Golgi and models

About single cisterna morphology

- Compressed cisterna lumen
   Osmotic pressure difference
   Ion channels
- Bent membrane at edge edge stabilizer protein (coatomer proteins?)
- Cisternae stacking
   Inter-membrane adhesion
   GRASPs, Golgins
- Membrane fusion(fission)
   Fusion machinery
   SNARE proteins







pH control by ion channels

Coatomer proteins at rim

## **Dynamical triangulation membrane**

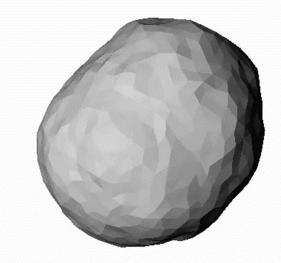
Gompper & Kroll '97, 01 Noguchi '09

- **Polygon representation for membrane shape** polygon ENERGY adsorb/desorb  $E = E_{osmo} + E_{bend} + N_p \cdot \varepsilon^{adsp}$ **r**<sub>i</sub>: vertex position  $E_{osmo} = -\Delta P \cdot \sum_{trianales} r_3 \cdot \frac{(r_1 \times r_3)}{6}$   $l_{ij}$ : edge length  $\sigma_{ij}$ : dual lattice lengtu  $E_{bend} = \kappa \sum_{vertices} \left[ \frac{1}{\sigma_i} \sum_{j(i)} \frac{\sigma_{ij}}{l_{ij}} (\boldsymbol{r}_i - \boldsymbol{r}_j) - c \boldsymbol{n}_i \right]$ edge length~20nm curvature Membrane-bending protein on vertices adsorb from/desorb to cytosol with energy change  $\mathcal{E}^{adsp}$ 
  - change spontaneous curvature locally
  - Monte-Carlo method for dynamics

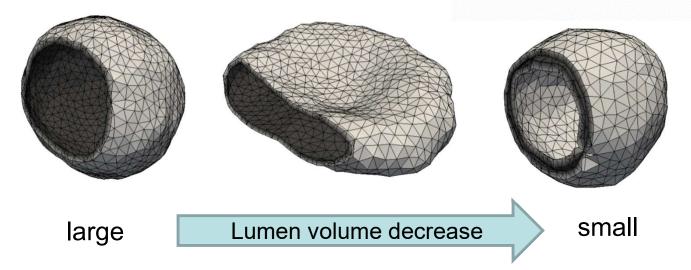
taking thermal fluctuation into account

### Simulator demo (without membrane-bending protein)

- Closed membrane bag (diameter~100nm)
- Increase osmotic pressure at t=0,  $0.0 \rightarrow 0.4(atm)$

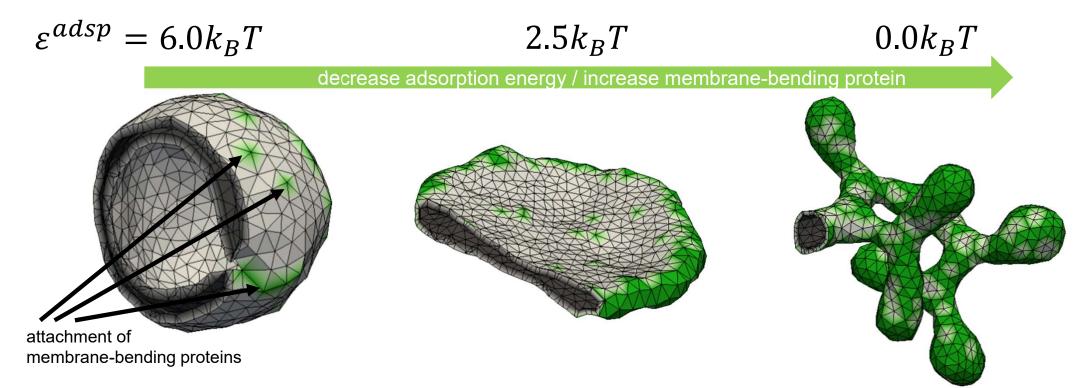


#### Shape variation



### Shapes by membrane-bending proteins

 $\Delta P = 5.0 \times 10^{-4} \text{atm}$ 



Discoid (cisterna-like) and tubular shapes are formed.

• Proteins are automatically arranged at the peripheral of disc. "Self-organization of protein distribution and membrane shape"

### Morphological aspects of Golgi and models

About single cisterna morphology
 Compressed cisterna lumen
 Osmotic pressure difference
 Ion channels

 Bent membrane at edge edge stabilizer protein (coatomer proteins?)

About cisternae assembly
 Cisternae stacking

Inter-membrane adhesion GRASPs, Golgins

Membrane fusion(fission)
 Fusion machinery
 SNARE proteins

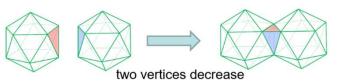
Model extension

Membrane adhesion (additional energy)



 $E^{adh} = \varepsilon^{adh} \times$ number of adhering vertex pairs

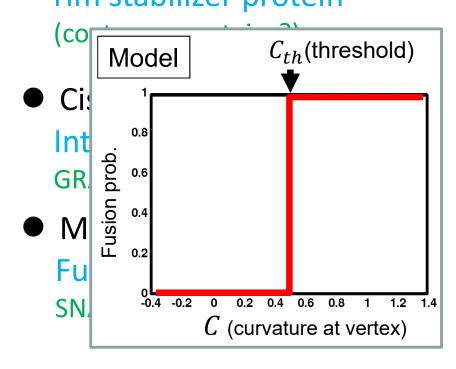
Membrane fusion (additional Monte-Caro step)

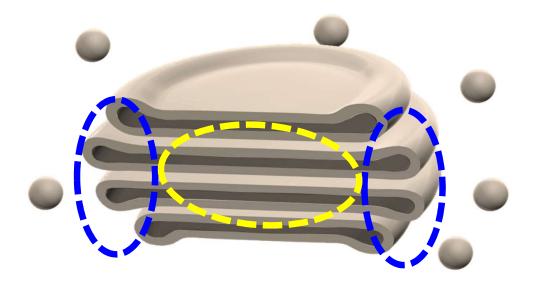


<u>Irreversible process (with ATP) : NO energetic control?</u>

### Morphological aspects of Golgi and models

- Compressed cisterna lumen
   Osmotic pressure difference
   Ion channels
- Bent cisternae rim rim stabilizer protein





Fusion should be restricted inside to keep cisternae separate

#### Model for fusion control "Only curved membrane can fuse."

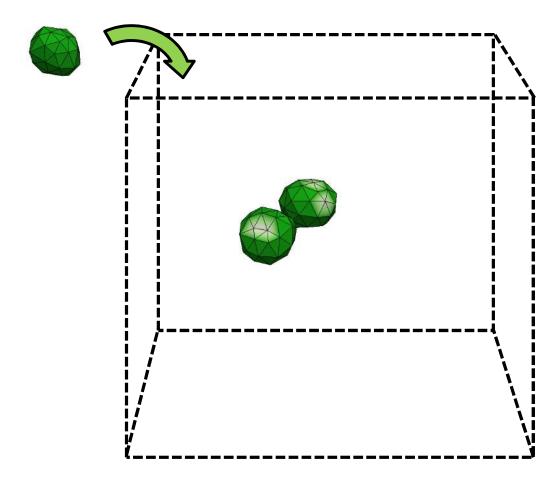
biological model

"Fusion machinery distribution depends on curvature."

## Golgi reassembly simulation

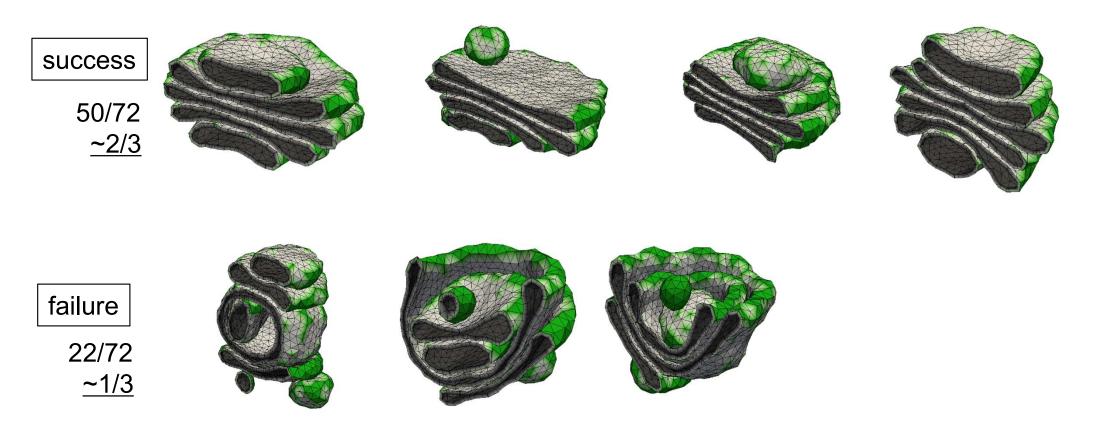
### Add vesicles with an interval

Vesicle size: 42 vertices Total number of vesicles: 75



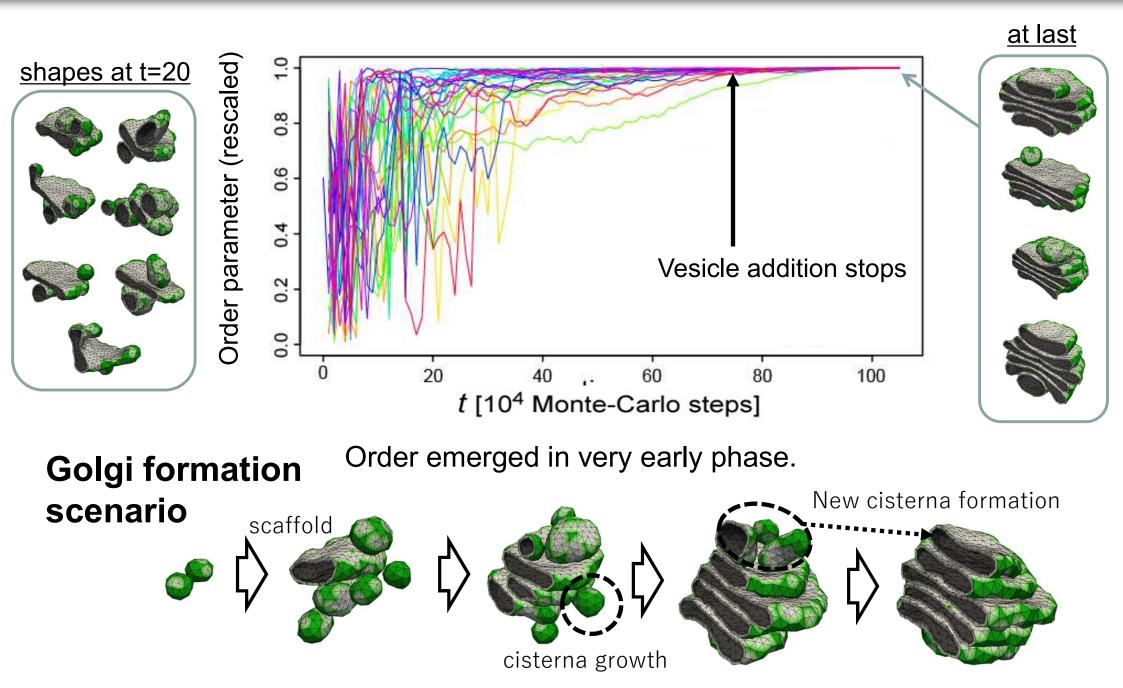
Best parameter set	
Osmotic pressure	$\Delta P \sim 7.0 \times 10^{-4}$ atm
Adsorption energy	$\varepsilon^{adsp} \sim 4.0 k_B T$
Adhesion energy	$\varepsilon^{ad} \sim 1.0 k_B T$
Vesicle adding interval	$\tau \sim 10^4 { m \ steps}$
Fusin threshold	$C_{th} \sim 0.8$

## Self-organization of Golgi shape did occur

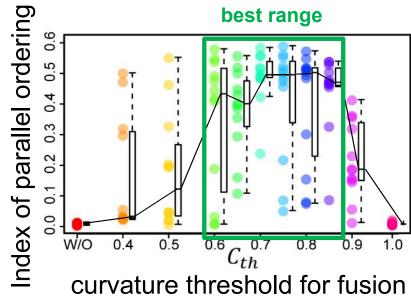


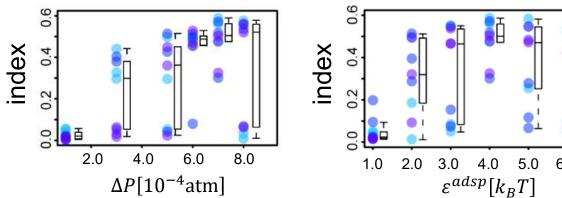
The physical model that is designed to stabilize the interphase Golgi shape and that comprises equilibrium reactions except the fusion process, reproduced(mimicked) the Golgi reassembly process from broad initial conditions.

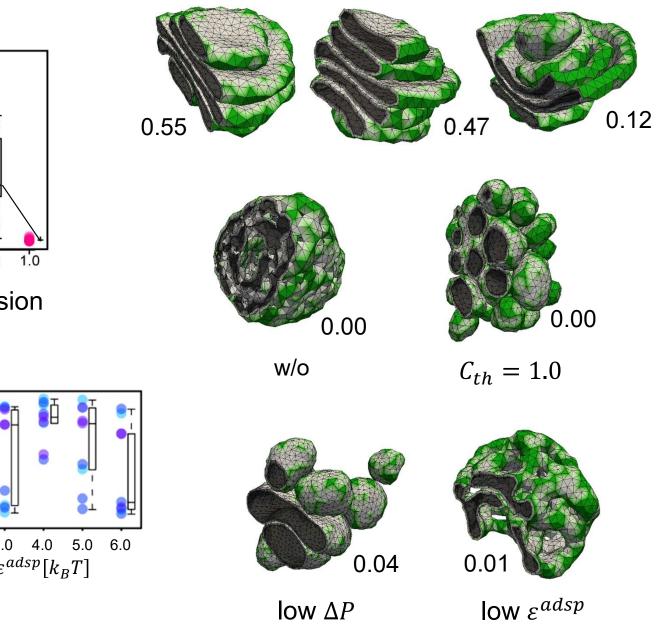
## Golgi formation dynamics



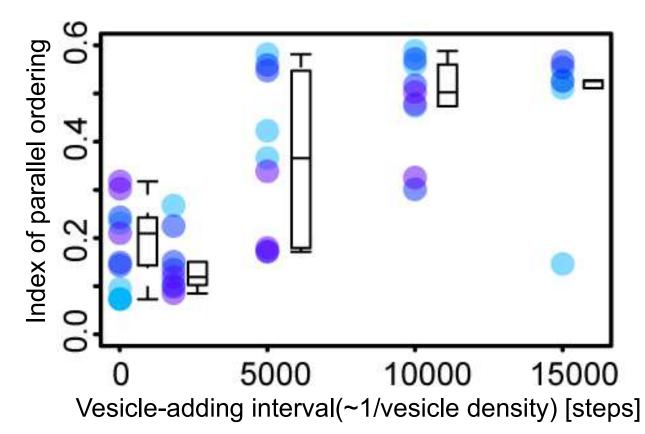
### order parameter statistics







## Aggregation speed is important

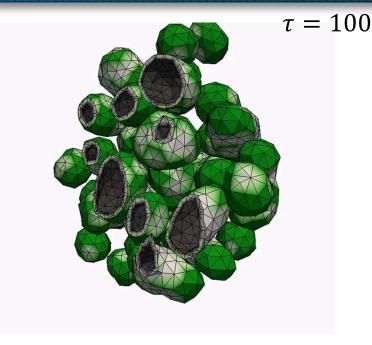


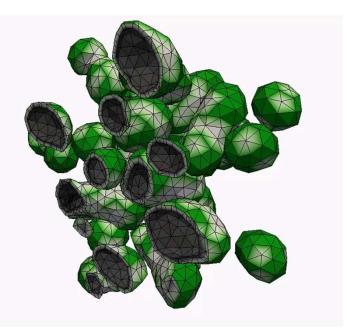
#### RESULT

Short interval aggregation (= high vesicle density) blocked clear layered structures

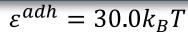
 $\Rightarrow$  shape relaxation after fusion is important.

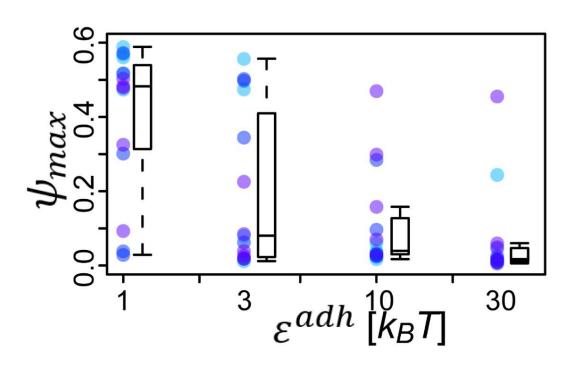
<u>Shape relaxation time scale < aggregation time scale</u>





# Adhesion energy (~ adhesion protein density)





#### RESULT

- High adhesion energy made nested structures.
- Adhesion energy should small enough not to change membrane shape.

#### Lee et al. (2014) PNAS

"Decrease in adhesion proteins made cisternae swell." "Adhesion energy may cause lumen compression."





### We created a recipe for **self-organization of Golgi body**.

We supposed **osmotic pressure, rim (curved membrane) stabilizer, fusion restriction** based on interphase Golgi shape, **which were enough.** (most reactions are equilibrium reactions.)

Self-organization of anisotropic layered structure from isotropic assembly of materials. **Anisotropy is formed in early stage.** 

Balances of time scales among vesicle aggregation, fusion and shape relaxation are necessary for formation of clear layered structures.

Acknowledgement

MT and Mochizuki (2017) PNAS

Prof. T. Kohyama, Shiga Univ.