

#### Methods for High Resolution Refinement in Single Particle Processing

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# Single Particle Reconstruction with EMAN

# GroEL

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EMAN: http://ncmi.bcm.tmc.edu/eman

# GroEL 2000 (15 Å)



5000 particles, JEOL 4000

# GroEL 2001 (11.5 Å)



5000 particles, JEOL 4000





30,000 particles, JEOL 2010F

# 







Jeol 3000

7 Days of imaging, 910 micrographs 1.06 Å/pix, Nikon 9000 scanner 135 used, 34,868 particles



























# Ca<sup>2+</sup> Release Channel

Irina Serysheva Wah Chiu Susan Hamilton



### Ca<sup>2+</sup> Release Channel

- SR membrane, triggered by DHPR in T-tubule
- Homotetramer
- ~2200 kDa
- Releases Ca<sup>++</sup> which initiates cross-bridge cycle

#### 200 kV image of ice-embedded RyR1 (no continuous CF)



### ~30 Å Resolution





# 20 Å Resolution



# 14 Å Resolution



### 9.6 Å Resolution







# Calcium Release Channel @9.6Å



#### Sequence assignment of observed helices



#### Sequence assignment of observed helices



#### CCD vs. Film


























# How do we get to Higher Resolutions?

- Get a better microscope
- Find a better microscopist
- Algorithm Improvements

#### **Contrast Transfer Function**

$$\overline{M}(s,\theta) = \overline{F}(s,\theta)C(s)E(s) + \overline{N}(s,\theta)$$

$$C(s) = \sqrt{1 - Q^2} \sin \gamma + Q \cos \gamma$$
  

$$\gamma = -\pi \left(\frac{1}{2}C_s\lambda^3 s^4 - \Delta Z \lambda s^2\right)$$
  

$$E(s) = e^{-Bs^2}$$
  

$$|N^2| = n_1 e^{n_2 s + n_3 s^2 + n_4 \sqrt{s}}$$

$$M(s)^{2} = F(s)^{2} C(s)^{2} E(s)^{2} + N(s)^{2}$$

# 8 Parameters

- $\Delta Z$  Defocus
- Q Amplitude Contrast
- B Gaussian Envelope Width
- k Signal Amplitude







## **CTF** Correction

$$\overline{T}(s,\theta) = \sum_{i} k_{i} \overline{M}_{i}(s,\theta)$$

$$k_{j}=?$$

- Maximize SNR of *T(s,q)*
- Minimize variance between T(s,q) and F(s,q)

#### **CTF** Correction



 $R_{i}(s) = \frac{C_{i}^{2}(s)E_{i}^{2}(s)}{N_{i}^{2}(s)}$ 

 $R(s) = \sum_{i} \frac{C_{i}^{2}(s)E_{i}^{2}(s)}{N_{i}^{2}(s)}$ 

#### Image Classification









← ? →



← ? →



#### Alignment/Registration



### Alignment/Registration



#### Alignment/Registration







# Measures of Similarity

- Correlation Coefficient
- Variance (transformed density)
- Variance (matched filter)
- Phase Residual
- Mutual Information
- etc.









### And the Answer is...

- Wiener filter particle
- Filter reference to match
- Normalize reference density to particle
- Calculate variance



#### Model Bias


















- Each particle -> best n classes
- More restrictive exclusion from class-avg

# The Future

- Better similarity criteria
- Improved CTF model
- Per-particle CTF (at least defocus)
- Beam tilt
- Better 3-D reconstruction
- New refinement methodologies