

## Advanced Applications in Solving Smoluchowski Equation

— Finite element Method Application

Yuhui Cheng

[ycheng@mccammon.ucsd.edu](mailto:ycheng@mccammon.ucsd.edu)

NBCR Summer School

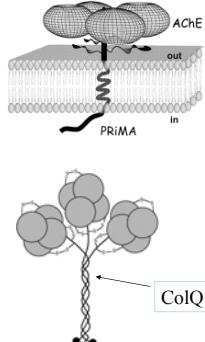
Aug. 10-11<sup>th</sup>, 2006

### Outline

- To apply the SSSE to study mAChE tetramers. conformations; visualization
- To introduce the reaction-determined reactive boundary conditions.
- Preliminary studies on the time-dependent SMOL solver and applications.
  - Analytical tests
  - mAChE monomer

### The Quaternary Association of AChE

- In mammalian CNS, AChE exists as an amphiphilic tetramer anchored to the membrane by a hydrophobic non-catalytic subunit (PRiMA)



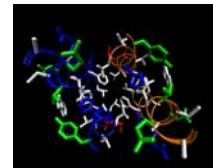
- In NMJ, AChE is an asymmetric form containing 1-3 tetramer associated with the basal lamina by a collagen-like structural subunit ColQ

### Dimer Interface

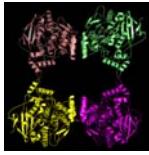
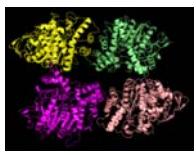
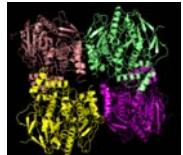
PDB:  
1J06  
1J07



- Four-helix bundle (371-383 and 525-541 in mouse sequence)
- Amphiphilic interface
- Weak affinity, only forms dimer at high concentration in solution

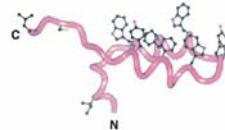


## Tetramer: Dimer of Dimers



- PDB: 1MAA
- Residues 549-583 deleted
- Only forms monomer or dimer in solution
- Dimer-dimer interaction similar to Fas2-AChE (omega loop = loop II), resulting in two occluded gorges
- PDB: 1C2O
- Trypsin released form of AChE from *E. electrocutor*
- Crystal grown at pH8 4°C
- Compact, square nonplanar
- four-helix bundle parallel
- two gorges partially blocked
- additional density for C-terminal t peptide observed, but not resolved.
- 1C2B(IEAA)
- pH6 20°C
- Loose, pseudo-square planar;
- anti-parallel
- all gorges open

## Heteromeric Association with PRAD



Giles, K. (1997) Protein Engineering, 6, 677-685

- t peptide sequence (40 or 41 res) highly conserved
- PRAD = Proline Rich Attachment Domain
- PRAD is required to form tetramer in solution

**ColQ<sub>+</sub> Mouse**

```
LPGLDQKRRG SHKACCLLMP PPPPLFPPPF FRGSRSPLLS PDMKNLLELE ASPSPCIQGS
LGSPPPPGQG PPGLIPGKTPG KGEKGDLGP GRKGKPGPPG VPGMPGPVGW PPEGPGRKEK
GDLGHMGGLPG SRGPMSKGF PGSRGEKGSR GERGDLGPKG EKGFPGPFGM LQQKGEMGPK
GESGLAGHRG PTGIPGKRGK QQQRGDSGIM GPHGKPGPSG QPGRQGPFGA PGPPSA
```

**PRMA<sub>-</sub> Mouse**

```
MLLRDLVPRH GCGWPSSLHH CALIFPLWGLV QVTHAEPKQS CSKVTDSCQH ICQCRPPPPL
PPPPPPPPPP RLLSAPAPNS TSCPDAEDSW SGLVIIIVAVV CASLVFLTVL VIICYKAIR
KPLRKDENGT SVAEYPMSSS QSHKGVDVNA
```

Bon, S., Coussen, F., Massoulie, J. (1997) JBC, 272, 3016-3021  
Bon, S. et al. (2004) Eur. J. Biochem., 271, 33-47

## A flexible Tetramer?

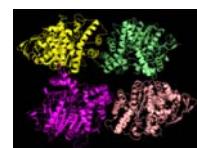


1C2B  
Flat square  
Quasi-planar

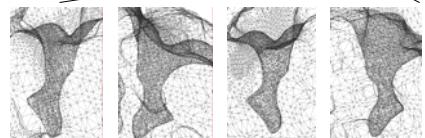
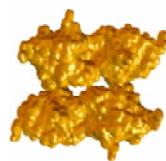


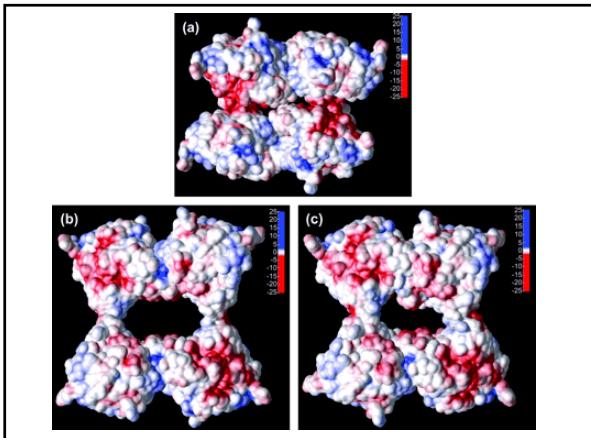
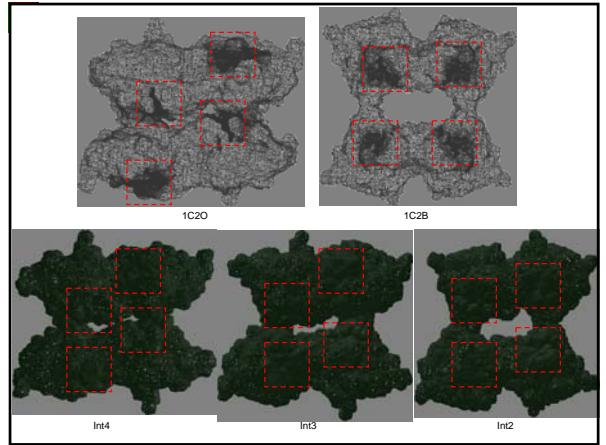
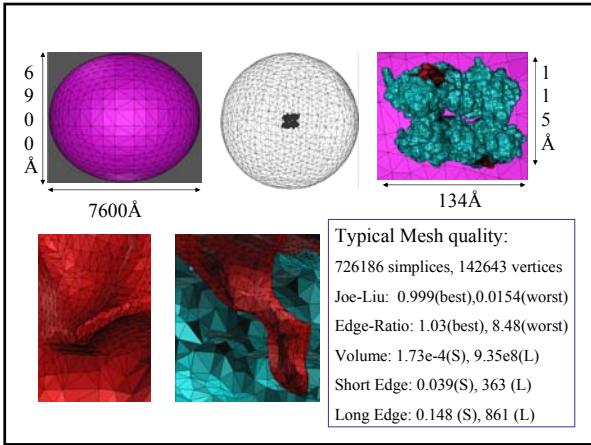
1C2O  
Compact

## Tetrahedral Mesh for mAChE Tetramer



Reactive surface is assigned according to previous studies on monomeric mAChE





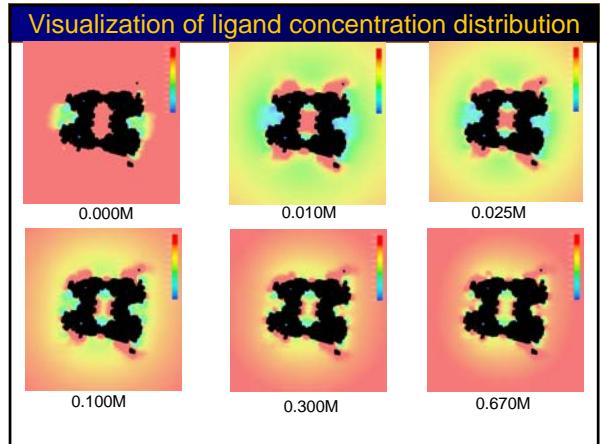
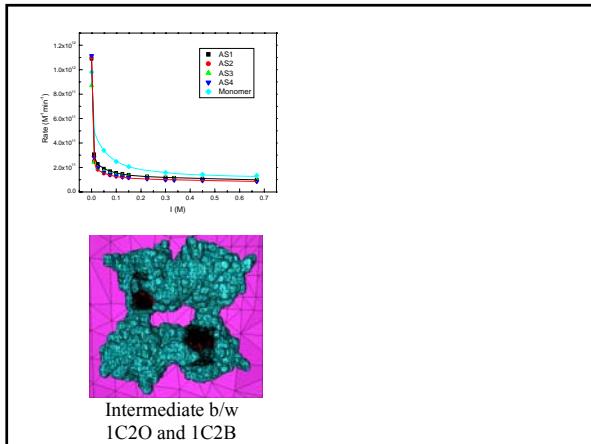
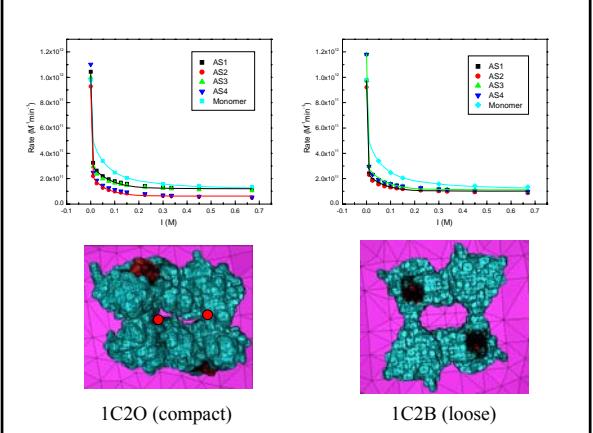
### PMF Calculation

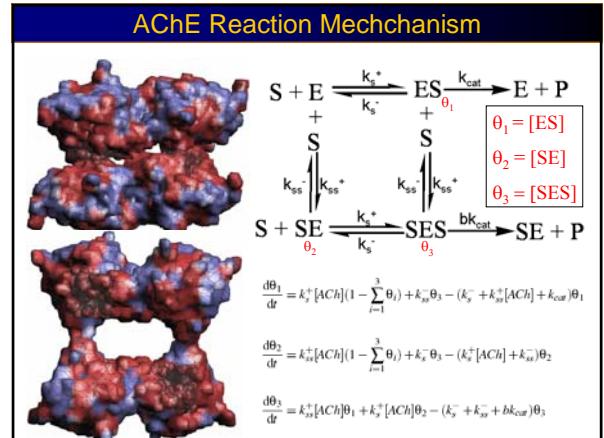
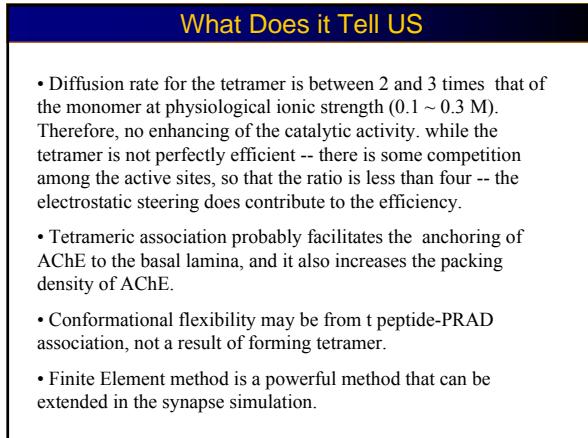
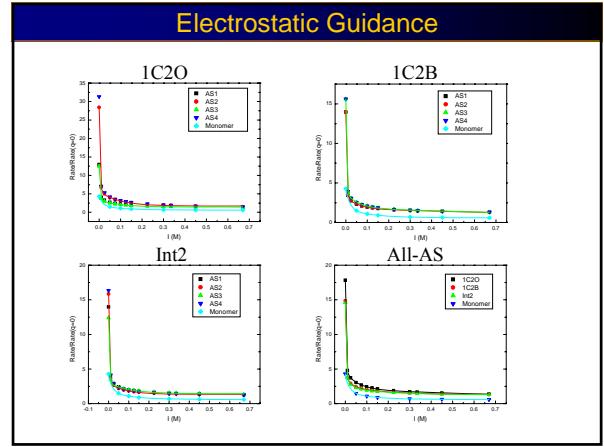
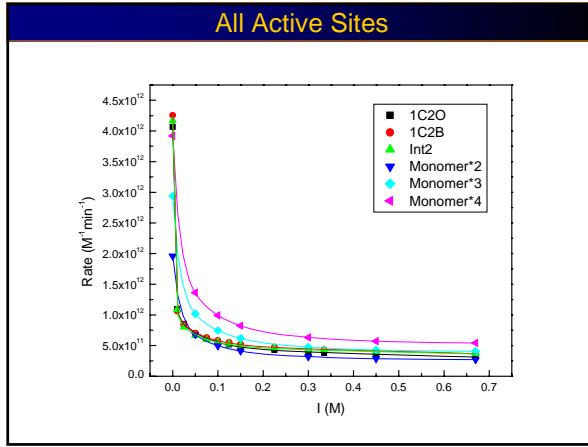
- APBS 0.4.0 (<http://agave.wustl.edu/>)
- Grid hierarchy (0-10)
- Apolar forces and dielectric boundary omitted
- No coupling b/w PMF and diffusing particle (Poisson-Nernst-Planck Eqn)
- No correlation b/w diffusing species

Grid#	$dx(\text{\AA})$	$dy(\text{\AA})$	$dz(\text{\AA})$	*x	*y	*z
0	0.44	0.38	0.38	-	-	-
1	0.89	0.78	0.80	2.0	2.0	2.0
2	1.33	1.16	1.20	1.5	1.5	1.5
3	2.00	1.73	1.80	1.5	1.5	1.5
4	3.00	2.60	2.71	1.5	1.5	1.5
5	4.49	3.91	4.07	1.5	1.5	1.5
6	6.73	5.87	6.11	1.5	1.5	1.5
7	10.11	8.80	9.16	1.5	1.5	1.5
8	15.16	13.20	13.73	1.5	1.5	1.5
9	22.73	19.80	20.60	1.5	1.5	1.5
10	34.09	29.71	30.89	1.5	1.5	1.5

## SSSE Solver Details

- Based on Mike Holst's Fetk (<http://www.fetk.org>)
- Diffusing particle (based on TFK+):  $q = +1e$ ,  $R=2.0 \text{ \AA}$ ,  $D = 78000 \text{ \AA}^2/\mu\text{s}$
- Ionic strengths: 0.00, 0.01, 0.05, 0.10, 0.20, 0.300, 0.450, and 0.670 M.
- Reactive surface is assigned with zero Dirichlet boundary condition (perfectly absorbing)
- $p_{bulk} = 1.0 \text{ M}$





## Reaction defined Boundary Conditions

$$\hat{n} \cdot D\nabla p_{ACh}(r,t|r_0,t_0) = \begin{cases} -k'_{act, AChe} [k_s^+ (1 - \sum_{i=1}^3 \theta_i) p_{ACh} - \frac{k_s^- \theta_1}{[ACh]_0}], & \text{on } \partial\Omega_{AChe}^{\text{act}} \\ 0, & \text{otherwise} \end{cases}$$

Find  $p_{ACh} \in V \subset H^1$  such that

$$\langle F(p_{ACh}), v \rangle = 0 \quad \forall v \in V,$$

where

$$\begin{aligned} \langle F(p_{ACh}, v) \rangle &= \int_{\Omega} (D\nabla p_{ACh} \cdot \nabla v + \frac{\partial p_{ACh}}{\partial t} v) dx \\ &\quad - \int_{\Omega_{AChe}^{\text{act}}} (-k'_{act, AChe} [k_s^+ (1 - \sum_{i=1}^3 \theta_i) p_{ACh} - \frac{k_s^- \theta_1}{[ACh]_0}]) dS \end{aligned}$$

## From SSSE to TDSE

$$\frac{\partial p(\vec{r}, t | \vec{r}_0, t_0)}{\partial t} = -\nabla \cdot D e^{-\beta U(\vec{r})} \nabla e^{\beta U(\vec{r})} p(\vec{r}, t | \vec{r}_0, t_0)$$

**SSSE:**

$$\int_{\Omega} \nabla v(\vec{r}) \cdot \bar{J}p(\vec{r}) d\vec{r}^3 - \int_{\Gamma_a} v(s) \alpha(s) p(s) ds - \int_{\Gamma_b} v(s) \bar{J}p(s) \cdot \bar{n}(s) ds = 0$$

**TDSE:**

$$\int_{\Omega} (\nabla v(\vec{r}) \cdot \bar{J}p(\vec{r}) + \frac{dp}{dt}) d\vec{r}^3 - \int_{\Gamma_a} v(s) \alpha(s) p(s) ds - \int_{\Gamma_b} v(s) \bar{J}p(s) \cdot \bar{n}(s) ds = 0$$

$$Au + \frac{M}{dt} (u - u^0) + Fu = 0$$

## Three schemes to do timestep marching

$$u_{n+1} = e^{-dt*M^{-1}*A} u_n \cong \frac{M - (1-\theta)*dt*A}{M + \theta*dt*A} u_n$$

1. Forward (explicit) Euler scheme

$$|1 - dt*M^{-1}*A| \leq 1, \theta = 0$$

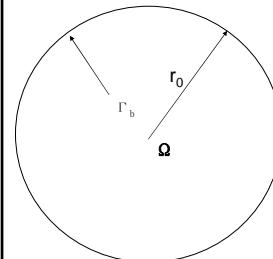
2. Backward (implicit) Euler scheme (unconditional stable)

$$|1 + dt*M^{-1}*A| \geq 1, \theta = 1$$

3. Crank-Nicholson (implicit) scheme (unconditional stable)

$$|2 + dt*M^{-1}*A| \geq |2 - dt*M^{-1}*A|, \theta = 0.5$$

## Analytical test



When the potential inside the sphere and the radius of the inner sphere are zero, the analytical solution can be easily written as below:

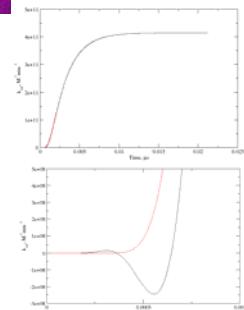
$$\left\{ \begin{array}{l} \frac{\partial p(r; t)}{\partial t} - D \Delta_3 p(r; t) = 0 \\ p(r; 0) = 0 \\ p(r_0; t) = p_{bulk} \end{array} \right.$$

$$p(r; t) = p_{bulk} + \frac{2p_{bulk}r_0}{\pi r} \sum_{n=1}^{\infty} \frac{(-1)^n}{n} \sin \frac{n\pi r}{r_0} \exp \left\{ -D \left( \frac{n\pi}{r_0} \right)^2 t \right\}$$

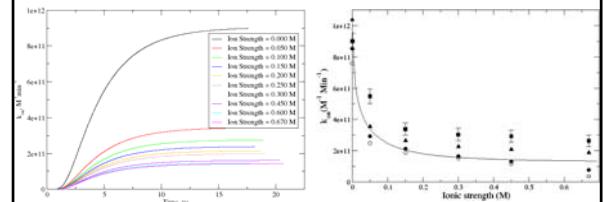
## Analytical test



- Vertex number: 109,478
- Simplex number: 629,760
- Vertex number: 857,610
- Simplex number: 5,038,080
- Inner radius: 10 Å
- Outer radius: 50 Å
- Time step: 5 ps



## TDSE on the mAChE monomer



- ✓ At zero ion-strength, the whole system need nearly 20 μ s to reach steady state, and the higher ion strength, the shorter time need to reach steady state.
- ✓ The steady state deriving from the TDSE is very close to the corresponding SSSE results.

## Acknowledgements

Prof. J. Andrew McCammon

Dr. David Zhang

Dr. Jason Suen

The McCammon group

**Washington University, St. Louis**

Prof. Nathan A. Baker

Dr. Yuhua Song

**University of Texas, Austin**

Prof. Chandrajit L. Bajaj

Yongjie (Jessica) Zhang

**UCSD, Mathematics**

Prof. Mike Holst