Simulación de Sistemas a la Nanoescala

Formación de un canal proteico en una membrana

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Introducción



Canal específico de K

Sistema que simular

Componente de la membrana lipídica

Introducción

Principales herramientas



MAD

Theoretical and Computational Biophysics Group
NIH Resource for Macromolecular Modeling and Bioinformatics
University of Illinois at Urbano-Champaign

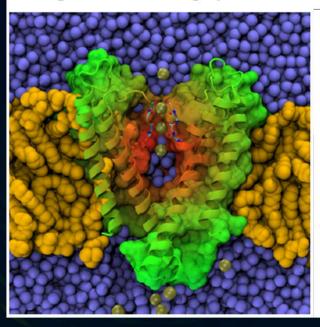
- R. Brunner, E. Caddigan, J. Cohen, A. Dalke, P. Grayson,
- J. Gullingsrud. D. Hardy. W. Humphrey. B. Isralewitz, S. Izrailev.
- A. Kohlmeyer, D. Norris, J. Saam, J. Stone, J. Ulrich, K. Vandivort

NAMD

Introducción

Fuente de apoyo

University of Illinois at Urbana-Champaign Beckman Institute for Advanced Science and Technology Theoretical and Computational Biophysics Group Computational Biophysics Workshop



Alek Aksimentiev
Marcos Sotomayor
David Wells
Current editor:
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\$sel writepdb KCSA-B.pdb

Obtención de ficheros .pdb y .psf

Primero abrir VMD # Cargar y guardar segmento A mol new 1k4c.pdb set sel [atomselect top "all"] \$sel set segname A \$sel writepdb KCSA-A.pdb # Hacemos segmento B set sel [atomselect top "all and not name K"] \$sel set segname B \$sel move {{-1.0 0.0 0.0 310.66} {0.0 -1.0 0.0 310.66}} {0.0 0.0 1.0 0.0} {0.0 0.0 0.0 0.0 1.0}}

```
# Proteinas

foreach S { A B C D } {

set seg [atomselect top "segname $S and chain C and protein"]

$seg writepdb seg$S.pdb

$seg delete
}

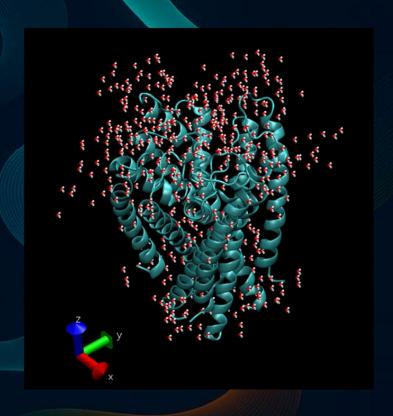
# Iones

set pot [atomselect top "name K and resid 3001 3003 3005 3006"]

$pot set name POT

$pot set resname POT

$pot writepdb pot.pdb
```



Tratamiento del Sistema

Código 3

Membrana

\$popc moveby [vecinvert [measure center
\$popc weight mass]]

\$popc writepdb PT.pdb

Canal, primera línea es seleccionar el centro de la proteína

set vest [atomselect \$mol "protein and resid 97 to 106"]

\$k moveby [vecinvert [measure center \$vest weight mass]]

\$k writepdb KT.pdb

Código 4

mol delete all

resetpsf

readpsf Mb.psf

coordpdb PT.pdb

readpsf../2Solvatacion/ProtSol.psf

coordpdb KT.pdb

writepsf K_Mb_Raw.psf

writepdb K_Mb_Raw.pdb

Código 5

Selección de lípidos

set bl [atomselect top "name Pl and beta > 0"]

set segll [\$bl get segid]

set resll [\$bl get resid]

Selección de aguas

set bw [atomselect top "name OH2 and beta > 0"]

set seglw [\$bw get segid]

set reslw [\$bw get resid]

Creación del Sistema (después de cargar el sistema de nuevo y reseteado los psf

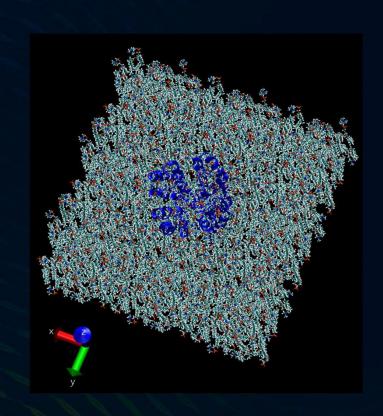
foreach segid \$segll resid \$resll {delatom \$segid \$resid}

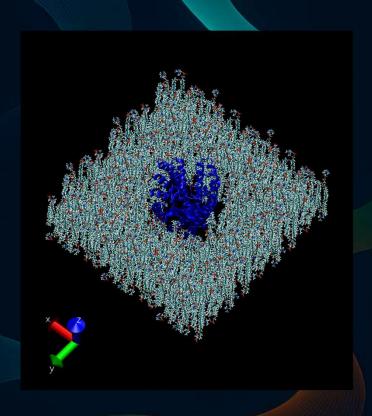
foreach segid \$seglw resid \$reslw {delatom \$segid \$resid}

writepsf K_Mb.psf

writepdb K_Mb.pdb

Tratamiento del Sistema





Simulaciones

Código 6

Indicar ficheros

mol new ../input/K_Mb.psf

mol addfile ../input/K_Mb.pdb

set all [atomselect top "all"]

\$all set beta 0

set fixed [atomselect top "water or name CLA POT or protein or (chain L / and name O2 P1 O3 O4 O1 C15 H52 H51 H11 C11 H12 N C14 H42 H43 H41 / C12 H22 H23 H21 C13 H33 H31 H32)"]

\$fixed set beta 1

 $\$ all\ writepdb\ K_Mb.fix$

Fichero melting.conf

Encontrar el origen de la celda

set all [atomselect top all]

measure center \$all

Encontrar Vectores de la base

set all [atomselect top all]

measure minmax \$all

Los valores que nos dan los restas y obtienes el valor total del vector

Valor de la red de un sistema periódico electrostático: Debe ser mayor al vector de la red y múltiplo de 2, 3 o 5.

Error

ERROR: Constraint failure in RATTLE algorithm for atom 37189!
ERROR: Constraint failure; simulation has become unstable.
ERROR: Constraint failure in RATTLE algorithm for atom 36408!
ERROR: Constraint failure; simulation has become unstable.
ERROR: Constraint failure in RATTLE algorithm for atom 17627!
ERROR: Constraint failure; simulation has become unstable.
ERROR: Constraint failure in RATTLE algorithm for atom 17210!
ERROR: Constraint failure; simulation has become unstable.
ERROR: Constraint failure in RATTLE algorithm for atom 13913!
ERROR: Constraint failure; simulation has become unstable.
ERROR: Constraint failure in RATTLE algorithm for atom 3828!
ERROR: Constraint failure; simulation has become unstable.
FATAL ERROR: Exiting prematurely; see error messages above.
[Partition 0][Node 0] End of program

Conclusiones

Estado Final del Trabajo



No he conseguido efectuar las simulaciones propuestas del flujo de iones por temas de tiempo y errores.



He aprendido comandos nuevos y métodos de trabajo en el campo de las simulaciones de sistemas nanométriocos diferentes a los vistos en clase.



