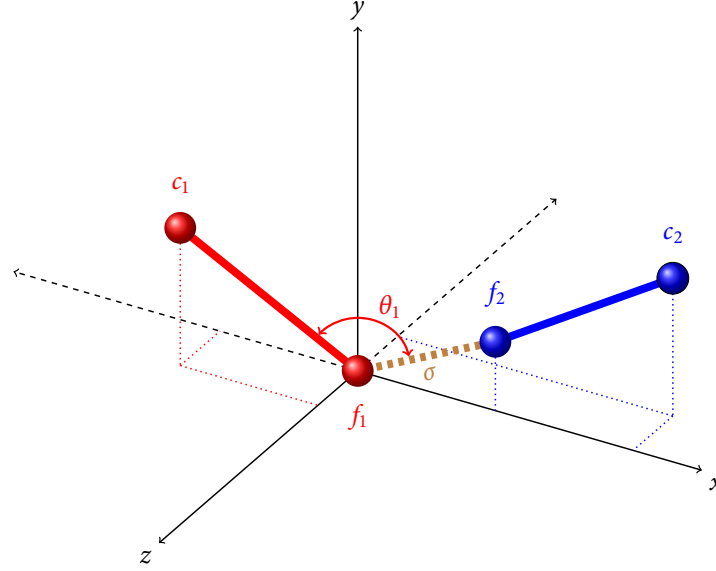


# 1 Theta



*Definitions:*

$\hat{\mathbf{v}} = \mathbf{f}_1 - \mathbf{c}_1$ , the center of mass to reacting interface vector for reactant molecule 1

$\hat{\sigma} = \mathbf{f}_2 - \mathbf{f}_1$ , vector between the two reacting interfaces

$\theta$ : angle between the  $\hat{\mathbf{v}}$  and  $\hat{\sigma}$

angle range:  $[0, \pi]$

*Procedure:*

Note that each reacting molecule is associated to a separate  $\theta$  angle. The indices 1 and 2 refer to the molecule to whom the  $\theta$  angle belongs to and the other molecule, respectively.

1. Determine angle to rotate each complex by

- (a) Calculate current angle,  $\theta_{\text{curr}}$

$$\theta_{\text{curr}} = \arccos\left(\frac{\hat{\mathbf{v}} \cdot \hat{\sigma}}{|\hat{\mathbf{v}}||\hat{\sigma}|}\right)$$

- (b) Determine difference from the target angle,  $\theta_{\text{targ}}$ ,  $\theta_{\text{rot}} = \theta_{\text{targ}} - \theta_{\text{curr}}$

- (c) Determine the angle to rotate each complex by (the complexes are rotated in opposite directions), according to their diffusion rotation constants,

$$\theta_{\text{pos.}} = \begin{cases} \frac{1}{2}(\theta_{\text{targ}} - \theta_{\text{curr}}) & \text{if } Dr_z^{\text{dom.}} = 0 \\ \frac{Dr_z}{Dr_{\text{tot}}}(\theta_{\text{targ}} - \theta_{\text{curr}}) & \text{if } Dr_z^{\text{dom.}} \neq 0 \end{cases}$$

$$\theta_{\text{neg.}} = \begin{cases} -\theta_{\text{pos.}} & \text{if } Dr_z^{\text{inf.}} = 0 \\ \frac{Dr_z}{Dr_{\text{tot}}}(\theta_{\text{targ}} - \theta_{\text{curr}}) & \text{if } Dr_z^{\text{inf.}} \neq 0 \end{cases}$$

- (d) If  $\theta_{\text{targ.}} - \theta_{\text{curr.}} < 1e^{-8}$ , no rotation is done for this angle.

2. Determine rotation axis (this could probably be simplified to just use  $\hat{\mathbf{x}}$  or  $\hat{\mathbf{y}}$  instead of  $\hat{\mathbf{v}} \times \hat{\mathbf{x}}$  or  $\hat{\mathbf{v}} \times \hat{\mathbf{y}}$ ),

$$\hat{\mathbf{u}} = \begin{cases} \hat{\mathbf{v}} \times \hat{\mathbf{x}} & \text{if } (\theta_{\text{curr.}} = 0 \parallel \theta_{\text{curr.}} = \pi) \ \& \ (\hat{\mathbf{v}} \cdot \hat{\mathbf{x}} \neq 0 \ \& \ \hat{\mathbf{v}} \cdot \hat{\mathbf{x}} \neq \pi) \\ \hat{\mathbf{v}} \times \hat{\mathbf{y}} & \text{if } (\theta_{\text{curr.}} = 0 \parallel \theta_{\text{curr.}} = \pi) \ \& \ (\hat{\mathbf{v}} \cdot \hat{\mathbf{x}} = 0 \parallel \hat{\mathbf{v}} \cdot \hat{\mathbf{x}} = \pi) \\ \hat{\sigma} \times \hat{\mathbf{v}} & \text{otherwise} \end{cases}$$

3. Set up rotation quaternions, which are then normalized,

$$Q_{\text{pos.}} = \cos\left(\frac{\theta_{\text{pos.}}}{2}\right) + \left[\sin\left(\frac{\theta_{\text{pos.}}}{2}\right) * \hat{\mathbf{u}}_x\right] \hat{\mathbf{i}} + \left[\sin\left(\frac{\theta_{\text{pos.}}}{2}\right) * \hat{\mathbf{u}}_y\right] \hat{\mathbf{j}} + \left[\sin\left(\frac{\theta_{\text{pos.}}}{2}\right) * \hat{\mathbf{u}}_z\right] \hat{\mathbf{k}}$$

$$Q_{\text{neg.}} = \cos\left(\frac{\theta_{\text{neg.}}}{2}\right) + \left[\sin\left(\frac{\theta_{\text{neg.}}}{2}\right) * \hat{\mathbf{u}}_x\right] \hat{\mathbf{i}} + \left[\sin\left(\frac{\theta_{\text{neg.}}}{2}\right) * \hat{\mathbf{u}}_y\right] \hat{\mathbf{j}} + \left[\sin\left(\frac{\theta_{\text{neg.}}}{2}\right) * \hat{\mathbf{u}}_z\right] \hat{\mathbf{k}}$$

4. Iterate over all vectors, (dominant interface)-(x), where x is every other center of mass/interface coordinate, and rotate with  $Q_{\text{pos.}}$  for the dominant complex and  $Q_{\text{neg.}}$  for the inferior complex,

$$\hat{\mathbf{v}}_{\text{rot.}} = Q_i (\hat{\mathbf{v}}) Q_i^{-1}$$

- When doing this,  $\hat{\mathbf{v}}$  is a quaternion with w component of 0.
- $Q^{-1}$  is the inverse quaternion,

$$Q^{-1} = \frac{[Q_w - Q_x \hat{\mathbf{i}} - Q_y \hat{\mathbf{j}} - Q_z \hat{\mathbf{k}}]}{|Q|}$$

- Quaternion multiplication:

$$Q_{\text{new}} = [(Q_{1,w} * Q_{2,w}) - (Q_{1,x} * Q_{2,x}) - (Q_{1,y} * Q_{2,y}) - (Q_{1,z} * Q_{2,z})]$$

$$+ [(Q_{1,w} * Q_{2,x}) + (Q_{1,x} * Q_{2,w}) + (Q_{1,y} * Q_{2,z}) - (Q_{1,z} * Q_{2,y})] \hat{\mathbf{i}}$$

$$+ [(Q_{1,w} * Q_{2,y}) + (Q_{1,y} * Q_{2,w}) + (Q_{1,z} * Q_{2,x}) - (Q_{1,x} * Q_{2,z})] \hat{\mathbf{j}}$$

$$+ [(Q_{1,w} * Q_{2,z}) + (Q_{1,z} * Q_{2,w}) + (Q_{1,x} * Q_{2,y}) - (Q_{1,y} * Q_{2,x})] \hat{\mathbf{k}}$$

## 2 Phi

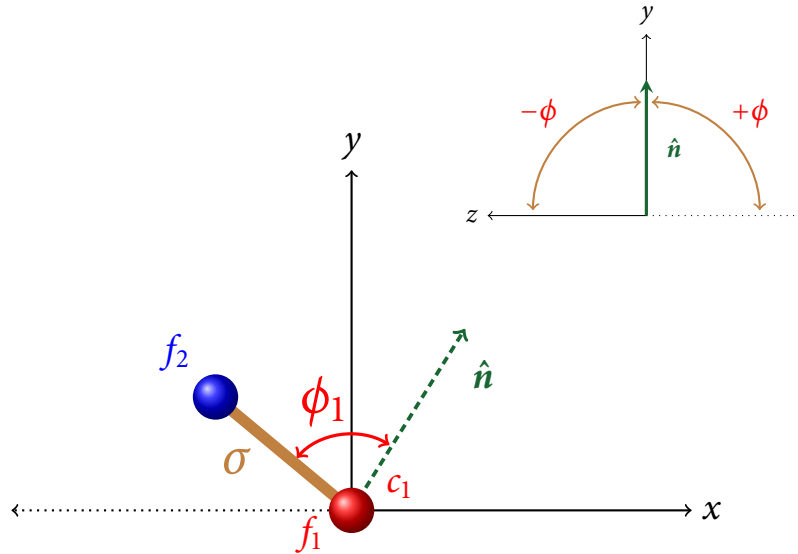


Figure 1: Definition of phi angle, the dihedral (torsion) angle between a predefined vector,  $\hat{n}$  and the interface to interface vector,  $\hat{\sigma}$ . The sign of the angle is determined by the position of vector  $\hat{n}$  relative to vector  $\hat{\sigma}$ , shown in the inset.

*Definitions:*

$\hat{\sigma} = f_2 - f_1$ , the vector between the two reacting interfaces

$\hat{n}$ : normal of the molecule, as given by the user (usually the  $z$  or  $y$  principle axis)

$\phi_i$ : dihedral angle between  $\hat{\sigma}$  and  $\hat{n}$

angle range:  $[\pi, -\pi]$

*Procedure:*

Note that each reacting molecule is associated to a separate  $\phi$  angle. The indices 1 and 2 refer to the molecule to whom the  $\phi$  angle belongs to and the other molecule, respectively.

1. Determine the current angle,  $\phi_{\text{curr}}$ , through an orthographic projection onto the  $xy$  plane

(a) Transform the molecule such that the axis of rotation,  $\hat{v}$ , is aligned with the  $z$  axis

- Get angle between the current  $\hat{\sigma}$  and the  $z$  axis,

$$\chi = \arccos\left(\frac{\hat{\sigma} \cdot \hat{z}}{|\hat{\sigma}||\hat{z}|}\right)$$

- Get the rotation axis,  $\hat{u} = \hat{\sigma} \times \hat{z}$
- Create quaternion and rotate,

$$Q = \cos\left(\frac{\chi}{2}\right) + \left[\sin\left(\frac{\mu_1}{2}\right) * \hat{u}_x\right] \hat{i} + \left[\sin\left(\frac{\mu_1}{2}\right) * \hat{u}_y\right] \hat{j} + \left[\sin\left(\frac{\mu_1}{2}\right) * \hat{u}_z\right] \hat{k}$$

(b) In the transformed coordinate system, get the two vectors,  $\hat{\sigma}$  and  $\hat{n}$ . The vector  $\hat{n}$  must be determined through a rotation to fit the coordinates to the provided molecule template internal coordinates, to obtain the current orientation (a dummy particle would be too computationally expensive).

- i. Center the molecule to origin  $(0, 0, 0)$  by subtracting all coordinates by the center of mass.
- ii. Get the angle  $(\mu_1)$  between  $\hat{\mathbf{f}}_{\text{curr.}} = \mathbf{f}_{\text{curr.}} - \mathbf{c}_{\text{curr.}}$ , the current center of mass to reacting interface vector, and  $\hat{\mathbf{f}}_{\text{targ.}} = \mathbf{f}_{\text{targ.}} - \mathbf{c}_{\text{targ.}}$ , the center of mass to reacting interface vector provided by the user
- iii. Create the rotation quaternion,

$$Q_1 = \cos\left(\frac{\mu_1}{2}\right) + \left[\sin\left(\frac{\mu_1}{2}\right) * \hat{\mathbf{u}}_x\right] \hat{\mathbf{i}} + \left[\sin\left(\frac{\mu_1}{2}\right) * \hat{\mathbf{u}}_y\right] \hat{\mathbf{j}} + \left[\sin\left(\frac{\mu_1}{2}\right) * \hat{\mathbf{u}}_z\right] \hat{\mathbf{k}}$$

where  $\hat{\mathbf{u}} = \hat{\mathbf{f}}_{\text{targ.}} \times \hat{\mathbf{f}}_{\text{curr.}}$ .

- iv. Rotate the molecule using this quaternion, as described above.
- v. If the molecule has more than one interface, repeat this process using the second interface, obtaining  $Q_2$ .
- vi. Return the quaternion,

$$Q_{\text{rot}}^{\hat{\mathbf{n}}} = \begin{cases} Q_1 & \text{if interfaces} = 1 \\ Q_2 Q_1 & \text{otherwise} \end{cases}$$

- vii. Rotate the provided normal with  $Q_{\text{rot}}^{\hat{\mathbf{n}}}$  to obtain the current normal,  $\hat{\mathbf{n}}$

(c) Still in the transformed coordinate system, project  $\hat{\boldsymbol{\sigma}}$  and  $\hat{\mathbf{n}}$  onto the  $xy$  plane. For example,

$$\hat{\boldsymbol{\sigma}}_{\text{proj.}} = \begin{bmatrix} 1 & 0 & 0 \\ 0 & 1 & 0 \\ 0 & 0 & 0 \end{bmatrix} \begin{bmatrix} \hat{\sigma}_x \\ \hat{\sigma}_y \\ \hat{\sigma}_z \end{bmatrix} = \begin{bmatrix} \hat{\sigma}_x \\ \hat{\sigma}_y \\ 0 \end{bmatrix}$$

- (d) Get  $\phi$  by the dot product,

$$\phi = \arccos\left(\frac{\hat{\boldsymbol{\sigma}}_{\text{proj.}} \cdot \hat{\mathbf{n}}_{\text{proj.}}}{|\hat{\boldsymbol{\sigma}}_{\text{proj.}}| |\hat{\mathbf{n}}_{\text{proj.}}|}\right)$$

2. Do steps 1b through 4 for the  $\theta$  rotation, replacing all angle calculations with the above procedure for  $\phi$

### 3 Omega

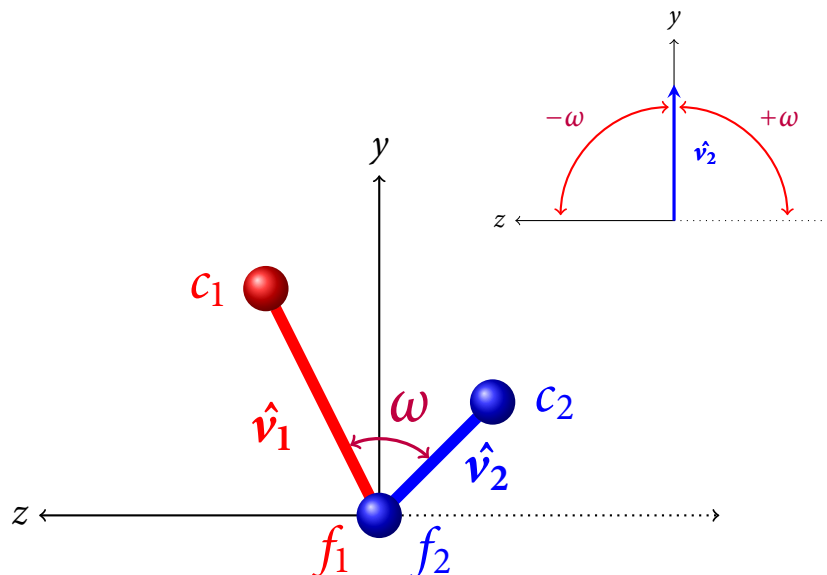


Figure 2: Definition of omega angle, comprised of the two reacting interface to center of mass vectors ( $\hat{v}_1$  and  $\hat{v}_2$ ) for each molecule. The sign of the angle is determined by the position of vector  $\hat{v}_1$  relative to vector  $\hat{v}_2$ , shown in the inset.

*Definitions:*

$\hat{v}_1$ :  $f_1 - c_1$ , center of mass to reacting interface vector for reactant molecule 1

$\hat{v}_2$ :  $f_2 - c_2$ , center of mass to reacting interface vector for reactant molecule 2

$\hat{n}_1$ : the normal of reactant molecule 1, provided by the user

$\hat{n}_2$ : the normal of reactant molecule 2, provided by the user

$\hat{\sigma}$ :  $f_2 - f_1$ , vector between the two reacting interfaces (current complex's interface to other complex's interface)

$\omega$ : dihedral between the  $\hat{v}_1$  and  $\hat{v}_2$ , or the dihedral between the normals of the two reacting molecules

angle range:  $[\pi, -\pi]$

*Procedure:*

1. Follows the same procedure for the  $\phi$  rotation, replacing  $\hat{n}$  and  $\hat{\sigma}$  with one of two sets of vectors:

$$\begin{cases} \hat{n}_1, \hat{n}_2 & \text{if } \theta_1 = \pi \parallel \theta_2 = \pi \\ \hat{v}_1, \hat{v}_2 & \text{otherwise} \end{cases}$$

This is necessary since if either  $\theta$  angle is equal to  $\pi$ , the dihedral between  $\hat{v}_1$  and  $\hat{v}_2$  is undefined, but an equivalent dihedral could still be necessary to properly align the two molecules (such as in the case of two planar clathrins associating)