#### Articulated-Body Forward Dynamics, Adaptive Dynamics ... & Proteins

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#### Motion



**Dynamics**: The branch of physics that treats the action of force on bodies in motion or at rest; kinetics, kinematics, and statics, collectively.

-- Webster Dictionary







#### **Molecular Dynamics**



 $O(n^2)$ 



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### **Forward Dynamics**

•A system of rigid bodies ...



•Bodies are connected together by joints & are acted on by various forces



Body positions, velocities, & acceleration-independent forces are known
The only unknown quantities are the accelerations and the kinematic constrain forces – Forward Dynamics problem



 $\mathbf{a}_i$ 

Φ

 $\Phi_{ij}$ f<sub>i</sub>

b

#### Featherstone: An Expression for the Acceleration of Bodies

$$\begin{bmatrix} \mathbf{a}_1 \\ \mathbf{a}_2 \\ \vdots \\ \mathbf{a}_m \end{bmatrix} = \begin{bmatrix} \Phi_1 & \Phi_{12} & \cdots & \Phi_{1m} \\ \Phi_{21} & \Phi_2 & \cdots & \Phi_{2m} \\ \vdots & \vdots & \ddots & \vdots \\ \Phi_{m1} & \Phi_{m2} & \cdots & \Phi_m \end{bmatrix} \begin{bmatrix} \mathbf{f}_1 \\ \mathbf{f}_2 \\ \vdots \\ \mathbf{f}_m \end{bmatrix} + \begin{bmatrix} \mathbf{b}_1 \\ \mathbf{b}_2 \\ \vdots \\ \mathbf{f}_m \end{bmatrix}$$

- = Spatial Acceleration of handle *i* 
  - = Articulated Body Inertia of handle *i*
  - = Cross-coupling inverse inertia between handles *i* & *j*
  - = External force applied to handle /
  - = Bias Acceleration of handle / (acceleration it would have if all external forces would zero).

#### Featherstone: Recursive Binary Assembly of Mechanism



#### **Featherstone: Connecting Two Articulated Bodies**



#### Featherstone: Branching, Link Splitting, Loops







#### Featherstone: Branching & Loops – Nonsingular Matrix



#### Which leads to a numerical solution



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#### **Redon – ADAPTIVE Dynamics**



Active region is composed of nodes which are simulated Force update regions contains the internal nodes which are directly influenced by an external force or an active joint force Update region is the union of the active region and the force update region

Determine the acceleration update region whose nodes matter the most according to an **Acceleration Metric** 



#### **For Proteins?**



-Automatic Generation of efficient assembly trees -A "dynamic" protein: bond breaking



### References

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