Chapter 3

- Applications of Newton's Laws in 1 dimension
 - Free Fall
 - Motion in a Fluid
 - Spring motion
 - Molecular Dynamics

Free fall

- Acceleration = $g = 9.8 \text{ m/s}^2 = \text{constant}$
- Constant acceleration implies constant force = weight
- Be careful when there is air friction then acceleration is not constant and a terminal velocity results



Constant acceleration Kinematics

If acceleration is constant then the average acceleration
= constant (instantaneous acceleration)

Then
$$a = \frac{d\mathbf{v}}{dt} = \frac{\Delta \mathbf{v}}{\Delta t}$$
 and $\mathbf{v}_f = \mathbf{v}_o + a\Delta t$

- Also $\int dv = \int a dt \rightarrow same result$
- Also, from the v_x vs t graph, the area under the line gives the displacement so

$$\Delta x = \mathbf{v}_o \Delta t + \frac{1}{2} a \Delta t^2$$



• We can get this result by integrating again also: $\Delta x = \int dx = \int v dt = \int [v_o + at] dt = v_o t + \frac{1}{2} at^2$ Eliminating ∆t from the first two boxed equations we get one more:

$$\mathbf{v}_f^2 = \mathbf{v}_o^2 + 2a\Delta x$$

Example problems

Motion in a Viscous Fluid



We'll discuss the buoyant force later

For now we focus on the friction force

The Reynolds number governs what happens: $\Re = \frac{L\rho v}{\eta}$. where L is the characteristic size of the object, ρ its density and η its

where L is the characteristic size of the object, ρ its density and η its viscosity.

For large Reynolds numbers, the flow is turbulent and the frictional force can often be written as $(\Re >> 1)$

$$F_f = \frac{1}{2} C \rho A v^2,$$

where $C \sim 1$



Notion of effective area – reduce to minimize friction resistance

Terminal velocity

• Returning to our falling object:

 $mg - F_B - F_f = ma$

• Soon after release, the object will have zero acceleration and a terminal velocity given by inserting the friction force and setting a = 0: $v_{term} = \sqrt{\frac{2(mg - F_B)}{C \rho A}}$.

Small Reynolds number

- The other limit is when the Reynolds number is very small – laminar flow – can occur for very small objects or larger viscosities
- The frictional force is linear in v and given by $F_f = f v$ $f = 6\pi\eta r$ for a sphere
- Bacterial motion is governed by this force

Another one-dimensional motion problem - springs





 $v = dx/dt = -A\omega \sin(\omega t)$





Springs 3

$$a = -\frac{k}{m}x = -\left(\frac{2\pi}{T}\right)^2 x = -\omega^2 A \cos \omega t \qquad a = -a_{\max} \cos \omega t$$

time (s)

$$f = \frac{1}{T} = \frac{1}{2\pi} \sqrt{\frac{k}{m}}.$$

Spring Problem

- P28 in text: Attached to a spring on a frictionless table top, a 1 kg mass is observed to undergo simple harmonic motion with a period of 2.5 s after stretching the spring. The spring is then held vertically and a 0.2 kg mass is attached.
- Find the distance the spring is stretched.
- If the spring is then stretched an additional 5 cm and released, find the period of the subsequent motion.
- What is the maximum acceleration of the 0.2 kg mass?
- What is its maximum velocity?

Elasticity of Solids



Shear /Pressure





Strength of Biomaterials



Collagen fibers – triple helix

Themes: filament subunits \rightarrow composites filaments \rightarrow fibers \rightarrow fiber bundle \rightarrow muscle



Fluids/Gels



Fluid/Gel systems behave differently



Molecular Dynamics



How do all the atoms of this hemoglobin molecule move around in time?

They undergo random thermal motions, known as diffusion, and each atom responds to all the forces acting on it according to Newton's laws. The problem is that there are many atoms in hemoglobin and many solvent molecules that collide with them and need to be accounted for.

Early crystal x-ray diffraction structures were pictured to be static – but really the atoms move about quite a bit

Mol. Dynamics 2

• In one dimension the acceleration of the ith atom is given by: $m_i a_i = \sum_i F_{ij} = F_{net \ on \ i}$,

From this we know that for a small time step (typically less than 1 ps = 10⁻¹² s) $x_i(t + \Delta t) = x_i(t) + v_i(t)\Delta t + a_i(t)\frac{\Delta t^2}{2}$ and $x_i(t - \Delta t) = x_i(t) - v_i(t)\Delta t + a_i(t)\frac{\Delta t^2}{2}$. $\sum_i F_{ij}(t)$

Adding these

$$x_i(t + \Delta t) = 2x_i(t) - x_i(t - \Delta t) + \frac{\sum_{j=0}^{j=0} \Delta t^2}{m_i} \Delta t^2.$$

While subtracting them gives

them gives $V_i(t) = \frac{x_i(t + \Delta t) - x_i(t - \Delta t)}{2\Delta t}$.

So if we know the forces and starting positions, we can iterate and predict the motion of each atom

Mol. Dynamics 3

- Molecular dynamics calculations are computer intensive – for each time step (sub – ps) you need to do several calculations for each atom in the molecule.
- For a reasonable protein (several 100 amino acids – or thousands of atoms) it takes many hours of supercomputing to map out the motions for nanoseconds
- Fast laser dynamic experiments are just starting to actually measure time courses of individual molecule motion in picoseconds
- Look at this web site for movies: <u>http://www.ks.uiuc.edu/Gallery/Movies/</u>