

# CE 530 Molecular Simulation

## Lecture 3

### Common Elements of a Molecular Simulation

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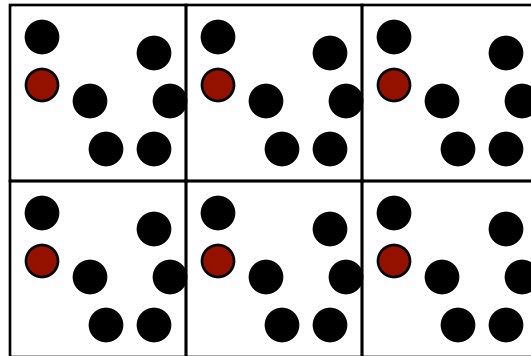
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# Boundary Conditions

- Impractical to contain system with a real boundary
  - *Enhances finite-size effects*
  - *Artificial influence of boundary on system properties*
- Instead surround with replicas of simulated system
  - *“Periodic Boundary Conditions” (PBC)*

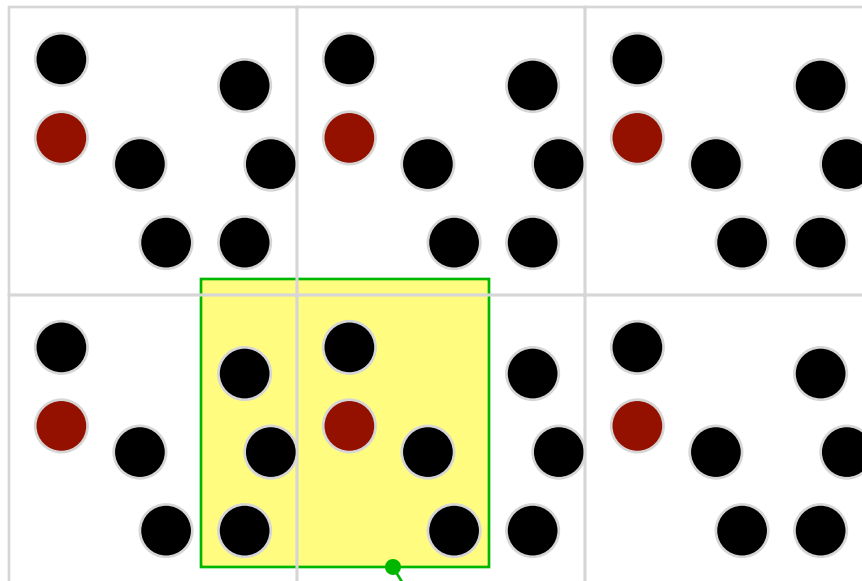


- [Click here](#) to view an applet demonstrating PBC

# Issues with Periodic Boundary Conditions 1.

## ○ Minimum image convention

- *Consider only nearest image of a given particle when looking for collision partners*

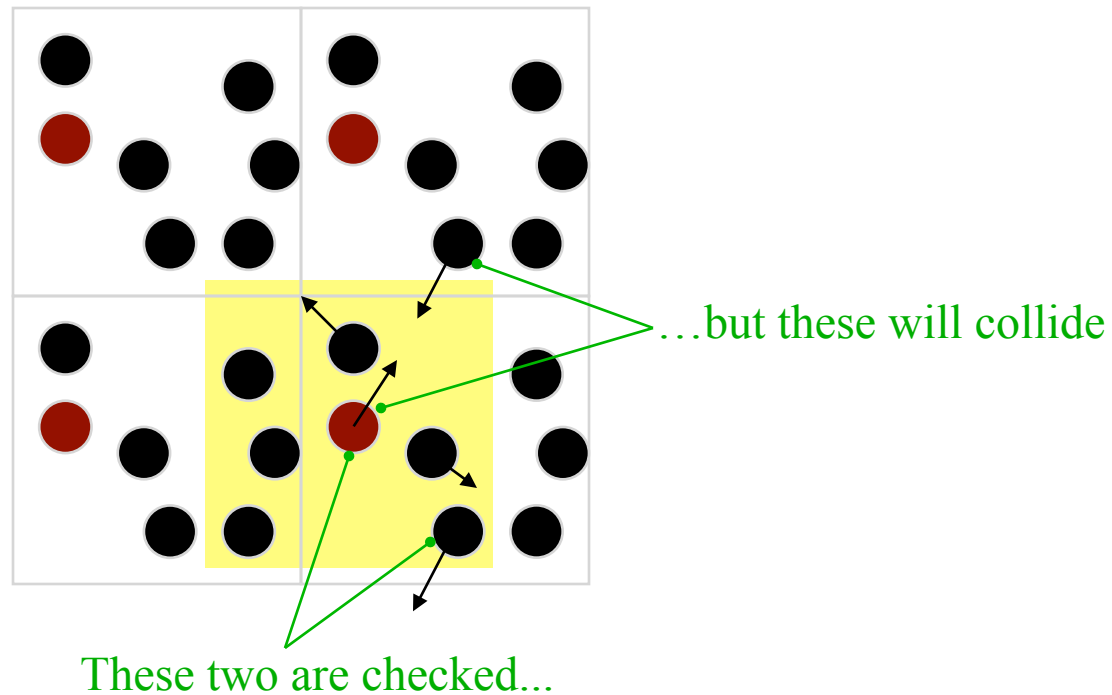


Nearest images of colored sphere

# Issues with Periodic Boundary Conditions 2.

## ○ Caution not to miss collisions

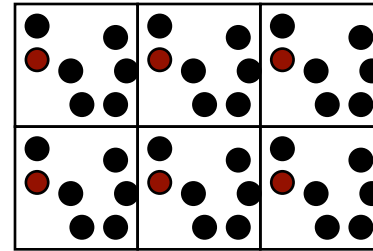
- [click here](#) for a bad simulation



# Issues with Periodic Boundary Conditions 3.

## ○ Correlations

- *new artificial correlations*
- *supressed long-range correlations*

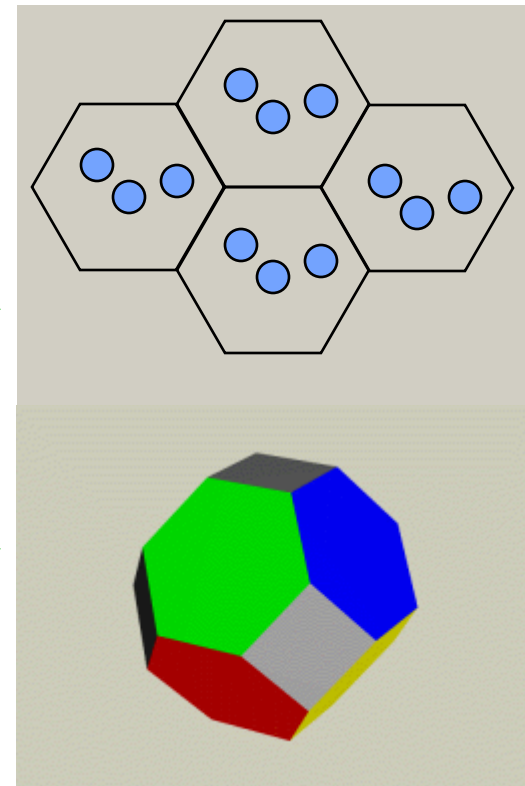


## ○ Other issues arise when dealing with longer-range potentials

- *accounting for long-range interactions*
- *nearest image not always most energetic*
- *splitting of molecules (charges)*
- *discuss details later*

## ○ Other geometries possible

- *any space-filling unit cell*
  - hexagonal in 2D*
  - truncated octahedron in 3D*
  - rhombic dodecahedron in 3D*
- *surface of a (hyper)sphere*
- *variable aspect ratio useful for solids*
  - relieves artificial stresses*



# Implementing Cubic Periodic Boundaries 1.

## ○ Details vary with representation of coordinates

- *Box size*

unit box, coordinates scaled by edge length

```
dr.x = dimensions.x * (r1.x - r2.x); //difference in x coordinates
```

full-size box, coordinates represent actual values

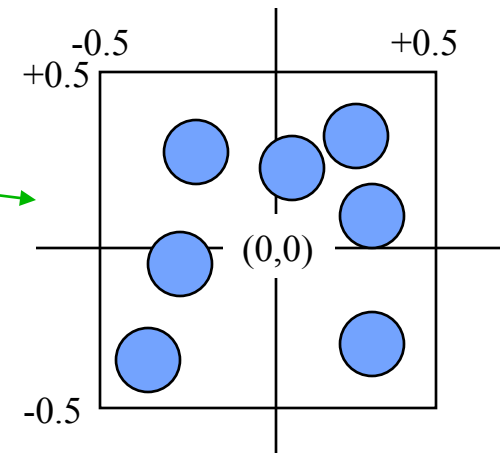
- *Box origin*

center of box, coordinates range from  $-L/2$  to  $+L/2$

corner of box, coordinates range from 0 to  $L$

## ○ Two approaches

- *decision based ("if" statements)*
- *function based (rounding (rint), truncation, modulo)*
- *relative speed of each approach may vary substantially from one computer platform to another*



# Implementing Cubic Periodic Boundaries 2.

## Central-image codes

○ Involved in most time-consuming part of simulation

○ (0,1) coordinates, decision based

- `r.x -= (r.x > 0.0) ? Math.floor(r.x) : Math.ceil(r.x-1.0); //Java syntax`
- *examples:* -0.2 → +0.8; -1.4 → +0.6; +0.4 → +0.4; +0.6 → +0.6; +1.5 → +0.5

○ (0,L) coordinates, decision based

- `r.x -= dimensions.x * ((r.x > 0.0) ? Math.floor(r.x/dimensions.x) : Math.ceil(r.x/dimensions.x-1.0));`

○ (-1/2, 1/2), decision based

- `if(r.x > 0.5) r.x -= 1.0; if(r.x < -0.5) r.x += 1.0; //only first shell`
- *examples:* -0.2 → -0.2; -1.4 → -0.4; +0.4 → +0.4; +0.6 → -0.4; +1.5 → +0.5

○ (-1/2, 1/2), function based

- `r.x -= Math.round(r.x); //nearest integer (r.x must be float, not double)`

○ (0,L), function based

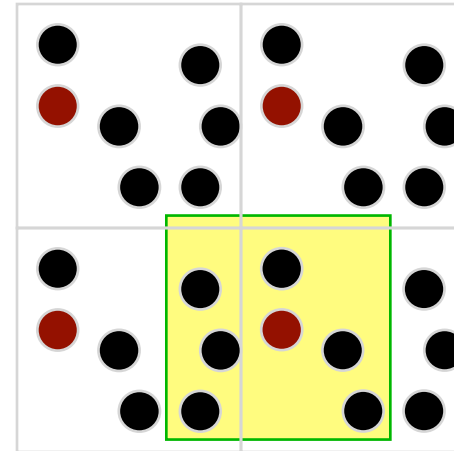
- `r.x %= dimensions.x; if(r.x < 0.0) r.x += dimensions.x; //modulo operator`

N.B. Most code segments are untested

# Implementing Cubic Periodic Boundaries 3. Nearest-image codes

## ○ Simply apply $(-1/2, 1/2)$ central-image code to raw difference!

- `dr.x = r1.x - r2.x; //unit box length`
- `if(dr.x > 0.5) dr.x -= 1.0;`
- `if(dr.x < -0.5) dr.x += 1.0;`
- `dr.x *= dimensions.x;`



## ○ Or...

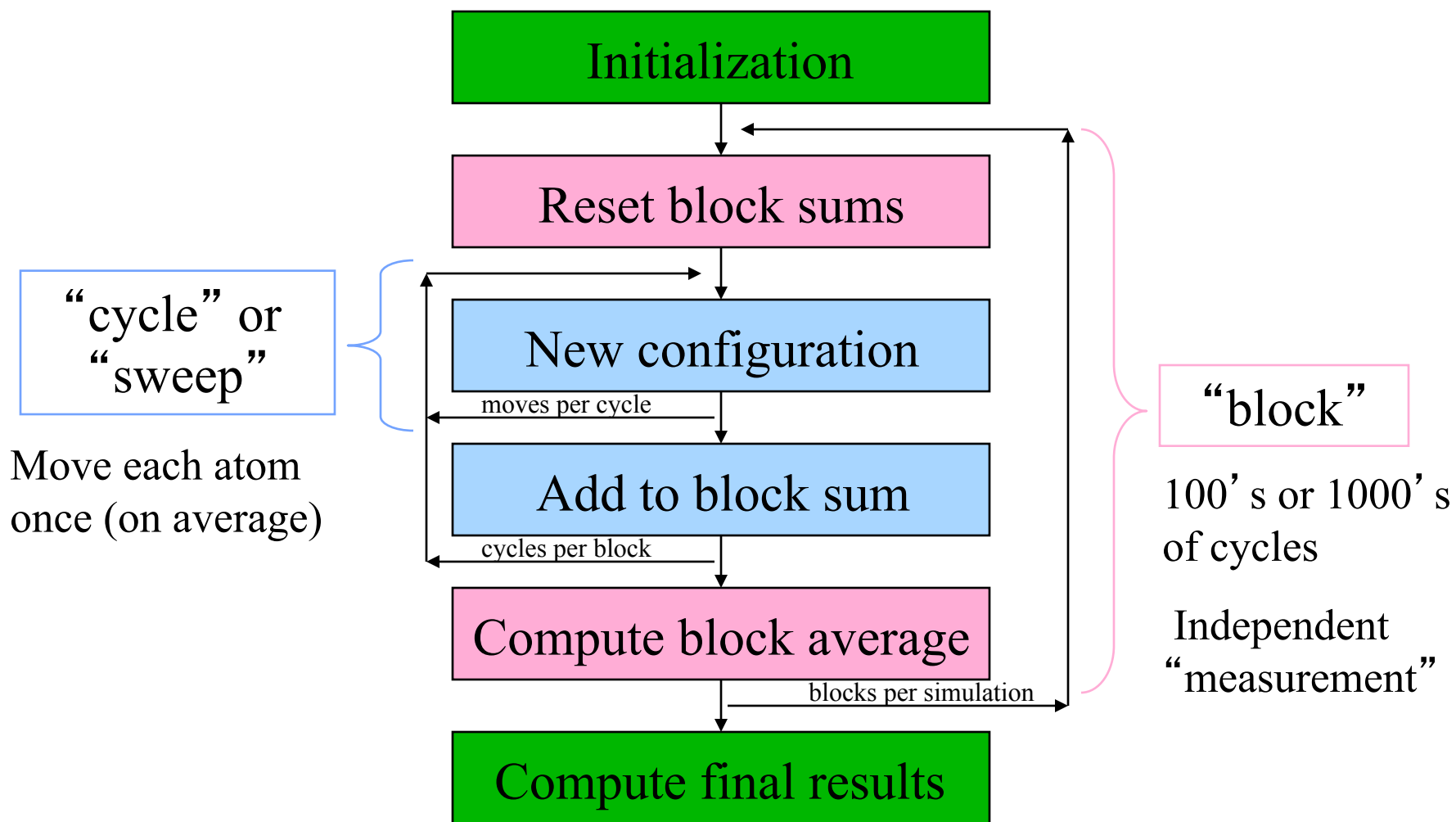
- `dr.x = r1.x - r2.x; //true box length`
- `dr.x -= dimensions.x * Math.round(dr.x/dimensions.x);`

## ○ Take care not to lose correct sign, if doing force calculation

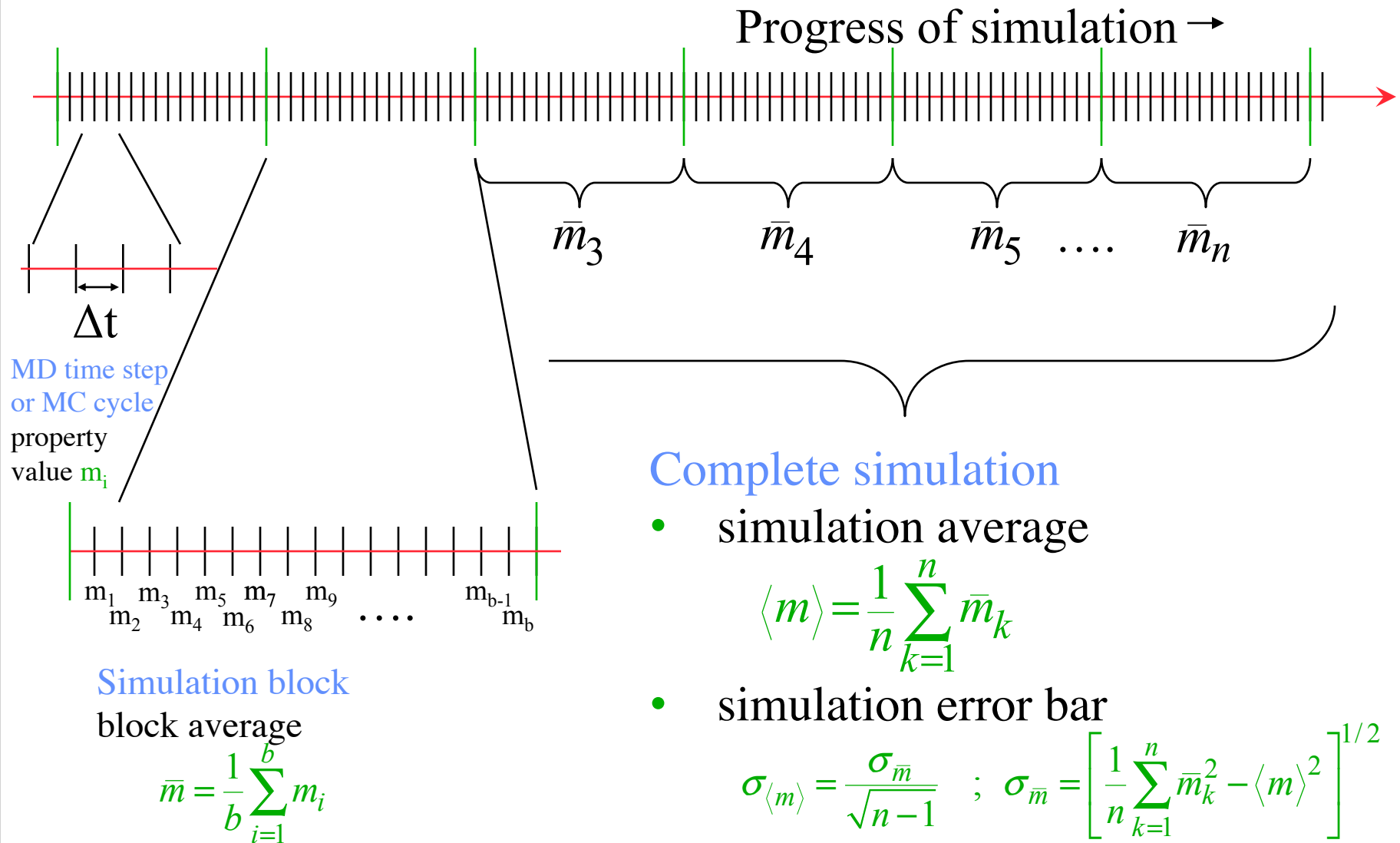
## ○ Nearest image for non-cubic boundary not always given simply in terms of a central-image algorithm



# Structure of a Molecular Simulation 1.

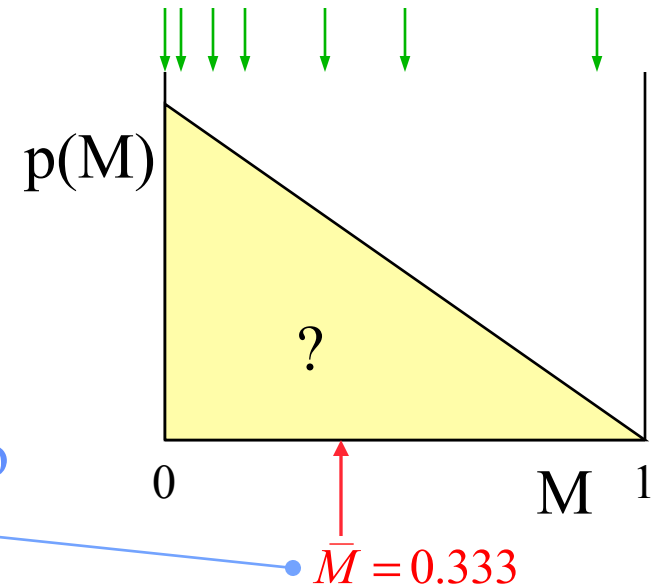


# Structure of a Molecular Simulation 2.



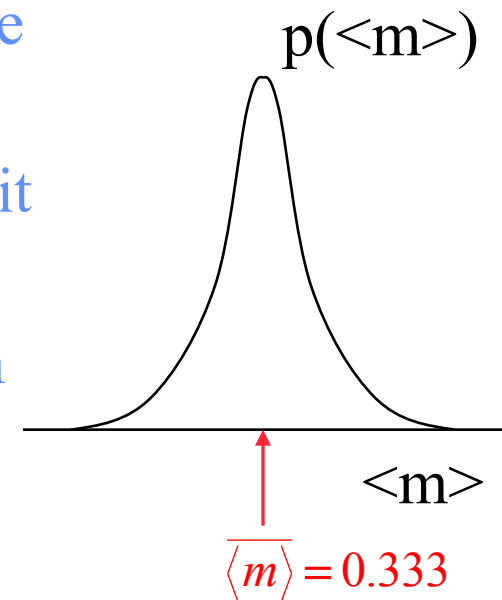
# Confidence Limits on Simulation Averages 1.

- Given a set of measurements  $\{m_i\}$ , for  $\{0.01, 0.1, 0.9, 0.06, 0.5, 0.3, 0.02\}$  some property  $M$
- There exists a distribution of values from which these measurements were sampled
- We do not know, *a priori*, any details of this distribution
- We wish to use our measurements  $\{m_i\}$  to estimate the mean of the true distribution
- Not surprisingly, the best estimate of the mean of the true distribution is given by the mean of the sample  $\bar{M} \approx \frac{1}{n} \sum m_i \equiv \langle m \rangle = (0.01+0.1+0.9+0.06+0.5+0.3+0.02)/7 = 0.27$
- We need to quantify our confidence in the value of this estimate for the mean  $\bar{M} \approx 0.27 \pm ?$
- We must do this using only the sample data



## Confidence Limits on Simulation Averages 2.

- Imagine repeating this experiment many (infinity) times, each time taking a sample of size  $n$ .
- If we say “68% of all the sample means  $\langle m \rangle$  lie within [some value] of the true mean.” ...
- ...then [some value] serves as a confidence limit
- According to the Central Limit Theorem, the distribution of observations of the sample mean  $\langle m \rangle$  will follow a gaussian, with
  - *mean*  $\overline{\langle m \rangle} = \bar{M}$
  - *variance*  $\sigma_{\langle m \rangle}^2 = \frac{1}{n} \sigma_M^2$
- Our confidence limit is then  $\sigma_{\langle m \rangle}$
- We can only estimate this using the sample variance



$$\sigma_{\langle m \rangle} = \frac{1}{\sqrt{n}} \sigma_M \approx \frac{1}{\sqrt{n}} \left[ \frac{1}{n} \sum m_i^2 - \left( \frac{1}{n} \sum m_i \right)^2 \right]^{1/2} = 0.12$$

$$\frac{1}{\sqrt{7}} \sigma_M = 0.09$$

(true value)

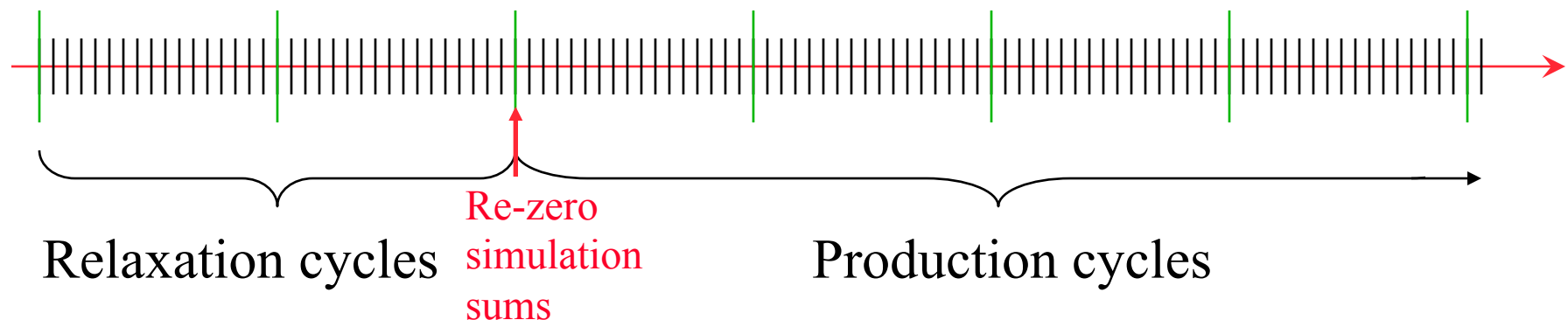
# Confidence Limits on Simulation Averages 3.

- Expression for confidence limit (error bar) assumes independent samples
  - *successive configurations in a simulation are (usually) not independent*
  - *block averages are independent for “sufficiently large” blocks*
- Often  $2\sigma$  is used for error bar (95% confidence interval)
  - *when reporting error bars it is good practice to state definition*
- Confidence limits quantify only statistical errors. Sometimes other sources of error are more significant
  - *systematic errors*
    - *poor sampling (non-ergodic)*
    - *finite-size effects*
    - *insufficient equilibration*
  - *programming errors*
  - *conceptual errors*
  - *limitations of the molecular model*

# Simulation Initialization

- Need to establish initial values for atom positions and momenta before simulation can begin
- Two options
  - *use values from end of another simulation*
  - *generate configuration from scratch*
- Often an equilibration period is warranted
  - *lets system “forget” artificial initial configuration*
  - *length of period depends on relaxation time of system*

5000 cycles typical



# Generating an Initial Configuration

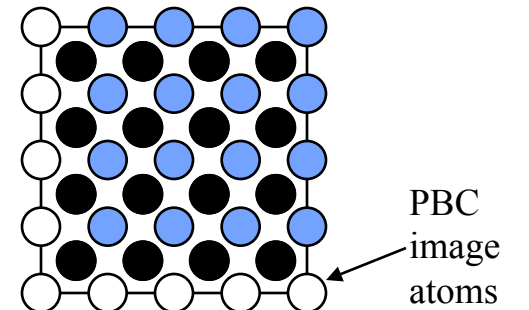
## ○ Placement on a lattice is a common choice

- *gives rise to “magic” numbers frequently seen in simulations*

2D;  $N = 2n^2$  (8, 18, 32, 50, 72, 98, 128, ...)

3D, face-center cubic (fcc);

$N = 4n^3$  (32, 128, 256, 500, 864, 1372, 2048, ...)

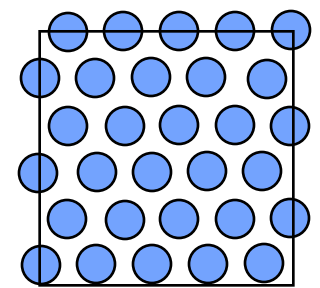


## ○ Other options involve “simulation”

- *place at random, then move to remove overlaps*
- *randomize at low density, then compress*
- *other techniques invented as needed*

## ○ Orientations done similarly

- *lattice or random, if possible*



hexagonal

incompatible  
with cubic PBC

# Initial Velocities

## ○ Random direction

- *randomize each component independently*
- *randomize direction by choosing point on spherical surface*

## ○ Magnitude consistent with desired temperature. Choices:

- *Maxwell-Boltzmann:  $\text{prob}(v_x) \propto \exp(-\frac{1}{2}mv_x^2 / kT)$*
- *Uniform over  $(-1/2, +1/2)$ , then scale so that  $\frac{1}{N} \sum v_{i,x}^2 = kT / m$*
- *Constant at  $v_x = \pm\sqrt{kT / m}$*
- *Same for y, z components*

## ○ Be sure to shift so center-of-mass momentum is zero

$$P_x \equiv \frac{1}{N} \sum p_{i,x}$$

$$p_{i,x} \rightarrow p_{i,x} - P_x$$

## ○ Unnecessary for Monte Carlo simulations (of course)



# Summary of Simulation Elements

- Specification of state
- Units and dimensions, scaling
- Initialization
- Generation of configurations
- Property measurement
- Confidence limits
- Cycles and blocks
- Periodic boundaries
- Organizing and cycling through atom lists