

Configurational-Bias Monte Carlo

Thijs J.H. Vlugt

Professor and Chair Engineering Thermodynamics
Delft University of Technology
Delft, The Netherlands

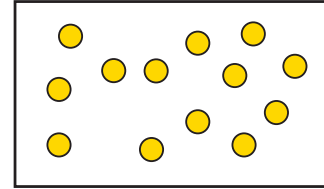
t.j.h.vlugt@tudelft.nl

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Random Sampling versus Metropolis Sampling (1)

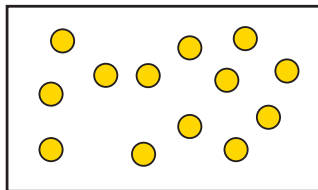
N interacting particles in volume V at temperature T



- vector representing positions of all particles in the system: $\mathbf{r}^N$
- total energy: $U(\mathbf{r}^N)$
- statistical weight of configuration $\mathbf{r}^N$ is $\exp[-\beta U(\mathbf{r}^N)]$ with $\beta = 1/(k_B T)$

Random Sampling versus Metropolis Sampling (2)

N interacting particles in volume V at temperature T
pair interactions $u(r_{ij})$



$$U(\mathbf{r}^N) = \sum_{i=1}^{N-1} \sum_{j=i+1}^N u(r_{ij}) = \sum_{i<j} u(r_{ij})$$

$$Q(N, V, T) = \frac{1}{\Lambda^{3N} N!} \int d\mathbf{r}^N \exp[-\beta U(\mathbf{r}^N)]$$

$$F(N, V, T) = -k_B T \ln Q(N, V, T)$$

Random Sampling versus Metropolis Sampling (3)

Computing the ensemble average $\langle \dots \rangle$ of a certain quantity $A(\mathbf{r}^N)$

- Random Sampling of $\mathbf{r}^N$:

$$\langle A \rangle = \lim_{n \rightarrow \infty} \frac{\sum_{i=1}^n A(\mathbf{r}_i^N) \exp[-\beta U(\mathbf{r}_i^N)]}{\sum_{i=1}^n \exp[-\beta U(\mathbf{r}_i^N)]}$$

Usually this leads to $\langle A \rangle = "0" / "0" = ???$

- Metropolis sampling; generate n configurations $\mathbf{r}^N$ with probability proportional to $\exp[-\beta U(\mathbf{r}_i^N)]$, therefore:

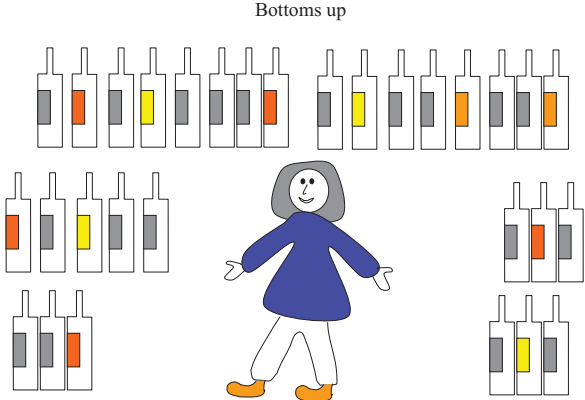
$$\langle A \rangle = \lim_{n \rightarrow \infty} \frac{\sum_{i=1}^n A(\mathbf{r}_i^N)}{n}$$

Simulation Technique (1)

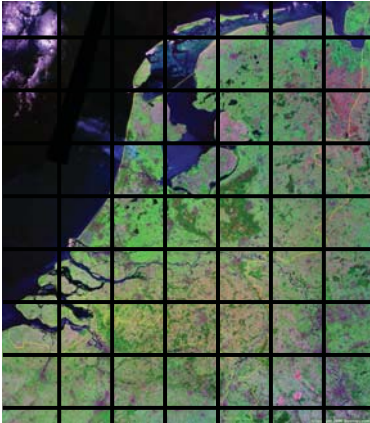
What is the ratio of red wine/white wine in the Netherlands?



Simulation Technique (2)



Simulation Technique (3)



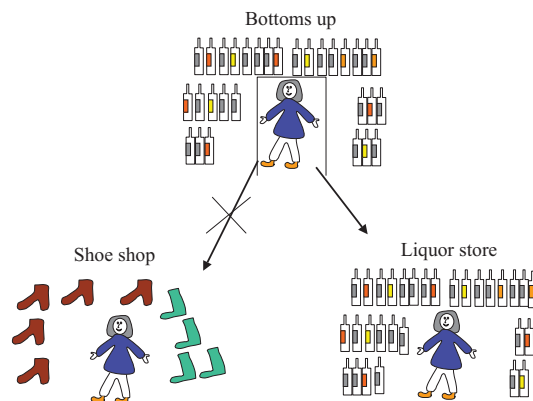
Simulation Technique (4)



Simulation Technique (5)

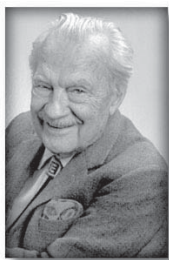


Simulation Technique (6)



Metropolis Monte Carlo (1)

How to generate configurations $\mathbf{r}_i$ with a probability proportional to $\mathcal{N}(\mathbf{r}_i) = \exp[-\beta U(\mathbf{r}_i)]$???

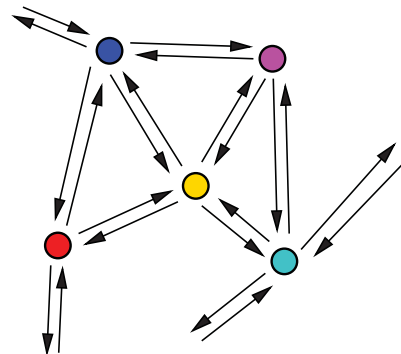


Nick Metropolis

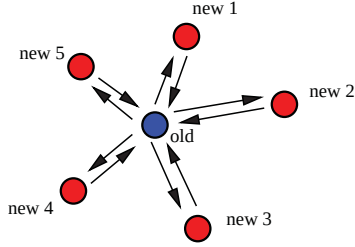
N. Metropolis, A.W. Rosenbluth, M.N. Rosenbluth, A.H. Teller and E. Teller, "Equation of State Calculations by Fast Computing Machines," J. Chem. Phys., 1953, 21, 1087-1092.

Metropolis Monte Carlo (2)

Whatever our rule is to move from one state to the next, the equilibrium distribution should not be destroyed



Move from the old state (o) to a new state (n) and back



leaving state o = entering state o

$$\mathcal{N}(o) \sum_n [\alpha(o \rightarrow n) \text{acc}(o \rightarrow n)] = \sum_n [\mathcal{N}(n) \alpha(n \rightarrow o) \text{acc}(n \rightarrow o)]$$

$\mathcal{N}(i)$: probability to be in state i (here: proportional to $\exp[-\beta U(\mathbf{r}_i)]$)

$\alpha(x \rightarrow y)$: probability to attempt move from state x to state y

$\text{acc}(x \rightarrow y)$: probability to accept move from state x to state y

Detailed Balance (1)

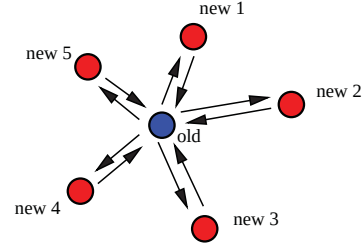
Requirement (balance):

$$\mathcal{N}(o) \sum_n [\alpha(o \rightarrow n) \text{acc}(o \rightarrow n)] = \sum_n [\mathcal{N}(n) \alpha(n \rightarrow o) \text{acc}(n \rightarrow o)]$$

Detailed balance: much stronger condition

$$\mathcal{N}(o) \alpha(o \rightarrow n) \text{acc}(o \rightarrow n) = \mathcal{N}(n) \alpha(n \rightarrow o) \text{acc}(n \rightarrow o)$$

for every pair o, n



Detailed Balance (2)

$$\mathcal{N}(o) \alpha(o \rightarrow n) \text{acc}(o \rightarrow n) = \mathcal{N}(n) \alpha(n \rightarrow o) \text{acc}(n \rightarrow o)$$

- $\alpha(x \rightarrow y)$; probability to select move from x to y
- $\text{acc}(x \rightarrow y)$; probability to accept move from x to y
- often (but not always); $\alpha(o \rightarrow n) = \alpha(n \rightarrow o)$

Therefore (note that $\Delta U = U(n) - U(o)$):

$$\frac{\text{acc}(o \rightarrow n)}{\text{acc}(n \rightarrow o)} = \frac{\alpha(n \rightarrow o) \exp[-\beta U(n)]}{\alpha(o \rightarrow n) \exp[-\beta U(o)]} = \frac{\alpha(n \rightarrow o)}{\alpha(o \rightarrow n)} \exp[-\beta \Delta U]$$

In case that $\alpha(o \rightarrow n) = \alpha(n \rightarrow o)$

$$\frac{\text{acc}(o \rightarrow n)}{\text{acc}(n \rightarrow o)} = \exp[-\beta \Delta U]$$

Metropolis Acceptance Rule

General:

$$\frac{\text{acc}(o \rightarrow n)}{\text{acc}(n \rightarrow o)} = X$$

Choice made by Metropolis (note: infinite number of other possibilities)

$$\text{acc}(o \rightarrow n) = \min(1, X)$$

Note that $\min(a, b) = a$ if $a < b$ and b otherwise

- always accept when $X \geq 1$
- when $X < 1$, generate uniformly distributed random number between 0 and 1 and accept or reject according to $\text{acc}(o \rightarrow n)$

Monte Carlo Casino



Smart Monte Carlo: $\alpha(o \rightarrow n) \neq \alpha(n \rightarrow o)$

Not a random displacement Δr uniformly from $[-\delta, \delta]$, but instead

$$\Delta r = r(\text{new}) - r(\text{old}) = A \times F + \delta r$$

F : force on particle

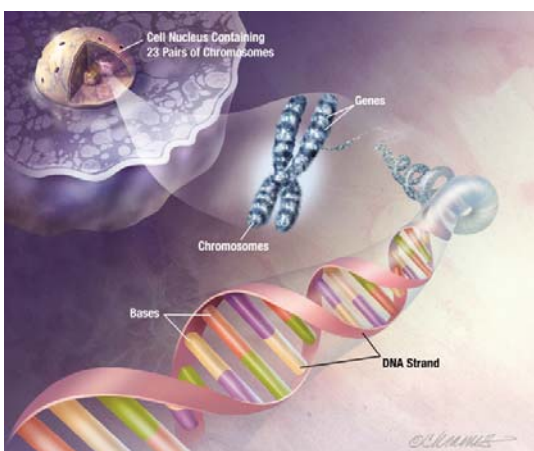
A : constant

δr : taken from Gaussian distribution with width $2A$
so $P(\delta r) \sim \exp[-(\delta r)^2/4A]$

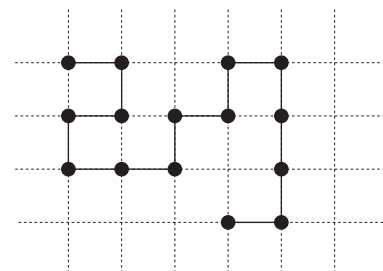
$$P(r_{\text{new}}) \sim \exp \left[-\frac{(r_{\text{new}} - (r_{\text{old}} + A \times F(o)))^2}{4A} \right]$$

$$\frac{\alpha(o \rightarrow n)}{\alpha(n \rightarrow o)} = \frac{\exp \left[-\frac{(\Delta r - A \times F(o))^2}{4A} \right]}{\exp \left[-\frac{(\Delta r + A \times F(n))^2}{4A} \right]}$$

Chain Molecules



Self-Avoiding Walk on a Cubic Lattice



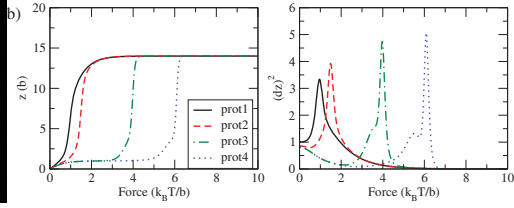
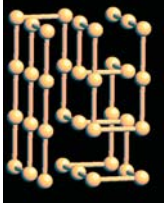
- 3D lattice; 6 lattice directions
- only 1 monomer per lattice site (otherwise $U = \infty$)
- interactions only when $|r_{ij}| = 1$ and $|i - j| > 1$

Simple Model for Protein Folding

20 by 20 interaction matrix Δ_{ij}

YPDLTQWHAMEAGKIRFSVPDACLNGEGIRQVTLN

(E. Jarkova, T.J.H. Vlught, N.K. Lee, J. Chem. Phys., 2005, 122, 114904)



Number of Configurations without Overlap

Random Chains:

$$\langle R \rangle = \lim_{n \rightarrow \infty} \frac{\sum_{i=1}^n R_i \exp[-\beta U_i]}{\sum_{i=1}^n \exp[-\beta U_i]}$$

Fraction of chains without overlap decreases exponentially as a function of chainlength (N)

N	total ($= 6^{N-1}$)	without overlap	fraction no overlap
2	6	6	1
6	7776	3534	0.454
8	279936	81390	0.290
10	10077696	1853886	0.183
12	362797056	41934150	0.115
13	2176782336	198842742	0.091
14	13060694016	943974510	0.072
15	78364164096	4468911678	0.057
16	470184984576	21175146054	0.045
50	...	...	1.3×10^{-5}

Rosenbluth Sampling (1)

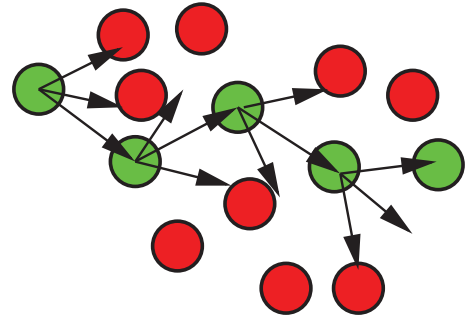
1. Place first monomer at a random position
2. For the next monomer (i), generate k trial directions ($j = 1, 2, \dots, k$) each with energy u_{ij}
3. Select trial direction j^* with a probability

$$P_{j^*} = \frac{\exp[-\beta u_{ij^*}]}{\sum_{j=1}^k \exp[-\beta u_{ij}]}$$

4. Continue with step 2 until the complete chain is grown (N monomers)

Rosenbluth Sampling (2)

$$P_{j^*} = \frac{\exp[-\beta u_{ij^*}]}{\sum_{j=1}^k \exp[-\beta u_{ij}]}$$



Rosenbluth Sampling (3)

Probability to choose trial direction j^* for the i th monomer

$$P_{j^*} = \frac{\exp[-\beta u_{ij^*}]}{\sum_{j=1}^k \exp[-\beta u_{ij}]}$$

Probability to grow this chain (N monomers, k trial directions)

$$P_{\text{chain}} = \prod_{i=1}^N P_{j^*(i)} = \frac{\prod_{i=1}^N \exp[-\beta u_{ij^*(i)}]}{\prod_{i=1}^N \sum_{j=1}^k \exp[-\beta u_{ij}]} = \frac{\exp[-\beta U_{\text{chain}}]}{W_{\text{chain}}}$$

Rosenbluth Sampling (4)

Probability to grow this chain (N monomers, k trial directions)

$$P_{\text{chain}} = \frac{\prod_{i=1}^N \exp[-\beta u_{ij^*(i)}]}{\prod_{i=1}^N \sum_{j=1}^k \exp[-\beta u_{ij}]} = \frac{\exp[-\beta U_{\text{chain}}]}{W_{\text{chain}}}$$

Therefore, weightfactor for each chain i is the Rosenbluth factor W_i :

$$\langle R \rangle_{\text{Boltzmann}} = \lim_{n \rightarrow \infty} \frac{\sum_{i=1}^n W_i \times R_i}{\sum_{i=1}^n W_i}$$

The unweighted distribution is called the Rosenbluth distribution:

$$\langle R \rangle_{\text{Rosenbluth}} = \lim_{n \rightarrow \infty} \frac{\sum_{i=1}^n R_i}{n}$$

Of course: $\langle R \rangle_{\text{Rosenbluth}} \neq \langle R \rangle_{\text{Boltzmann}}$

Intermezzo: Ensemble Averages at Different Temperatures

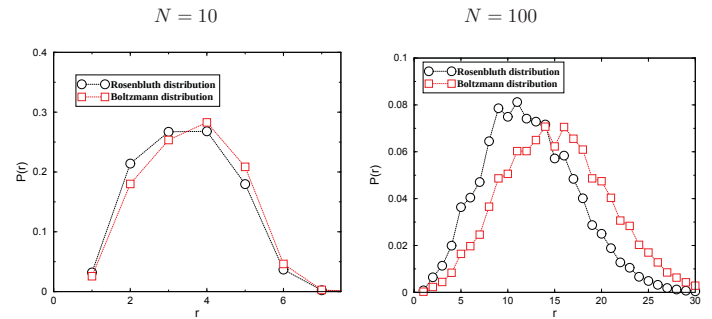
Ensemble averages at β^* can (in principle) be computed from simulations at β :

$$\begin{aligned} \langle U \rangle_{\beta} &= \frac{\int d\mathbf{r}^N U(\mathbf{r}^N) \exp[-\beta U(\mathbf{r}^N)]}{\int d\mathbf{r}^N \exp[-\beta U(\mathbf{r}^N)]} \\ &= \frac{\int d\mathbf{r}^N U(\mathbf{r}^N) \exp[-\beta^* U(\mathbf{r}^N)] \exp[(\beta^* - \beta) \times U(\mathbf{r}^N)]}{\int d\mathbf{r}^N \exp[-\beta^* U(\mathbf{r}^N)] \exp[(\beta^* - \beta) \times U(\mathbf{r}^N)]} \\ &= \frac{\langle U(\mathbf{r}^N) \exp[(\beta^* - \beta) \times U(\mathbf{r}^N)] \rangle_{\beta^*}}{\langle \exp[(\beta^* - \beta) \times U(\mathbf{r}^N)] \rangle_{\beta^*}} \\ &= \frac{\langle U(\mathbf{r}^N) \exp[\Delta\beta \times U(\mathbf{r}^N)] \rangle_{\beta^*}}{\langle \exp[\Delta\beta \times U(\mathbf{r}^N)] \rangle_{\beta^*}} \end{aligned}$$

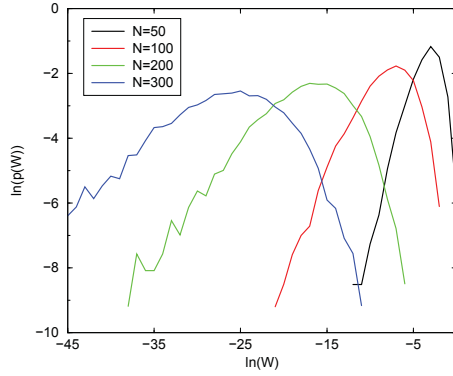
Useful or not???

Rosenbluth Distribution Differs from Boltzmann Distribution

Probability distribution for the *end-to-end distance* r



Distribution of Rosenbluth Weights



Of course, $\text{Probability}(W = 0) \neq 0$ (not shown in this figure)

Pruned-Enriched Rosenbluth Method (1)

Grassberger (1997); grow chains using Rosenbluth Method:

$$W = \sum_{j=1}^6 \frac{\exp[-\beta u_{2j}]}{6} \times \prod_{i=3}^N \sum_{j=1}^5 \frac{\exp[-\beta u_{ij}]}{5} = \prod_{i=3}^N \sum_{j=1}^5 \frac{\exp[-\beta u_{ij}]}{5}$$

Two additional elements:

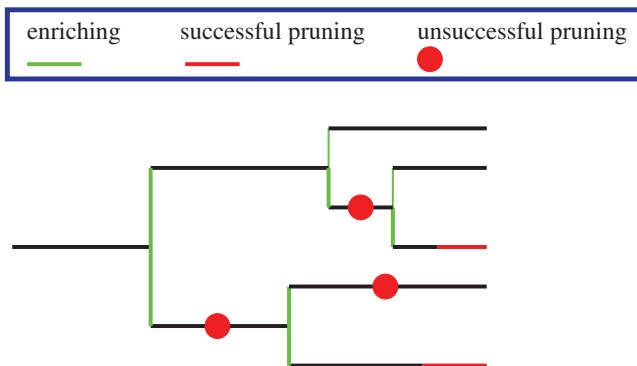
- Enriching**

If $W > W_{\max}$ during the construction of the chain, k copies of the chain are generated, each with a weight of W/k . This is a deterministic process. The growth of those k chains is continued.

- Pruning**

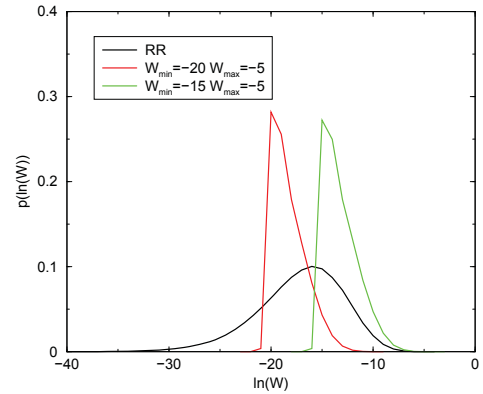
If $W < W_{\min}$ during the construction of a chain, with a probability of $1/2$ the chain is pruned resulting in $W = 0$. If the chain survives, the Rosenbluth weight is multiplied by 2 and the growth of the chain is continued.

Pruned-Enriched Rosenbluth Method (2)



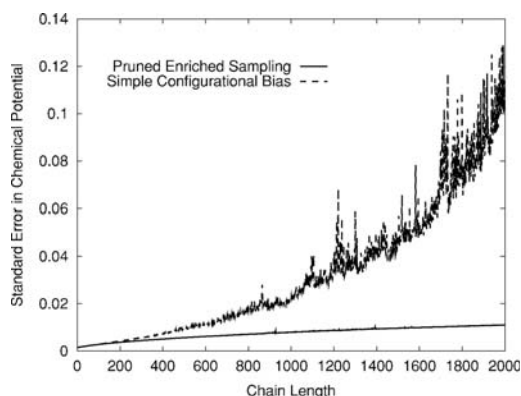
Pruned-Enriched Rosenbluth Method (3)

Example: $N = 200$, $k = 2$, $\beta\mu_{\text{ex}} = -\ln \langle W \rangle = -12.14$



Pruned-Enriched Rosenbluth Method (4)

$\beta\mu_{\text{ex}} = -\ln \langle W \rangle$, Ann. Rev. of Phys. Chem. 1999, 50, 377-411



Static versus Dynamic Monte Carlo

• Static Monte Carlo

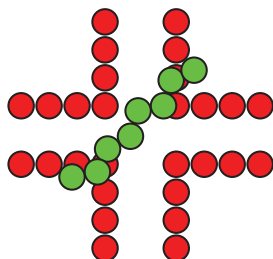
- create single chain conformations, and use correct weight factor (random insertion, Rosenbluth scheme, PERM) to compute single chain averages
- **single chain only; no Markov chain**

• Dynamic Monte Carlo

- create Markov chain, accept/reject new configuration, acceptance rules should obey detailed balance
- **multi-chain system, usable for all ensembles (e.g. Gibbs, μVT)**
- Configurational-Bias Monte Carlo (CBMC), Recoil Growth (RG), Dynamic PERM (DPERM)

Random Insertion of Chains is Useless

Chain Length	Probability without overlaps
1	10^{-2}
2	10^{-4}
3	10^{-6}
...	...
8	10^{-16}



Configurational-Bias Monte Carlo

- Generate configurations using the Rosenbluth scheme
- Accept/Reject these configurations in such a way that detailed balance is obeyed
- Split potential energy into "**bonded**" (bond-stretching, bending, torsion) and "**non-bonded**" (i.e. Lennard-Jones and/or Coulombic) interactions
- Generate (k) trial positions according to **bonded** interactions (unbranched chain: l , θ , ϕ are independent)

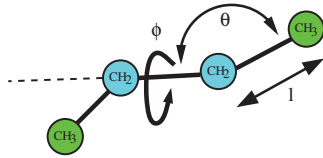
$$U_{\text{bonded}} = U_{\text{stretch}}(l) + U_{\text{bend}}(\theta) + U_{\text{tors}}(\phi)$$

$$P(l) \sim dl l^2 \exp[-\beta u(l)]$$

$$P(\theta) \sim d\theta \sin(\theta) \exp[-\beta u(\theta)]$$

$$P(\phi) \sim d\phi \exp[-\beta u(\phi)]$$

Generate Trial Configurations: Linear Alkane



$$u(l) = (k_l/2) (l - l_0)^2$$

$$u(\theta) = (k_\theta/2) (\theta - \theta_0)^2$$

$$u(\phi) = \sum_{i=0}^5 c_i \cos^i(\phi)$$

$$P(l) \sim dl l^2 \exp[-\beta u(l)]$$

$$P(\theta) \sim d\theta \sin(\theta) \exp[-\beta u(\theta)]$$

$$P(\phi) \sim d\phi \exp[-\beta u(\phi)]$$

Generate a Random Number from a Distribution (1)

$$F(y) = \int_0^y p(y') dy'$$

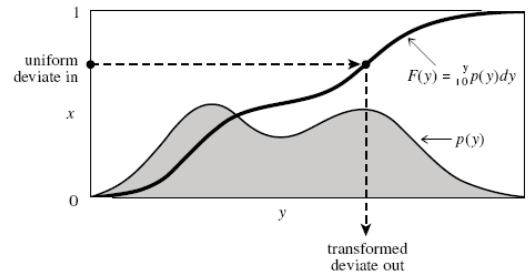


Figure 7.2.1. Transformation method for generating a random deviate y from a known probability distribution $p(y)$. The indefinite integral of $p(y)$ must be known and invertible. A uniform deviate x is chosen between 0 and 1. Its corresponding y on the definite-integral curve is the desired deviate.

Generate a Random Number from a Distribution (2)

$$F(y) = \int_0^y f(y') dy' \quad f(x) > p(x)$$

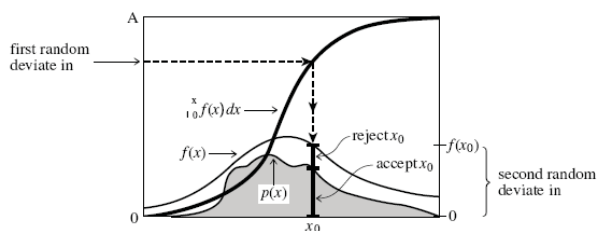


Figure 7.3.1. Rejection method for generating a random deviate x from a known probability distribution $p(x)$ that is everywhere less than some other function $f(x)$. The transformation method is first used to generate a random deviate x of the distribution f (compare Figure 7.2.1). A second uniform deviate is used to decide whether to accept or reject that x . If it is rejected, a new deviate of f is found; and so on. The ratio of accepted to rejected points is the ratio of the area under p to the area between p and f .

Generate a Random Number from a Distribution (3)

```

subroutine bend-tors                                generate appropriate  $\theta$  and  $\phi$ 

lready=.false
do while (.not.lready)
  call ransphere(dx,dy,dz)                          random vector on unit sphere
  x = xold + dx                                       monomer position
  y = yold + dy
  z = zold + dz
  call bend(ubend,x,y,z)                             bending energy
  call tors(utors,x,y,z)                             torsion energy
  if(ranf().lt.exp(-beta*(ubend+utors)))               accept or reject
    + lready=.true
enddo

```

CBMC Algorithm

- Generate a trial configuration using the Rosenbluth scheme. k trial segments $\{\mathbf{b}\}_k = \{\mathbf{b}_1 \cdots \mathbf{b}_k\}$, each trial segment is generated according to

$$P(\mathbf{b}) \sim \exp[-\beta u_{\text{bonded}}(\mathbf{b})]$$

- Compute non-bonded energy, select configuration i with a probability

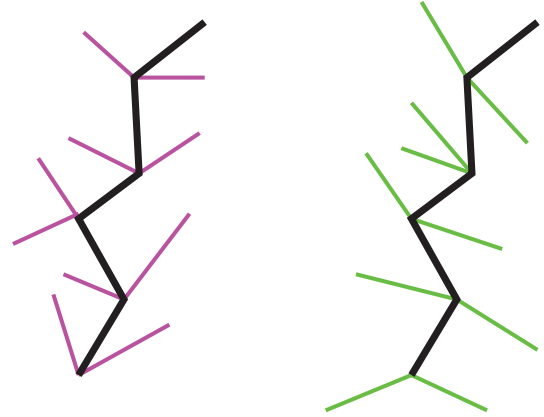
$$P(\mathbf{b}_i) = \frac{\exp[-\beta u_{\text{non-b}}(\mathbf{b}_i)]}{\sum_{j=1}^k \exp[-\beta u_{\text{non-b}}(\mathbf{b}_j)]} = \frac{\exp[-\beta u_{\text{non-b}}(\mathbf{b}_i)]}{w_l}$$

- Continue until chain is grown, $W(n) = \prod_{l=1}^n w_l$
- Similar procedure for old configuration, generate $k - 1$ trial positions (trial position 1 is the old configuration itself), leading to $W(o)$
- Accept/reject according to

$$\text{acc}(o \rightarrow n) = \min(1, W(n)/W(o))$$

Super-Detailed Balance (1)

Same chain can be grow for different sets of trial directions...



Super-Detailed Balance (2)

Flux of configurations

$$\begin{aligned} K(o \rightarrow n) &= \sum_{\mathbf{b}_n \mathbf{b}_o} K(o \rightarrow n | \mathbf{b}_n \mathbf{b}_o) \\ K(n \rightarrow o) &= \sum_{\mathbf{b}_n \mathbf{b}_o} K(n \rightarrow o | \mathbf{b}_n \mathbf{b}_o) \end{aligned}$$

Detailed balance requires

$$K(o \rightarrow n) = K(n \rightarrow o)$$

Possible solution (**super-detailed balance**):

$$K(o \rightarrow n | \mathbf{b}_n \mathbf{b}_o) = K(n \rightarrow o | \mathbf{b}_n \mathbf{b}_o)$$

for each $\mathbf{b}_n \mathbf{b}_o$.

Super-Detailed Balance (3)

Detailed balance for each set $\mathbf{b}_n \mathbf{b}_o$:

$$\begin{aligned} K(o \rightarrow n | \mathbf{b}_n \mathbf{b}_o) &= N(o) \times \alpha(o \rightarrow n | \mathbf{b}_n \mathbf{b}_o) \times \text{acc}(o \rightarrow n | \mathbf{b}_n \mathbf{b}_o) \\ &= \exp[-\beta U(o)] \times C \exp[-\beta u_{\text{bonded}}(n)] \times \\ &\quad \frac{\exp[-\beta u_{\text{non-b}}(n)]}{W(n)} \times P(\mathbf{b}_n \mathbf{b}_o) \times \text{acc}(o \rightarrow n | \mathbf{b}_n \mathbf{b}_o) \\ K(n \rightarrow o | \mathbf{b}_n \mathbf{b}_o) &= \exp[-\beta U(n)] \times C \exp[-\beta u_{\text{bonded}}(o)] \times \\ &\quad \frac{\exp[-\beta u_{\text{non-b}}(o)]}{W(o)} \times P(\mathbf{b}_n \mathbf{b}_o) \times \text{acc}(n \rightarrow o | \mathbf{b}_n \mathbf{b}_o) \end{aligned}$$

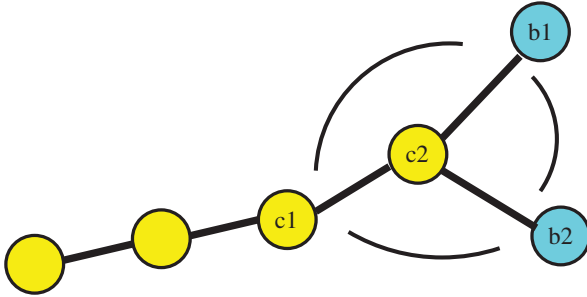
As

$$U = u_{\text{non-b}} + u_{\text{bonded}}$$

therefore

$$\frac{\text{acc}(o \rightarrow n)}{\text{acc}(n \rightarrow o)} = \frac{W(n)}{W(o)}$$

Branched Molecules (1)



$$P(\mathbf{b}_1, \mathbf{b}_2) \sim \exp[-\beta[u_{\text{bend}}(\mathbf{c}_1, \mathbf{c}_2, \mathbf{b}_1)] + u_{\text{bend}}(\mathbf{c}_1, \mathbf{c}_2, \mathbf{b}_2)] + u_{\text{bend}}(\mathbf{b}_1, \mathbf{c}_2, \mathbf{b}_2)]]$$

Branched Molecules (2)

Use CBMC to generate internal configurations:

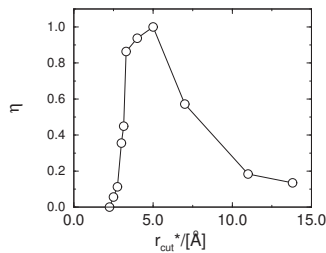
- Generate n_t random trial positions and select one (i) with a probability

$$P^{\text{int}}(i) = \frac{\exp[-\beta U_{\text{bonded}}(i)]}{\sum_{j=1}^{n_t} \exp[-\beta U_{\text{bonded}}(j)]} = \frac{\exp[-\beta U_{\text{bonded}}(i)]}{W^{\text{int}}(n)}$$

- Repeat until k trial orientations are found; these are fed into CBMC leading to $W(n)$
- Repeat procedure for old configuration, leading to $W^{\text{int}}(o)$ and $W(o)$.
- Accept or reject according to

$$\text{acc}(o \rightarrow n) = \min \left(1, \frac{W(n) \times W^{\text{int}}(n)}{W(o) \times W^{\text{int}}(o)} \right)$$

Significant Speedup: Dual-Cutoff CBMC



- Grow chain with approximate (cheaper) potential; W^*
- Correct for difference later (δu , difference real and approximate potential for *selected* configuration)

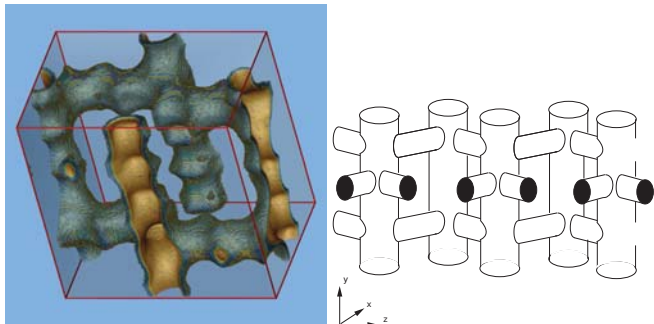
$$\text{acc}(o \rightarrow n) = \min \left(1, \frac{W^*(n)}{W^*(o)} \times \exp[-\beta[\delta u(n) - \delta u(o)]] \right)$$

Application 1: Adsorption of Alkanes in MFI-type zeolite (1)

Zeolites:

- microporous channel structure
- crystalline, SiO_2 building blocks
- substitution of Si^{4+} by Al^{3+} and a cation (Na^+ or H^+)
- typical poresize: 4 – 12 Å
- synthetic and natural; >190 framework types

Application 1: Adsorption of Alkanes in MFI-type zeolite (2)

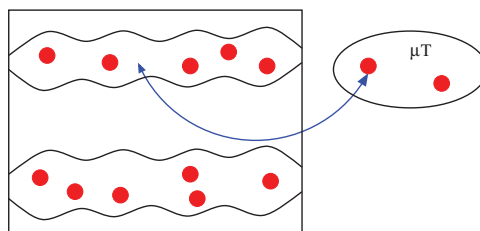


straight channels (y direction), zig-zag channels (xz plane) and intersections

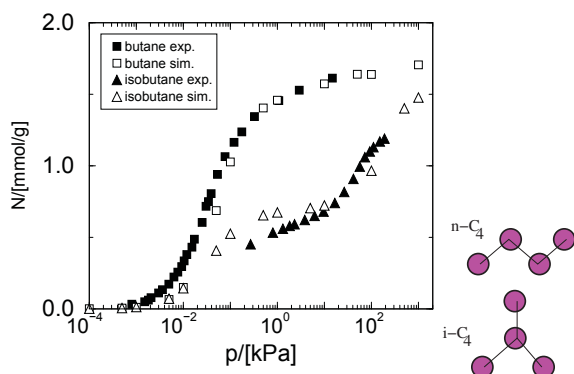
Application 1: Adsorption of Alkanes in MFI-type zeolite (3)

Grand-canonical (μVT) ensemble; number of particles (N) fluctuates

- system is coupled to particle reservoir at chemical potential μ and temperature T , statistical weight $\sim V^N \exp[\beta\mu N - \beta U(\mathbf{r}^N)] / (\Lambda^{3N} N!)$
- trial moves to exchange particles between zeolite and reservoir (using CBMC)
- equilibrium: $\mu_{\text{gas}} = \mu_{\text{zeolite}}$; measure average $\langle N \rangle$ for given μ and β

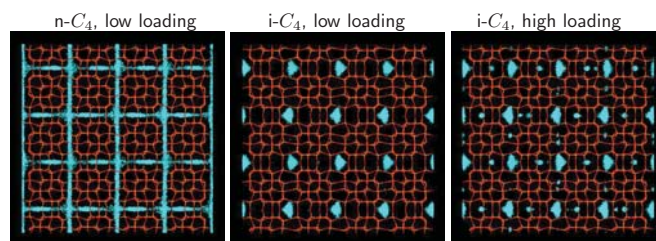


Application 1: Adsorption of Alkanes in MFI-type zeolite (4)



Vlugt et al, J. Am. Chem. Soc., 1998, 120, 5599

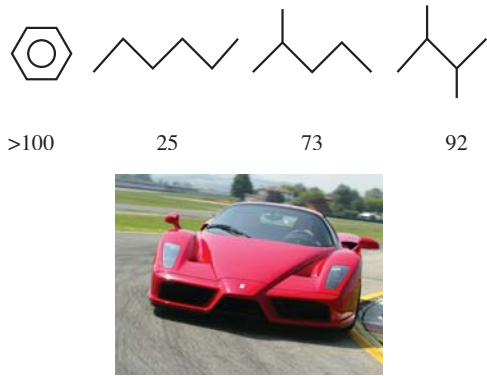
Application 1: Adsorption of Alkanes in MFI-type zeolite (5)



Vlugt et al, J. Am. Chem. Soc., 1998, 120, 5599

Application 1: Adsorption of Alkanes in MFI-type zeolite (6)

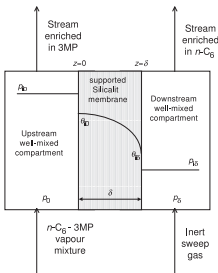
Research Octane Number (RON)



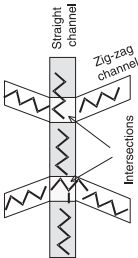
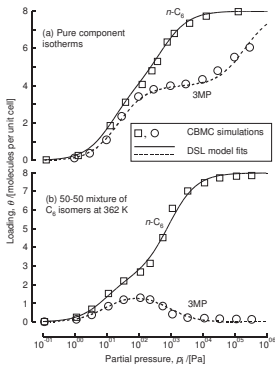
Application 1: Adsorption of Alkanes in MFI-type zeolite (7)

Flux	$n - C_6$	$i - C_6$	selectivity
pure	179	136	1.3
50%-50%	46	1.9	24

Experiments by J. Falconer, Univ. Colorado

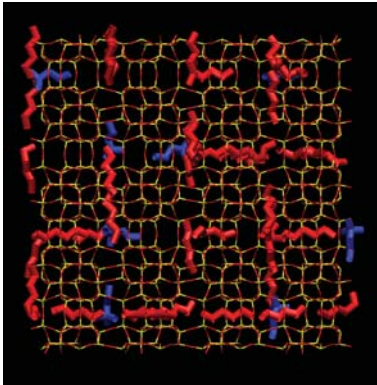


Application 1: Adsorption of Alkanes in MFI-type zeolite (8)

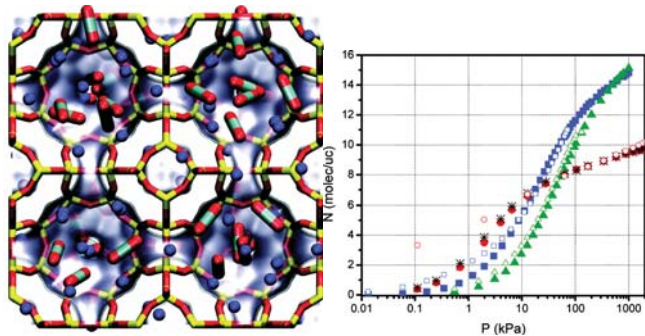


Application 1: Adsorption of Alkanes in MFI-type zeolite (9)

blue = branched ($i-C_6$) red = linear ($n-C_6$)

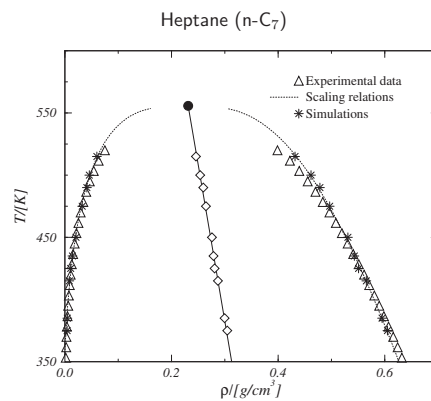


Application 2: Adsorption of CO₂ in Na⁺ containing zeolites



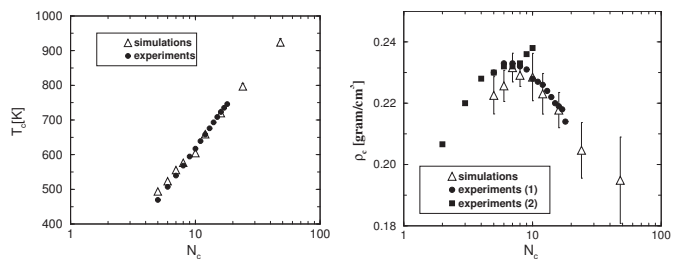
Sofia Calero et al., J. Phys. Chem. C, 2009, 113, 8814-8820

Application 3: Gibbs Ensemble Monte Carlo (1)



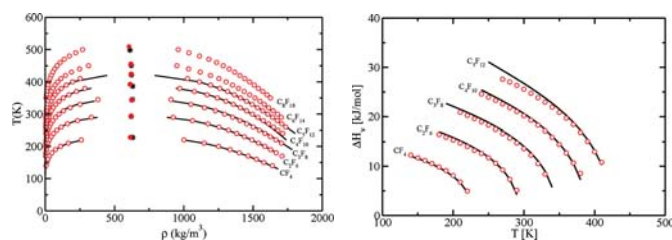
B. Smit, S. Karaborni, and J.I. Siepmann, J. Chem. Phys. 102, 2126 (1995)

Application 3: Gibbs Ensemble Monte Carlo (2)



B. Smit, S. Karaborni, and J.I. Siepmann, J. Chem. Phys. 102, 2126 (1995)

Application 4: GCMC Histogram Reweighting



J.J. Potoff et al., J. Phys. Chem. B, 2009, 113, pp 14725-14731

Efficiency of CBMC

- k : number of trial directions
- a : probability that trial direction has a “favorable” energy
- growth can continue as long as at least 1 trial direction is “favorable”
- generate chain of length N successfully

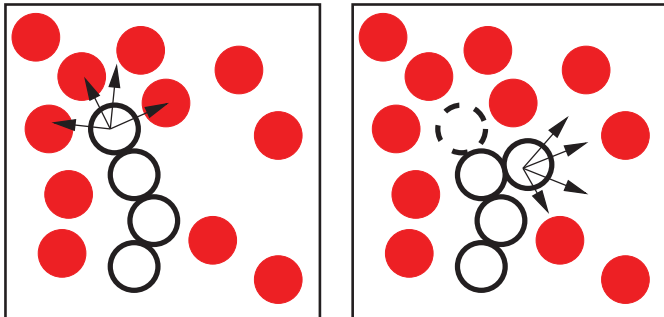
$$P_{\text{success}} = (1 - (1 - a)^k)^N = \exp[-cN]$$

- increasing k means increasing CPU time.

Dead-End Alley

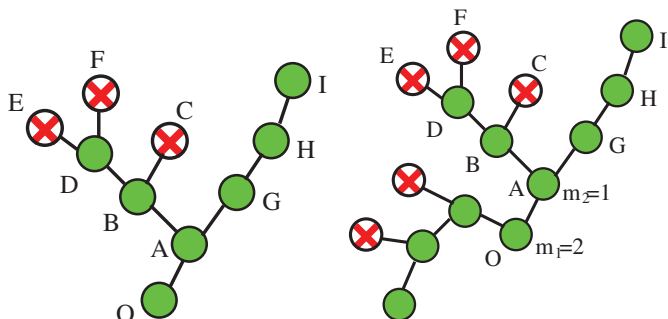


Recoil Growth: Avoiding Dead-End Alley

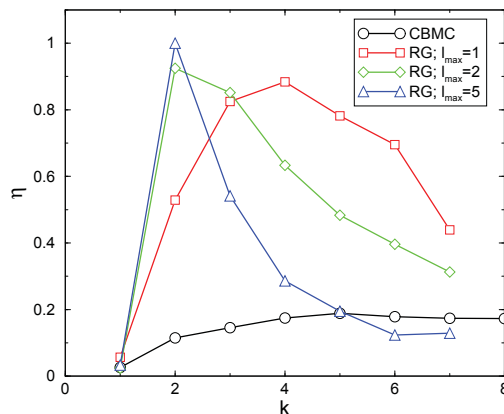


Recoil Growth Algorithm (1)

- Place first bead at random position
- Position (i) can be “open” or “closed” depending on the environment (energy u_i); here we use $p_{\text{open}} = \min(1, \exp[-\beta u_i])$ and toss a coin.
- If “open”, continue with next segment
- If “closed”, try another trial direction up to a maximum of k
- If all k directions are closed, retract by one step
- Maximum retraction length: $l_{\text{max}} - l + 1$
- l : recoil length, l_{max} : maximum length obtained during the growth of the chain
- Computed weight $W(n)$ and repeat procedure for old configuration
- Accept or reject using $\text{acc}(o \rightarrow n) = \min(1, W(n)/W(o))$

Computing the Weight ($k = 2, l = 3$)

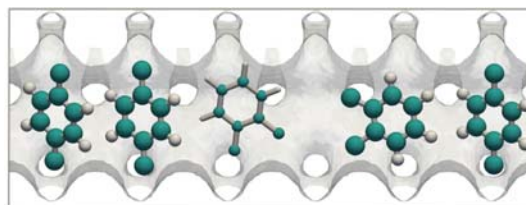
Efficiency of RG Compared to CBMC



Other Methods

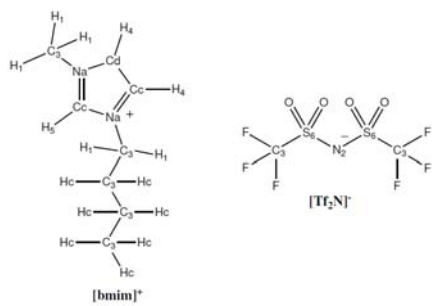
- Continuous Fractional Component Monte Carlo
 - system contains N molecules and one “fractional” molecule
 - interactions of the fractional molecule are described by order parameter λ
 - include trial-moves to change λ
 - “fractional” molecule can become a “real” molecule or disappear
 - Maginn, J. Chem. Theory Comput., 2007, 3, 451-1463
- Wormhole move
 - create an artificial “hole” in the system
 - use reptation steps to gradually insert the chain
 - accept/reject individual reptation steps
 - move is completed when the whole chain is transferred through the hole
 - Houdayer, Journal of Chemical Physics, 2002, 116, 1783-1787

Continuous Fractional Component Monte Carlo

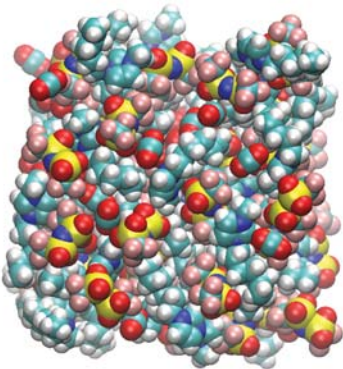


- Not inserting whole molecules, but step by step
- Slowly switching on/off interactions of a “ghost molecule”
- Maginn and co-workers; Dubbeldam, Vlugt et al., Journal of Chemical Theory and Computation, 2014, 10, 942-952.

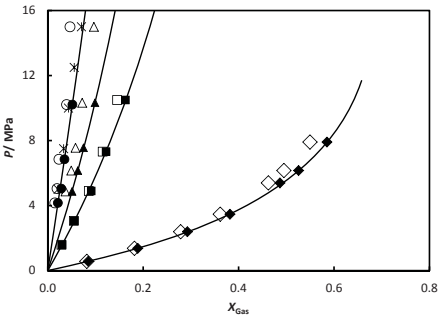
[bmim][Tf2N]



[bmim][Tf2N]



Solubility of precombustion gasses in [bmim][Tf2N]



Solubility of CO₂, CH₄, CO, H₂ and N₂ in [bmim][Tf₂N] from MC simulations (open symbols) and experiments (filled symbols) at 333.15 K. CO₂ experiments (filled diamonds) and MC data (open diamonds); CH₄ experiments (filled squares) and MC data (open squares); CO experiments (filled triangles) and MC data (open triangles); H₂ experiments (filled circles) and MC data (open circles), and MC data of N₂ (stars). Lines: PR-EOS modeling

Henry constants of CO₂, CH₄, CO, H₂, N₂, and H₂S in Selexol and [bmim][Tf2N] at 333.15 K

solute	$H_{\text{Selexol}}^{\text{exp.}}/\text{MPa}$	$H_{\text{IL}}^{\text{exp.}}/\text{MPa}$	$H_{\text{IL}}^{\text{sim.}}/\text{MPa}$	difference/%
CO ₂	6.81 ^a	6.56	7.10	8.2
CH ₄	40.13 ^a	52.4	53.7	2.5
CO	-	95	125.9	33.0
H ₂	193 ^b	199	271.7	36.3
N ₂	151 ^b	-	225.7	-
H ₂ S (3S)	1.01 ^c	2.17	1.15	47.0
H ₂ S (4S)	1.01	2.17	1.16	46.5
H ₂ S (5S)	1.01	2.17	1.17	46.1

^a Taken from Rayer *et al.* ^b Calculated from Gainar *et al.* ^c Taken from Xu *et al.*

Kirkwood-Buff theory for finite systems (1)

Integrals of pair correlation functions (PCFs) are related to fluctuations in the grand-canonical ensemble

$$\begin{aligned} G_{\alpha\beta}^V &\equiv 4\pi \int_0^\infty (g_{\alpha\beta}^{\mu VT}(r) - 1) r^2 dr \\ &= V \frac{\langle N_\alpha N_\beta \rangle - \langle N_\alpha \rangle \langle N_\beta \rangle}{\langle N_\alpha \rangle \langle N_\beta \rangle} - \frac{V \delta_{\alpha\beta}}{\langle N_\alpha \rangle} \end{aligned}$$

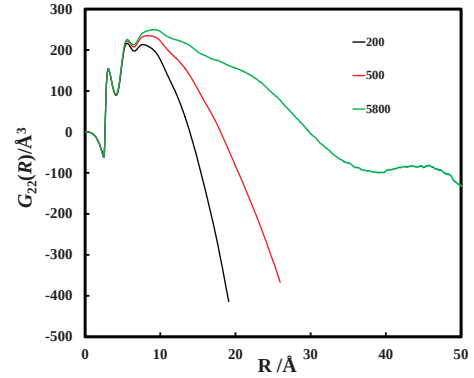
Using PCFs from MD:

$$G_{\alpha\beta}^V \approx \hat{G}_{\alpha\beta}(R) = 4\pi \int_0^R (g_{\alpha\beta}^{NVT}(r) - 1) r^2 dr$$

Often used, but is it correct?

Kirkwood-Buff theory for finite systems (2)

$$\hat{G}_{\alpha\beta}(R) = 4\pi \int_0^R (g_{\alpha\beta}^{NVT}(r) - 1) r^2 dr$$



Kirkwood-Buff theory for finite systems (3)

$$\hat{G}_{\alpha\beta}(R) = 4\pi \int_0^R (g_{\alpha\beta}^{NVT}(r) - 1) r^2 dr$$

$\hat{G}_{\alpha\beta}(R)$ is not a valid approximation for the KB coefficient. For finite volumes, the exact expression is:

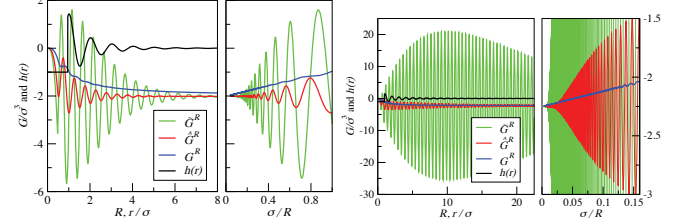
$$\begin{aligned} G_{\alpha\beta}^V &\equiv \frac{1}{V} \int_V \int_V (g_{\alpha\beta}^{NVT}(r_{12}) - 1) d\mathbf{r}_1 d\mathbf{r}_2 \\ &= 4\pi \int_0^{2R} (g_{\alpha\beta}^{NVT}(r) - 1) r^2 \left(1 - \frac{3r}{4R} + \frac{r^3}{16R^3}\right) dr \\ &\equiv G_{\alpha\beta}(R) \end{aligned}$$

One can rigorously show that $G_{\alpha\beta}(R)$ scales as $1/R$.

P. Krüger, S.K. Schnell, D. Bedeaux, S. Kjelstrup, T.J.H. Vlugt, J.M. Simon
J. Phys. Chem. Lett., 2013, 4, 235-238.

Kirkwood-Buff theory for finite systems (4)

$\chi = 2$ (left) and $\chi = 20$ (right)



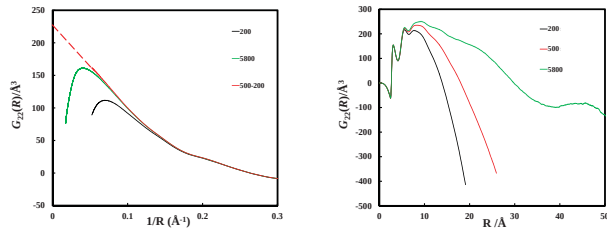
$$h(r) = g(r) - 1 = \begin{cases} \frac{3/2}{r/\sigma} \exp\left(\frac{1-r/\sigma}{\chi}\right) \cos\left[2\pi\left(\frac{r}{\sigma} - \frac{21}{20}\right)\right], & r/\sigma \geq \frac{19}{20} \\ -1, & r < \frac{19}{20}\sigma. \end{cases}$$

P. Krüger, S.K. Schnell, D. Bedeaux, S. Kjelstrup, T.J.H. Vlugt, J.M. Simon
J. Phys. Chem. Lett., 2013, 4, 235-238.

Kirkwood-Buff theory for finite systems (5)

MD simulations: beware of the finite-size effect of $g(r)$

$$g_{\alpha\beta}^{\infty}(r) \approx g_{\alpha\beta}^N(r) + \frac{c(r)}{N}$$



Equimolar mixture of methanol and acetone, LJ+electrostatics, 298K, 1atm

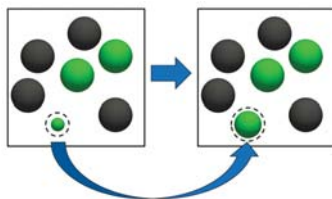
The End

Questions ??



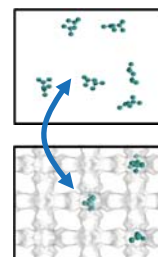
Continuous Fractional Component Monte Carlo

Ali Poursaeidesfahani
Delft University of Technology, The Netherlands
a.poursaeidesfahani@tudelft.nl

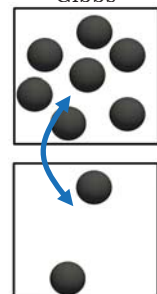


Grand-Canonical and Gibbs Ensembles
Critically Rely on Molecule Transfer

Grand-Canonical

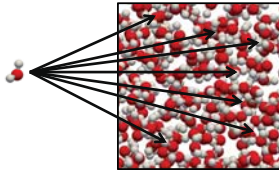


Gibbs



Insertion/Deletion of Molecules

- Very low acceptance probability at high densities
 - **Problem:** Molecules inserted in one MC step
 - **Problem:** Depends on occurrence of spontaneous cavities
 - **Dense liquids:** water at room temperature
 - **Deletion:** Molecule has very favourable interactions



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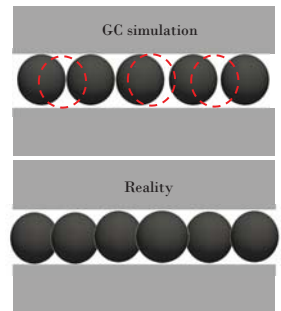
Adsorption in a nearly full pore

- At high loadings acceptance probability is almost zero

- Sampled configurations are not representative of real configurations

- No spontaneous cavity is formed

- Same problem with Widom Test particle insertion (zero * ∞ problem)

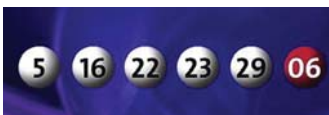


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Probability of wining 1 M Euro in Lottery

$$P(\text{Winning}) = \frac{\# \text{ Won}}{\# \text{ Entered}}$$



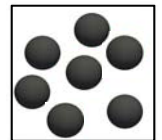
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Expanded Ensembles

- Conventional (NVT)

$$Q(N, V, T) = \frac{V^N}{\Lambda^{3N} N!} \int dr^N \exp[-\beta u(r^N)]$$



- Expanded ensemble
 - Ensemble is expanded by number of parameters

$$Q_{\text{Ex}}(N, V, T, x, y, z, \dots) = \dots$$

Escobedo, et. al., J. Chem. Phys., 1995, 7, 2703–2710

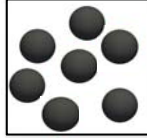
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Continuous Fractional Component Mote Carlo

- Conventional (NVT)

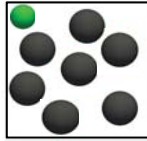
$$Q(N, V, T) = \frac{V^N}{\Lambda^{3N} N!} \int dr^N \exp[-\beta u(r^N)]$$



- CFCMC

- 1 molecule with interactions scaled with Additional parameter λ

$$Q_{\text{CFCMC}}(N, V, T, \lambda) = \frac{V^{N+1}}{\Lambda^{3(N+1)} N!} \int_0^1 d\lambda \int dr^N \exp[-\beta u(r^N)] \int dr_F \exp[-\beta u_F(r^N, r_F, \lambda)]$$

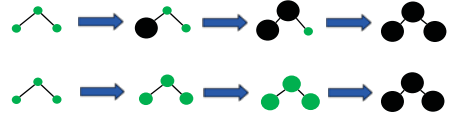


CFCMC

- Interactions of fractional molecule with whole molecules are scaled with scaling parameter λ

$$u_{ij}(r, \lambda) = \lambda 4\epsilon \left[\frac{1}{\left[\frac{1}{2}(1-\lambda)^2 + \left(\frac{r}{\sigma}\right)^6 \right]^{\frac{1}{2}}} - \frac{1}{\left[\frac{1}{2}(1-\lambda)^2 + \left(\frac{r}{\sigma}\right)^{12} \right]^{\frac{1}{2}}} \right]$$

- When $\lambda = 0$ → Ideal gas Molecule
- When $\lambda = 1$ → Whole Molecule



CFCMC

$$Q_{\text{CFCMC}}(N, V, T, \lambda) = \frac{V^{N+1}}{\Lambda^{3(N+1)} N!} \int_0^1 d\lambda \int dr^N \exp[-\beta u(r^N)] \int dr_F \exp[-\beta u_F(r^N, r_F, \lambda)]$$

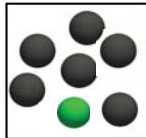
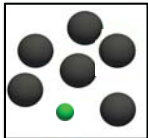
- Additional trial move: changing the value of λ
- Acceptance rule

$$\mathcal{N}(o) = \frac{V^{N+1}}{\Lambda^{3(N+1)} N!} \exp[-\beta U_o(r^N, r_F, \lambda_o)]$$

$$\mathcal{N}(n) = \frac{V^{N+1}}{\Lambda^{3(N+1)} N!} \exp[-\beta U_n(r^N, r_F, \lambda_n)]$$

$$\text{acc}(o \rightarrow n) = \frac{p(n)}{p(o)}$$

$$\text{acc}(o \rightarrow n) = \min[1, \exp[-\beta \Delta U]]$$



Chemical Potential

$$p(\lambda=1) = \frac{V^{N+1}}{\Lambda^{3(N+1)} N!} \int dr^N \exp[-\beta u(r^N)] \int dr_F \exp[-\beta u_F(r^N, r_F, \lambda=1)]$$

$$= \frac{Q_{\text{CFCMC}}(N, V, T, \lambda)}{Q_{\text{CFCMC}}(N, V, T, \lambda)}$$

$$p(\lambda=0) = \frac{V^{N+1}}{\Lambda^{3(N+1)} N!} \int dr^N \exp[-\beta u(r^N)] \int dr_F \exp[-\beta u_F(r^N, r_F, \lambda=0)]$$

$$= \frac{Q_{\text{CFCMC}}(N, V, T, \lambda)}{Q_{\text{CFCMC}}(N, V, T, \lambda)}$$

$$\frac{p(\lambda=1)}{p(\lambda=0)} = \frac{\int dr^{N+1} \exp[-\beta u(r^{N+1})]}{\int dr^N \exp[-\beta u(r^N)]}$$

CFCMC

• Chemical Potential

$$\mu_{\text{ex}} = -k_B T \ln \left[\frac{\int dr^{N+1} \exp[-\beta u(r^{N+1})]}{\int dr^N \exp[-\beta u(r^N)]} \right] = -k_B T \ln \left[\frac{p(\lambda=1)}{p(\lambda=0)} \right]$$

$$\mu = -k_B T \ln \left[\frac{Q(N+1, V, T)}{Q(N, V, T)} \right] \Rightarrow \mu = -k_B T \ln \left[\frac{V / \Lambda^3}{N+1} \right] - k_B T \ln \left[\frac{\int dr^{N+1} \exp[-\beta u(r^{N+1})]}{\int dr^N \exp[-\beta u(r^N)]} \right]$$

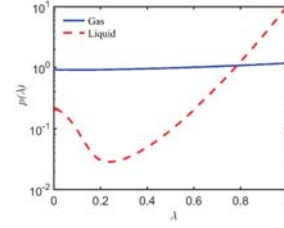
$\downarrow$ μ_{id} $\downarrow$ μ_{ex}

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CFCMC

- Flat probability distribution of λ is preferred
- Biasing functions are used to make the observed probability distribution flat



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CFCMC

Modified Ensemble:

$$Q_{\text{Modified}}(N, V, T, \lambda) = \frac{V^{N+1}}{\Lambda^{3(N+1)} N!} \int_0^1 d\lambda \int dr^N \exp[-\beta u(r^N)] \int dr^N \exp[-\beta u_F(r^N, r_F, \lambda)] \exp[-W(\lambda)]$$

- Using biasing function, we are not computing Boltzmann averages anymore
- To obtain the correct Boltzmann averages of observable X

$$\langle X \rangle_{\text{Boltzmann}} = \frac{\langle X \exp[-W(\lambda)] \rangle_{\text{Modified}}}{\langle \exp[-W(\lambda)] \rangle_{\text{Modified}}}$$

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Wang-Landau Algorithm

- Initially Histogram and Weight Function are set to zero

$$H(\lambda) = 0 \text{ and } W(\lambda) = 0$$

- When certain λ is visited

$$H(\lambda) = H(\lambda) + 1 \text{ and } W(\lambda) = W(\lambda) - F$$

- F is the modification factor
- When Histogram ($H(\lambda)$) is flat enough the value of F is reduced and the $H(\lambda)$ is set to zero and $W(\lambda)$ is kept
- Iterate until $W(\lambda)$ converges
- Note: detailed balance is violated

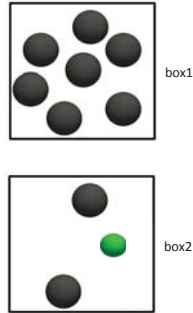
Wang et. al., Phys. Rev. Lett., 2001, 86, 2050 - 2053

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Formulation of CFCMC GE

- One fractional molecule per component
- Fractional molecule can be in either of the simulation boxes
- Three additional trial moves to facilitate particle exchange



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Partition function CFCMC Gibbs Ensemble

$$Q_{\text{CFCMC}} = \frac{1}{\Lambda^{3(N_T+1)} (N_T)!} \sum_{i=1}^2 \sum_{N_i=0}^{N_T} \int_0^1 d\lambda \int dV_1 V_1^{N_i+\delta_{i,1}} (V_T - V_1)^{N_T-N_i+\delta_{i,2}}$$

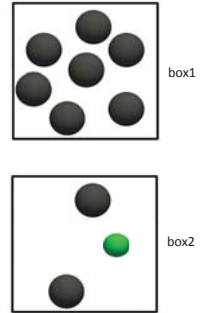
$$\frac{(N_T)!}{(N_1)!(N_T-N_1)!} \times \int ds^{N_1} \exp[-\beta U_{\text{int},1}(s^{N_1})]$$

$$\int ds^{N_T-N_1} \exp[-\beta U_{\text{int},2}(s^{N_T-N_1})] \times$$

$$\left(\delta_{i,1} \int ds_{\text{fac}}^1 \exp[-\beta U_{\text{fac},1}(s_{\text{fac}}^1, s^{N_1}, \lambda)] + \delta_{i,2} \int ds_{\text{fac}}^2 \exp[-\beta U_{\text{fac},2}(s_{\text{fac}}^2, s^{N_T-N_1}, \lambda)] \right)$$

- where $\delta_{i,1}=1$ when the fractional molecule is in box 1 and otherwise $\delta_{i,1}=0$

Poursaidesfahani, et. al., J. Chem. Theo. Comp., 2016, 12, 1481-1490
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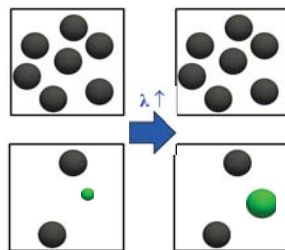
Changing the Strength of Interactions between the Fractional Molecule and Whole Molecules

- Acceptance rule

$$\text{acc}(o \rightarrow n) = \min(1, \exp[-\beta \Delta U])$$

- Rejected when

$$\lambda \notin (0,1)$$



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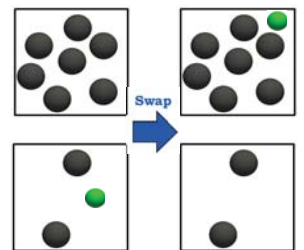
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Swapping the Fractional Molecule to the Other Box

- Very efficient at low values of λ

- Acceptance rule

$$\text{acc}(o \rightarrow n) = \min\left(1, \frac{V_T - V_1}{V_1} \exp[-\beta \Delta U]\right)$$



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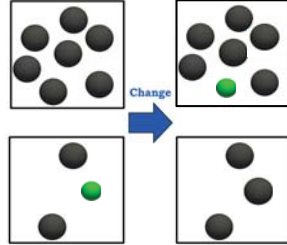
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Changing the identity of the Fractional Molecule with a Whole Molecule in the other Box

- Very efficient at high values of λ

- Acceptance rule

$$\text{acc}(o \rightarrow n) = \min \left(1, \frac{N_r - N_l}{N_l + 1} \exp[-\beta \Delta U] \right)$$

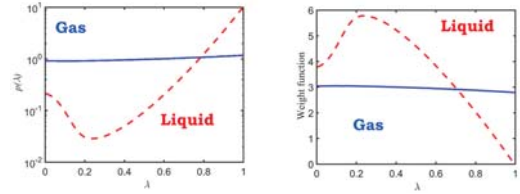


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Chemical Potential

$$\mu_j \approx -k_b T \ln \left(\frac{V_i / \Lambda^3}{N_i + 1} \right) - k_b T \ln \left(\frac{p_i(\lambda \uparrow 1)}{p_i(\lambda \downarrow 0)} \right)$$

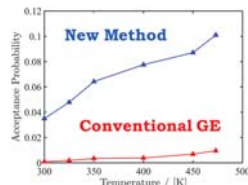


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Performance

- Excellent agreement in densities and chemical potentials for TiP3P-EW water model
- **30 times higher** acceptance for molecule exchange at low temperatures



GE					
T / [K]	ρ_l / [kg m ⁻³]	ρ_g / [kg m ⁻³]	μ_l / [kJ mol ⁻¹]	μ_g / [kJ mol ⁻¹]	$P_{\text{acc}}(\text{Swap})_{\text{GE}}$
400	882 (2)	1.7 (1)	-32 (2)	-33.1 (1)	2.80×10^{-3}
450	798 (2)	6.8 (1)	-32.2 (8)	-32.9 (2)	6.83×10^{-3}
473	754 (5)	12.2 (5)	-32.4 (7)	-33.0 (3)	9.52×10^{-3}

CFMCGE					
T / [K]	ρ_l / [kg m ⁻³]	ρ_g / [kg m ⁻³]	μ_l / [kJ mol ⁻¹]	μ_g / [kJ mol ⁻¹]	$P_{\text{acc}}(\text{Change})_{\text{CFMCGE}}$
400	882 (2)	1.7 (1)	-33.2 (6)	-33.0 (1)	7.75×10^{-2}
450	798 (2)	6.7 (1)	-33.3 (5)	-32.8 (1)	8.71×10^{-2}
473	753 (2)	12.2 (2)	-33.4 (5)	-32.9 (1)	1.01×10^{-1}

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Chemical Potential

- Widom insertion method fails to compute the correct chemical potential of the liquid phase

$$\mu_j \approx -k_b T \ln \left(\frac{V_i / \Lambda^3}{N_i + 1} \right) - k_b T \ln \left(\frac{p_i(\lambda \uparrow 1)}{p_i(\lambda \downarrow 0)} \right)$$

T=350K	New Method		Widom	
	μ_l / [kJ mol ⁻¹]	μ_g / [kJ mol ⁻¹]	μ_l / [kJ mol ⁻¹]	μ_g / [kJ mol ⁻¹]
SPC	-33.3(4)	-33.6(1)	-31(2)	-33.6(1)
TiP3P-EW	-33.3(4)	-33.6(1)	-31(2)	-36.6(1)
TiP4P-EW	-35.6(4)	-36.5(2)	-32(1)	-36.5(1)
TiP5P-EW	-31.1(5)	-31.5(1)	-29(1)	-31.5(1)

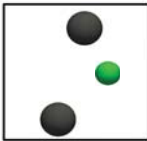
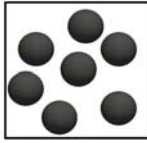
- New method does not rely on occurrence of spontaneous cavities in liquid

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Today's Exercise

- Simulate the VLE of LJ particles using CFCMC GE algorithm
 - Calculate the chemical potential of the two phases
 - How Wang-Landau algorithm works?
 - Importance of using an appropriate weight function
 - Effect of the density on acceptance probabilities
 - Comparison of conventional GE / CFCMC GE in terms of results/efficiency



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Questions?

References:

- Poursaeidesfahani, et al, J. Chem. Theo. Comp., 2016, 12, 1481–1490
- Poursaeidesfahani, et al, J. Mol. Sim., 2017, 43.3, 189-195

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Gibbs Ensemble

- Vapour-Liquid Equilibria (VLE) is very important for many processes
- Simulations in the Gibbs Ensemble are widely used to study VLE
- Fixed temperature $\Rightarrow T_1 = T_2$
- Volume exchange $\Rightarrow P_1 = P_2$
- Molecule exchange $\Rightarrow \mu_1 = \mu_2$
- Very low number of molecule exchange at low temperatures (high liquid density)



$$\mu_1 \stackrel{?}{=} \mu_2$$

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