## Single Point Energies And Geometry Optimizations

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## Single Point Energy Calculations

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- Solution of Schrödinger Equation for Molecule with Specified Geometric Structure - E and geometry
- $v$ and thermodynamic properties
- NMR
- Electronic distributions
- Other static properties
- Validity
- Reasonable structure
- Choice of level
- Choice of basis set
- Purpose
- Only "affordable" calculation
- Starting point for optimization
- Estimate time of optimization
- Calculate specific molecular properties after optimization
- Calculate accurate values of $E$ and related properties at a higher level of theory following lower level optimization


## Potential Energy Surfaces (PES)

$E$ and other properties are function of geometry

- Mathematical relationship of $E$ as a function of structure
- Surface has as many dimensions as number of internal degrees of freedom in molecule
- Diatomic molecule AB
$-r_{\mathrm{AB}}$
- Nonlinear triatomic molecule ABC
$-r_{\mathrm{AB}}$ and $r_{\mathrm{BC}}$ (unless identical)
- A-B-C bond angle

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## PES Features

Minima

- Bottom of "Valley" on PES
- Changing any geometric parameter increases $E$
- Equilibrium structures of molecule
- Different conformers
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- Structural isomers
- Reactant and product $\qquad$
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## Geometry Optimization

- Locating Extremum of PES
- Minimization gives equilibrium structure(s)
- Saddle point corresponds to transition structure
- Calculus at Extremum for Multidimensional Function
- Gradient $=\mathbf{g}_{\mathrm{i}}=\partial E / \partial \mathbf{v}_{\mathrm{i}}=0$
- Force $=-($ gradient $)=0$
- "stationary point" is location on PES where forces $=0$
- Force constant $=\partial^{2} E / \partial \mathbf{v}_{i}^{2}$
- Specifies "curvature" of surface at point
- All > 0 at stationary point
- All >0 except one $<0$ at (1st order) saddle point
- "Hessian" is matrix of second derivatives

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## Optimization Methods

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"Simple" Method $\qquad$
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- Procedure
- Minimize E with respect to only one variable $\qquad$ holding all others constant
- Change variable to optimum value
- Repeat minimization with respect to a second
$\qquad$ variable holding all others constant
- Change second variable to optimum value
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- Continue for each variable

Problems

- Variables are not independent
- Linear molecules like acetylene are often problems
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- Several cycles are needed
- "Expensive" for large molecules
- "Real" methods
- Use all variables
- Three general approaches: SD, CG, NR


## Optimization Methods

- Change coordinates in direction opposite the maximum of gradient using a unit vector $\mathbf{s}_{\mathbf{i}}=$
$\qquad$ $-g_{i}\left|g_{i}\right|$
- Line search method for distance
- Find 3 points such that inner point is lower in $E$ than outer points
- Thus at least one minimum lies between outer points
- Iterate decreasing distance
- Recalculate $\mathbf{g}_{i+1}$ and repeat

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## Optimization Methods

## Conjugate Gradient Method (CG)

- Mixture of current gradient and previous search direction
- Procedure
- First step: SD
- Subsequent steps: $\mathbf{v}_{i+1}=-\mathbf{g}_{i+1}+\gamma_{i+1} \mathbf{v}_{\mathrm{i}}$
- Fletcher-Reeves: $\gamma_{i+1}=\left(\mathbf{g}_{i+1} \bullet \mathbf{g}_{i+1}\right) /\left(\mathbf{g}_{i} \bullet \mathbf{g}_{\mathrm{i}}\right)$
- Polak-Ribiere (common): $\mathrm{y}_{i+1}=\left[\left(\mathbf{g}_{i+1}-\mathbf{g}_{i}\right) \cdot \mathbf{g}_{i+1}\right] /\left(\mathbf{g}_{i} \cdot \mathbf{g}_{i}\right)$
- Hestenes-Stifel: $\gamma_{i+1}=\left[\left(\mathbf{g}_{i+1}-\mathbf{g}_{i}\right) \cdot \mathbf{g}_{i+1}\right] /\left[\mathbf{v}_{i} \bullet\left(\mathbf{g}_{i+1}-\mathbf{g}_{i}\right)\right]$
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## Optimization Methods

## Newton-Raphson (NR)

## - Includes Hessian

- Advantages
- Locates minima and saddle points
- Convergence is second order near stationary point
- Problems
- Control of step size
- Calculation of Hessian required
- Several variations of NR


## Global Minimum

- Optimization Results
- Above methods locate the "nearest" minimum (local?)
- Conformers and transition structures are related to local minima and saddle points
- Molecular properties are related to global minimum--the most stable structure
- Several approaches to finding the global minimum - NO Guarantees!!!

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## Global Minimum Methods

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Grid Search

- Simple
- Calculate all possible energies
- Prepare energy map or table
- Choose best structure
- Problems
- Number of minima increases exponentially with the number of variables
- Not practical for large or biomolecules
- Build structures from optimized fragments
- Optimize portions of molecule

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Example: $\mathrm{CH}_{3}\left(\mathrm{CH}_{2}\right)_{n+1} \mathrm{CH}_{3}$

| $n=1$ | $N=3^{1}=3$ | $t=3 \mathrm{~s}$ |
| :--- | :--- | :--- |
| $n=2$ | $N=3^{2}=9$ | $t=9 \mathrm{~s}$ |
| $n=5$ | $N=3^{5}=243$ | $t=\sim 4 \mathrm{~min}$ |
| $n=10$ | $N=3^{10}=59 \mathrm{k}$ | $t=\sim 16 \mathrm{~h}$ |
| $n=15$ | $N=3^{15}=14 \mathrm{M}$ | $t=\sim 160 \mathrm{~d}$ |

## Global Minimum Methods

Other

- Monte Carlo
- Usually start at a minimum
- Randomly change one or several angles or bond

lengths to generate new geometry
-
$\quad$ Calculate $E$

- If $E$ is lower, accept new geometry

distribution related to the energy change and $T$

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- Molecular Dynamics
- Based on Newton's equations of motion for atoms
- Molecule overcomes barrier between minima if kinetic energy is great enough
- Similar to climbing out a valley over a mountain
- Kinetic energy is proportional to $T$
- Use elevated temperatures ( $600-1200 \mathrm{~K}$ )
- High temperatures reduce chance of trapping molecule in a local minimum
- Essentially searches PES in the region of the starting minimum
- Simulated Annealing
- Molecular dynamics variation
- Start with high $T$ ( $2000-3000 \mathrm{~K}$ )
- Reduce $T$
- Molecule trapped in a minimum
- Similar to playing roulette
- Very slow cooling might give global minimum
- Repeat to get many results
- Choose best
- Genetic Algorithm
- Use several low energy structures as "parents" to generate "off spring" that might be better
- Distance Geometry
- Based on establishing minimum and maximum distances between all pairs of atoms

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