

# 43384 – Digital Alchemy

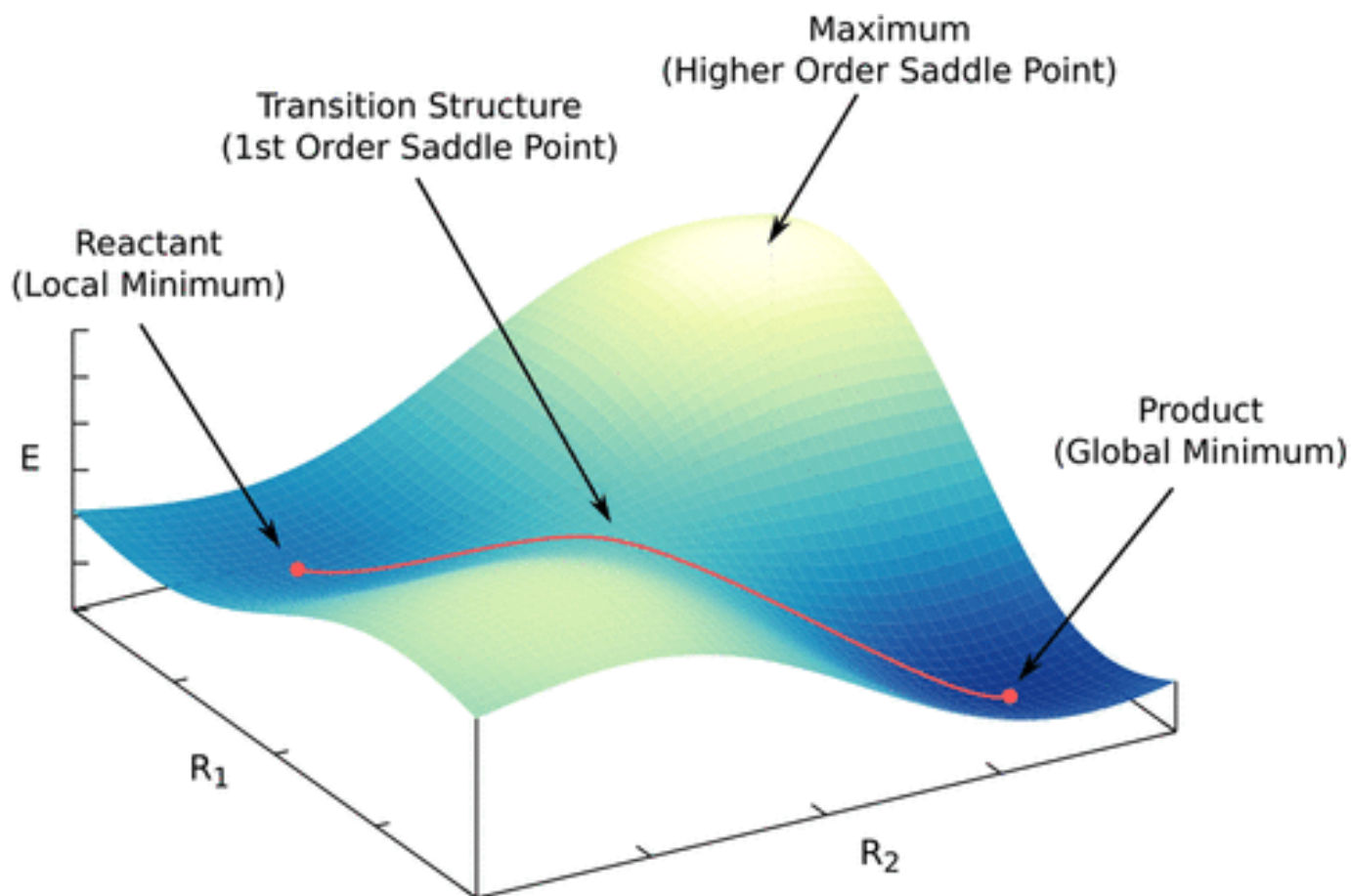
Unit 05 – Molecular Structure Optimization

**Prof. Dr. Carolin Müller**

November 11, 2025

# Optimization of Molecular Structures


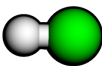
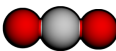
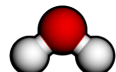
## Concept: Potential Energy Surface (PES)



# Potential Energy Surfaces (PESs)

## Internal degrees of freedom


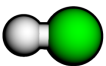
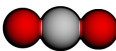
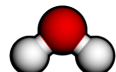
- A molecule with  $N$  atoms has  $3N$  degrees of freedom:

Type of molecule	$N$	$3N$	modes
monoatomic,	1	3	
e.g., Ne 			
diatomic,	2	6	
e.g., HCl 			
triatomic linear,	3	9	
e.g. CO <sub>2</sub> 			
triatomic non-linear,	3	9	
e.g. H <sub>2</sub> O 			

# Potential Energy Surfaces (PESs)

## Internal degrees of freedom



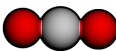
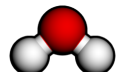
- A molecule with  $N$  atoms has  $3N$  degrees of freedom:
  - translational modes: 3

Type of molecule	$N$	$3N$	modes
monoatomic, e.g., Ne 	1	3	<b>3</b> translational
diatomic, e.g., HCl 	2	6	<b>3</b> translational
triatomic linear, e.g. CO <sub>2</sub> 	3	9	<b>3</b> translational
triatomic non-linear, e.g. H <sub>2</sub> O 	3	9	<b>3</b> translational

# Potential Energy Surfaces (PESs)

## Internal degrees of freedom



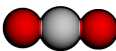
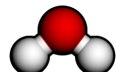
- A molecule with  $N$  atoms has  $3N$  degrees of freedom:
  - translational modes: 3
  - rotational modes:
    - ▶ **non-linear** molecule: 3
    - ▶ **linear** molecule: 2

Type of molecule	$N$	$3N$	modes
monoatomic, e.g., Ne 	1	3	<b>3</b> translational
diatomic, e.g., HCl 	2	6	<b>3</b> translational
triatomic linear, e.g. CO <sub>2</sub> 	3	9	<b>3</b> translational
triatomic non-linear, e.g. H <sub>2</sub> O 	3	9	<b>3</b> translational

# Potential Energy Surfaces (PESs)

## Internal degrees of freedom



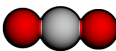
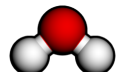
- A molecule with  $N$  atoms has  $3N$  degrees of freedom:
  - translational modes: 3
  - rotational modes:
    - ▶ **non-linear** molecule: 3
    - ▶ **linear** molecule: 2

Type of molecule	$N$	$3N$	modes
monoatomic, e.g., Ne 	1	3	<b>3</b> translational <b>0</b> rotational
diatomic, e.g., HCl 	2	6	<b>3</b> translational <b>2</b> rotational
triatomic linear, e.g. CO <sub>2</sub> 	3	9	<b>3</b> translational <b>2</b> rotational
triatomic non-linear, e.g. H <sub>2</sub> O 	3	9	<b>3</b> translational <b>3</b> vibrational

# Potential Energy Surfaces (PESs)

## Internal degrees of freedom


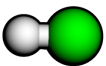
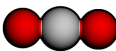
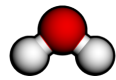
- A molecule with  $N$  atoms has  $3N$  degrees of freedom:
  - translational modes: 3
  - rotational modes:
    - ▶ **non-linear** molecule: 3
    - ▶ **linear** molecule: 2
  - vibrational modes:
    - ▶ **non-linear** molecule:  $3N - 6$
    - ▶ **linear** molecule:  $3N - 5$

Type of molecule	$N$	$3N$	modes
monoatomic, e.g., Ne 	1	3	<b>3</b> translational <b>0</b> rotational
diatomic, e.g., HCl 	2	6	<b>3</b> translational <b>2</b> rotational
triatomic linear, e.g. CO <sub>2</sub> 	3	9	<b>3</b> translational <b>2</b> rotational
triatomic non-linear, e.g. H <sub>2</sub> O 	3	9	<b>3</b> translational <b>3</b> vibrational

# Potential Energy Surfaces (PESs)

## Internal degrees of freedom

- A molecule with  $N$  atoms has  $3N$  degrees of freedom:
  - translational modes: 3
  - rotational modes:
    - ▶ **non-linear** molecule: 3
    - ▶ **linear** molecule: 2
  - vibrational modes:
    - ▶ **non-linear** molecule:  $3N - 6$
    - ▶ **linear** molecule:  $3N - 5$


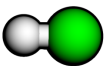
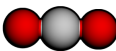
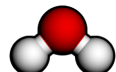
Type of molecule	$N$	$3N$	modes
monoatomic, e.g., Ne 	1	3	3 translational 0 rotational 0 vibrational
diatomic, e.g., HCl 	2	6	3 translational 2 rotational 1 vibrational
triatomic linear, e.g. CO <sub>2</sub> 	3	9	3 translational 2 rotational 4 vibrational
triatomic non-linear, e.g. H <sub>2</sub> O 	3	9	3 translational 3 rotational 3 vibrational



# Potential Energy Surfaces (PESs)

## Internal degrees of freedom

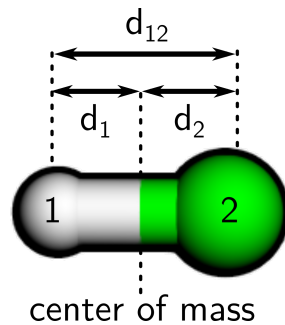
- A molecule with  $N$  atoms has  $3N$  degrees of freedom:
  - translational modes: 3
  - rotational modes:
    - ▶ **non-linear** molecule: 3
    - ▶ **linear** molecule: 2
  - vibrational modes:
    - ▶ **non-linear** molecule:  $3N - 6$
    - ▶ **linear** molecule:  $3N - 5$
- Once a linear molecule bends, it is no longer linear, so even a linear molecule can have its internal coordinates described by  $3N - 6$  coordinates.

Type of molecule	$N$	$3N$	modes
monoatomic, e.g., Ne 	1	3	3 translational 0 rotational 0 vibrational
diatomic, e.g., HCl 	2	6	3 translational 2 rotational 1 vibrational
triatomic linear, e.g. CO <sub>2</sub> 	3	9	3 translational 2 rotational 4 vibrational
triatomic non-linear, e.g. H <sub>2</sub> O 	3	9	3 translational 3 rotational 3 vibrational

# PESs of diatomic molecules: 1D case

## Example: HCl

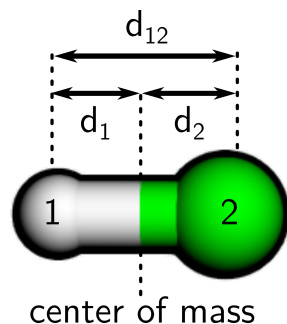
Internal coordinate in HCl:  $d(\text{H}, \text{Cl})$



# PESs of diatomic molecules: 1D case

## Example: HCl

Internal coordinate in HCl:  $d(\text{H}, \text{Cl})$



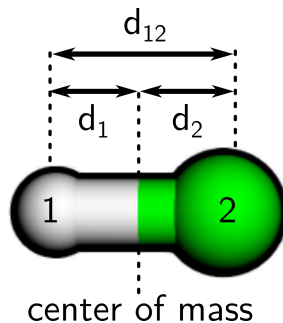
Scan of internal coordinate with VeloxChem:

```
1 import veloxchem as vlx
2
3 # Molecule specification
4 hcl_xyz = '2
5 XYZ of HCl
6 H    0.00 0.00 0.00
7 Cl   0.00 0.00 1.10'
8 hcl_mol = vlx.Molecule.
   read_xyz_string(hcl_xyz)
```

# PESs of diatomic molecules: 1D case

## Example: HCl

Internal coordinate in HCl:  $d(\text{H}, \text{Cl})$



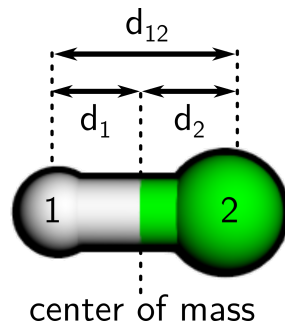
Scan of internal coordinate with VeloxChem:

```
1 import veloxchem as vlx
2
3 # Molecule specification
4 hcl_xyz = '2
5 XYZ of HCl
6 H    0.00 0.00 0.00
7 Cl   0.00 0.00 1.10'
8 hcl_mol = vlx.Molecule.
9           read_xyz_string(hcl_xyz)
10
11 # Optimization method
12 scf_drv = vlx.XtbDriver()
13 opt_drv = vlx.OptimizationDriver
14           (scf_drv)
```

# PESs of diatomic molecules: 1D case

## Example: HCl

Internal coordinate in HCl:  $d(\text{H}, \text{Cl})$



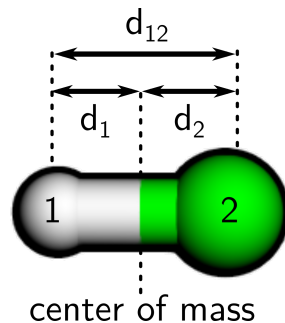
Scan of internal coordinate with VeloxChem:

```
1  import veloxchem as vlx
2
3  # Molecule specification
4  hcl_xyz = '2
5  XYZ of HCl
6  H    0.00 0.00 0.00
7  Cl   0.00 0.00 1.10'
8  hcl_mol = vlx.Molecule.
9             read_xyz_string(hcl_xyz)
10
11 # Optimization method
12 scf_drv = vlx.XtbDriver()
13 opt_drv = vlx.OptimizationDriver
14           (scf_drv)
15
16 # Constrained coordinate
17 opt_drv.constraints = ['scan
18                        distance 1 2 1 3 30']
```

# PESs of diatomic molecules: 1D case

## Example: HCl

Internal coordinate in HCl:  $d(\text{H}, \text{Cl})$



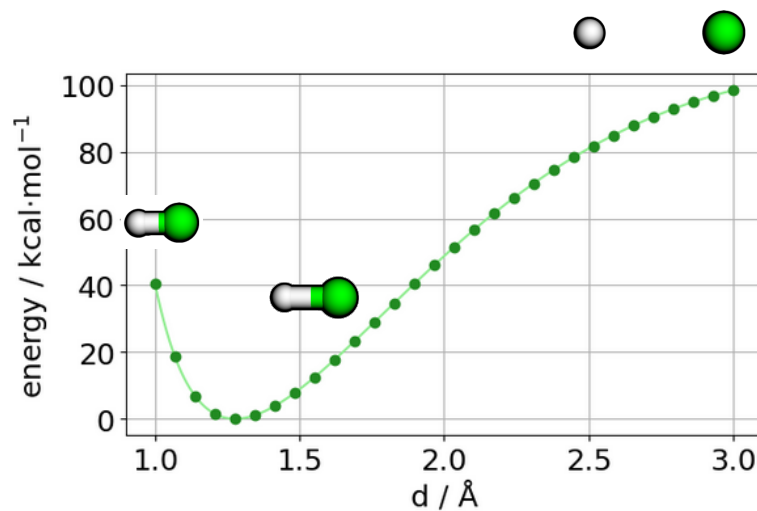
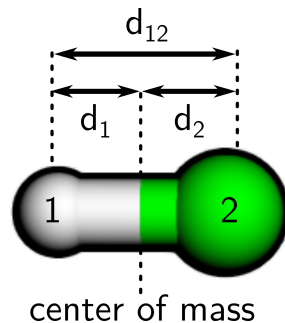
Scan of internal coordinate with VeloxChem:

```
1 import veloxchem as vlx
2
3 # Molecule specification
4 hcl_xyz = '2
5 XYZ of HCl
6 H    0.00 0.00 0.00
7 Cl   0.00 0.00 1.10'
8 hcl_mol = vlx.Molecule.
9         read_xyz_string(hcl_xyz)
10
11 # Optimization method
12 scf_drv = vlx.XtbDriver()
13 opt_drv = vlx.OptimizationDriver
14         (scf_drv)
15
16 # Constrained coordinate
17 opt_drv.constraints = ['scan
18                        distance 1 2 1 3 30']
19
20 opt_res_scan = opt_drv.compute(
21     hcl_mol)
```

# PESs of diatomic molecules: 1D case

## Example: HCl

Internal coordinate in HCl:  $d(\text{H}, \text{Cl})$



Scan of internal coordinate with VeloxChem:

```
1 import veloxchem as vlx
2
3 # Molecule specification
4 hcl_xyz = '2
5 XYZ of HCl
6 H    0.00 0.00 0.00
7 Cl   0.00 0.00 1.10'
8 hcl_mol = vlx.Molecule.
9         read_xyz_string(hcl_xyz)
10
11 # Optimization method
12 scf_drv = vlx.XtbDriver()
13 opt_drv = vlx.OptimizationDriver
14         (scf_drv)
15
16 # Constrained coordinate
17 opt_drv.constraints = ['scan
18                        distance 1 2 1 3 30']
19
20 opt_res_scan = opt_drv.compute(
21     hcl_mol)
```

# PESs triatomic non-linear molecules

## Example: Water

Scan of internal coordinate with VeloxChem:

```
1 import veloxchem as vlx
2
3 # Molecule and optimizer
4 h2o_mol = vlx.Molecule.
   read_xyz_string(h2o_xyz)
5 scf_drv = vlx.XtbDriver()
6 opt_drv = vlx.OptimizationDriver
   (scf_drv)
7
8 # Constrained coordinates
9 opt_drv.constraints = [
10     'scan distance 1 2 0.6 1.5 18'
11     ,
12     'scan distance 1 3 0.6 1.5 18'
13     ]
14
15 opt_res_scan = opt_drv.compute(
16     h2o_mol)
```



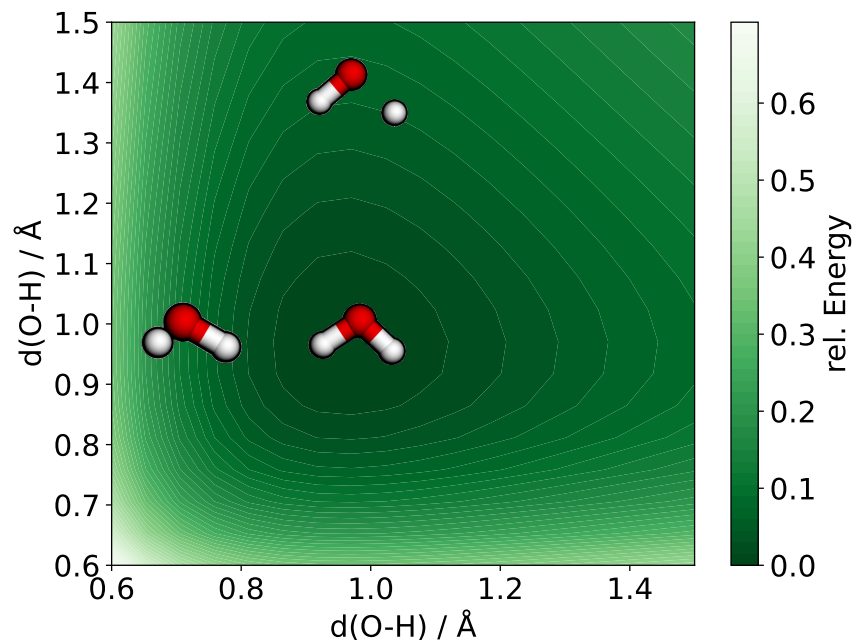
# PESs triatomic non-linear molecules

## Example: Water

Scan of internal coordinate with VeloxChem:

```
1 import veloxchem as vlx
2
3 # Molecule and optimizer
4 h2o_mol = vlx.Molecule.
   read_xyz_string(h2o_xyz)
5 scf_drv = vlx.XtbDriver()
6 opt_drv = vlx.OptimizationDriver
   (scf_drv)
7
8 # Constrained coordinates
9 opt_drv.constraints = [
10     'scan distance 1 2 0.6 1.5 18'
11     ,
12     'scan distance 1 3 0.6 1.5 18'
13     ]
14
15 opt_res_scan = opt_drv.compute(
16     h2o_mol)
```

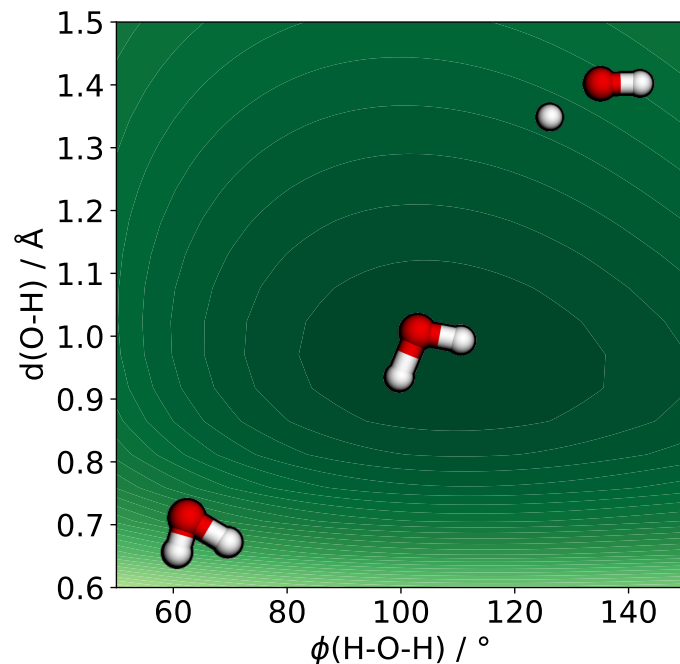
Symmetric stretching mode:



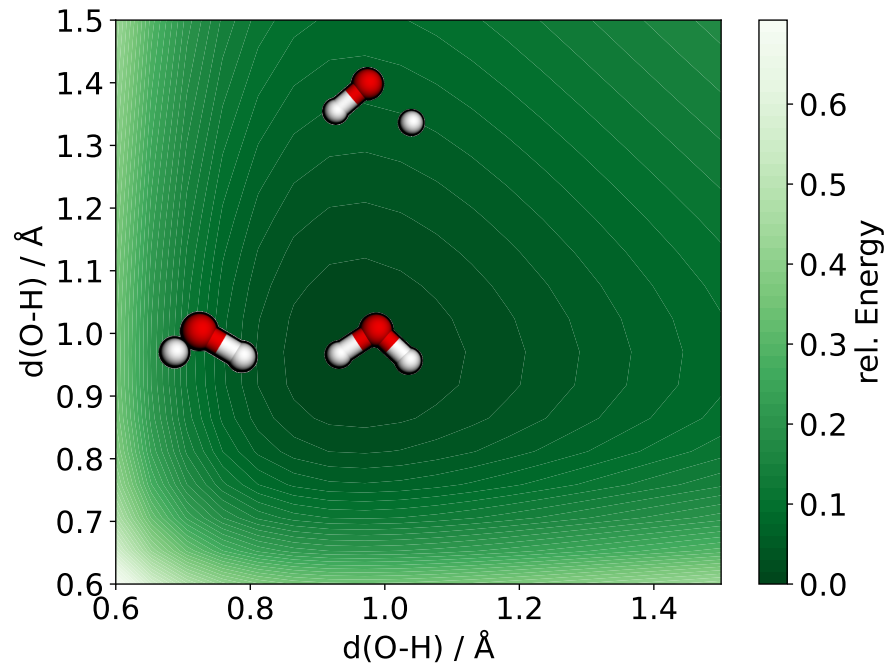
# PESs triatomic non-linear molecules

## Example: Water

Asymmetric stretching and bending modes:



Symmetric stretching mode:



# PESs 4-atomic non-linear molecules

Example: Hydrogen peroxide ( $\text{H}_2\text{O}_2$ )

---

- 12 degrees of freedom:

# PESs 4-atomic non-linear molecules

Example: Hydrogen peroxide ( $\text{H}_2\text{O}_2$ )

---

- 12 degrees of freedom:
  - 3 translational

# PESs 4-atomic non-linear molecules

Example: Hydrogen peroxide ( $\text{H}_2\text{O}_2$ )

---

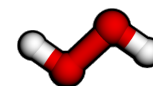
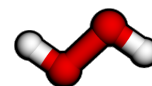
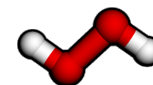
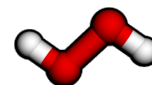
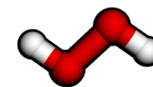
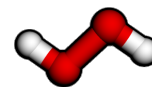
- 12 degrees of freedom:
  - 3 translational
  - 3 rotational

# PESs 4-atomic non-linear molecules

Example: Hydrogen peroxide ( $\text{H}_2\text{O}_2$ )

- 12 degrees of freedom:

- 3 translational
- 3 rotational
- **6 vibrational** →



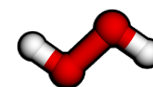
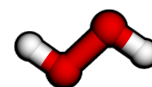
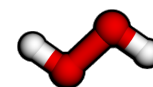
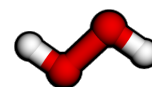
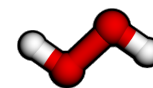
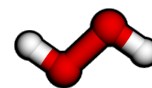
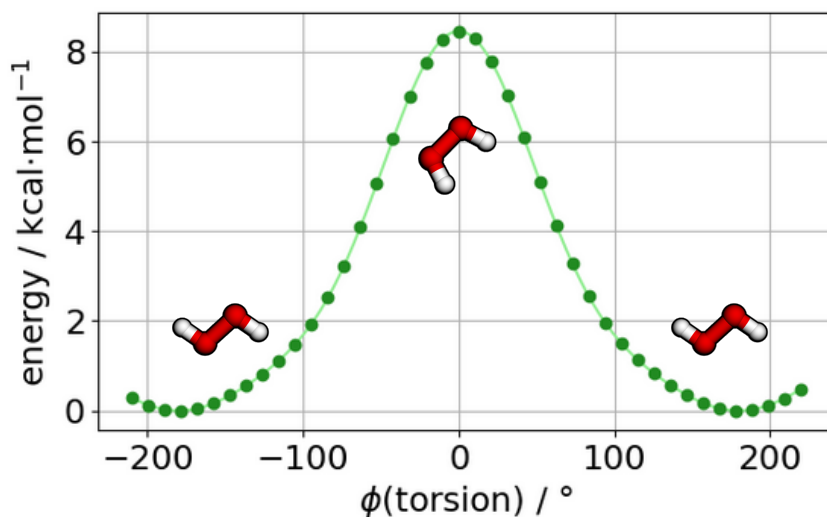
# PESs 4-atomic non-linear molecules

## Example: Hydrogen peroxide ( $\text{H}_2\text{O}_2$ )

- 12 degrees of freedom:

- 3 translational
- 3 rotational
- **6 vibrational** →

Torsion scan,  $\delta(\text{H-O-O-H})$ :

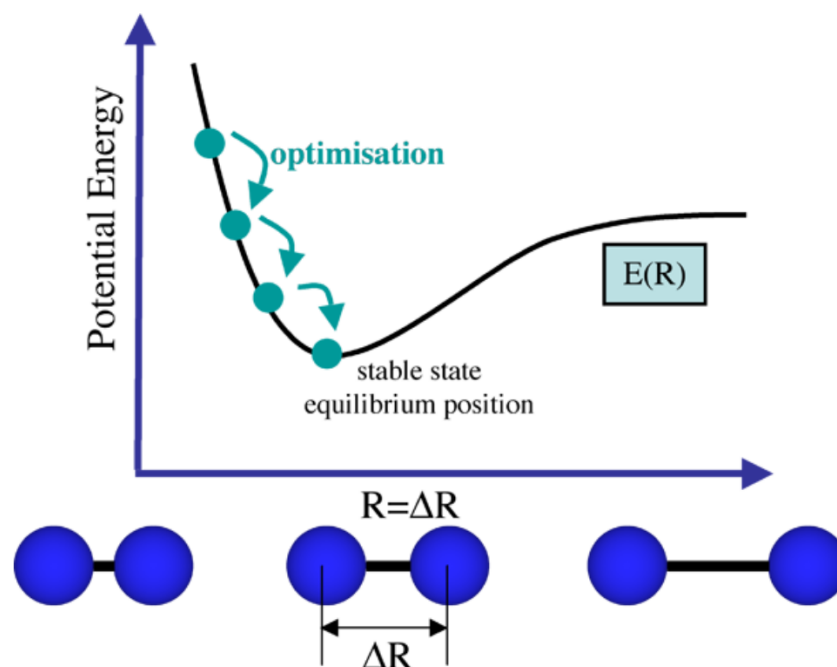


# Optimization of Molecular Structures

## Ingredients of structure optimization

### Structure Optimization

Structure optimization refers to the process of finding the **atomic coordinates** that **minimize** the **energy** of a molecular system, typically corresponding to a local energy minimum on the potential energy surface (PES). A local minimum represents an equilibrium molecular structure, where the first-order energy derivative vanishes, and the Hessian matrix has only positive eigenvalues.





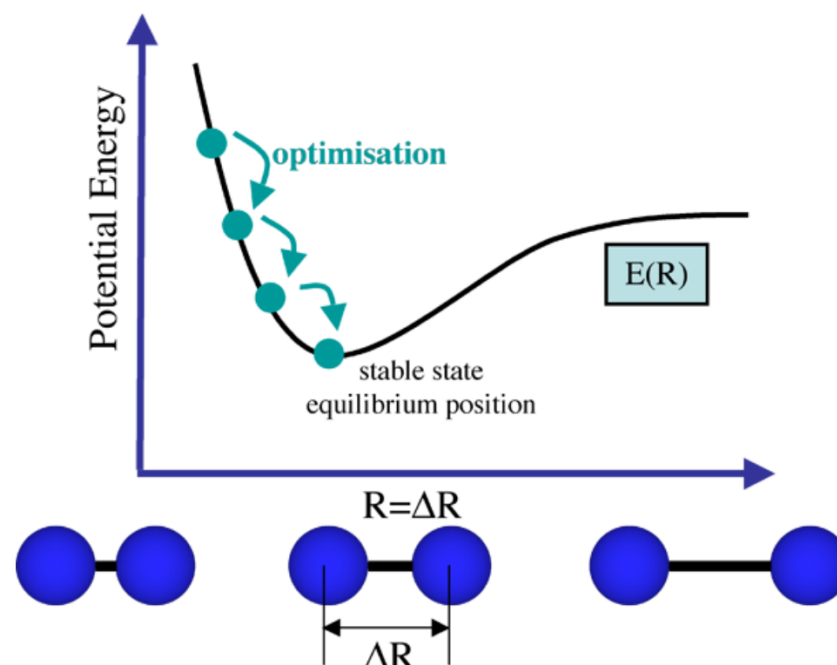
## Ingredients of structure optimization

### Structure Optimization

Structure optimization refers to the process of finding the **atomic coordinates** that **minimize** the **energy** of a molecular system, typically corresponding to a local energy minimum on the potential energy surface (PES). A local minimum represents an equilibrium molecular structure, where the first-order energy derivative vanishes, and the Hessian matrix has only positive eigenvalues.

Ingredients of structure optimization:

1. initial molecular coordinates



# Optimization of Molecular Structures

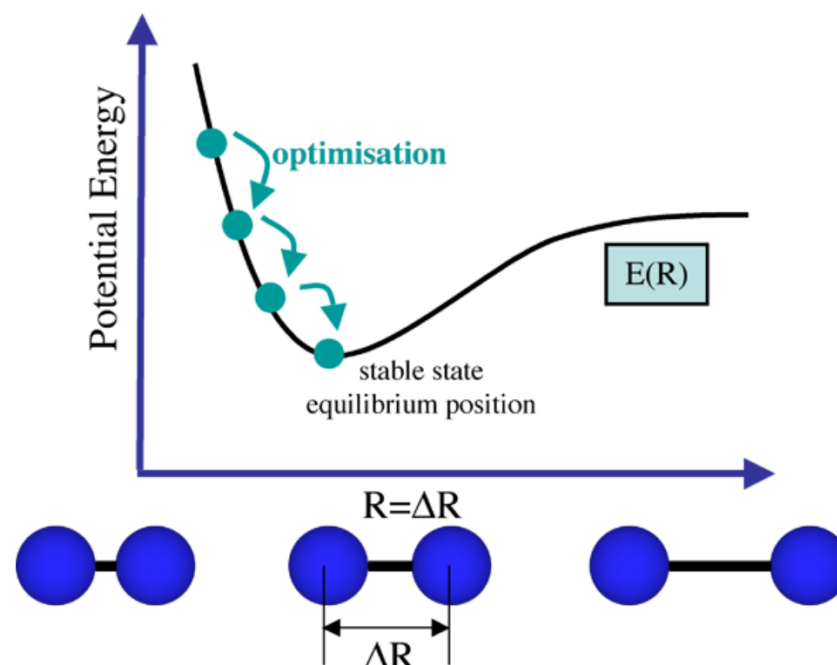
## Ingredients of structure optimization

### Structure Optimization

Structure optimization refers to the process of finding the **atomic coordinates** that **minimize** the **energy** of a molecular system, typically corresponding to a local energy minimum on the potential energy surface (PES). A local minimum represents an equilibrium molecular structure, where the first-order energy derivative vanishes, and the Hessian matrix has only positive eigenvalues.

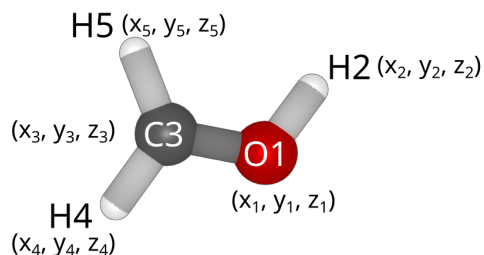
Ingredients of structure optimization:

1. initial molecular coordinates
2. choice of coordinate system



## Choice of coordinates

### Cartesian coordinates



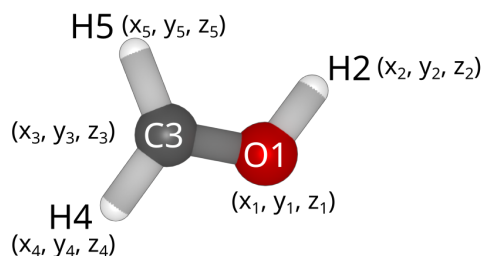
$$3N = 15$$

- Each atomic position is specified by its x, y, and z coordinates.

O	x <sub>1</sub>	x <sub>1</sub>	x <sub>1</sub>
H	x <sub>2</sub>	x <sub>2</sub>	x <sub>2</sub>
C	x <sub>3</sub>	x <sub>3</sub>	x <sub>3</sub>
H	x <sub>4</sub>	x <sub>4</sub>	x <sub>4</sub>
H	x <sub>5</sub>	x <sub>5</sub>	x <sub>5</sub>

## Choice of coordinates

### Cartesian coordinates

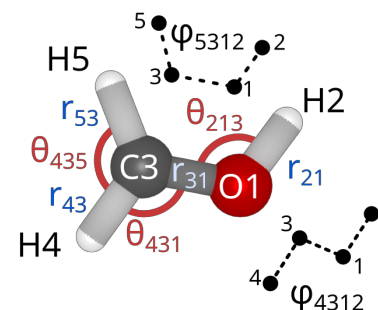


$$3N = 15$$

- Each atomic position is specified by its x, y, and z coordinates.

O	x <sub>1</sub>	x <sub>1</sub>	x <sub>1</sub>
H	x <sub>2</sub>	x <sub>2</sub>	x <sub>2</sub>
C	x <sub>3</sub>	x <sub>3</sub>	x <sub>3</sub>
H	x <sub>4</sub>	x <sub>4</sub>	x <sub>4</sub>
H	x <sub>5</sub>	x <sub>5</sub>	x <sub>5</sub>

### Internal coordinates



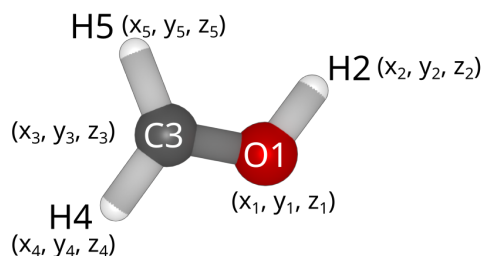
$$3N-6 = 9$$

- bond lengths, valence angles, and dihedrals instead of atomic positions (e.g. Z-matrix)

O						
H	1	r <sub>21</sub>				
C	1	r <sub>31</sub>	2	θ <sub>213</sub>		
H	3	r <sub>43</sub>	1	θ <sub>431</sub>	2	φ <sub>4312</sub>
H	3	r <sub>53</sub>	1	θ <sub>531</sub>	2	φ <sub>5312</sub>

## Choice of coordinates

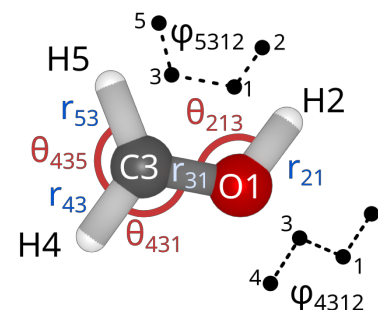
### Cartesian coordinates



$$3N = 15$$

- Each atomic position is specified by its x, y, and z coordinates.
- Advantage: Simplifies calculations of total energy and energy gradients.
- Disadvantage: Not ideal for geometry optimization due to strong coupling between coordinates.

### Internal coordinates

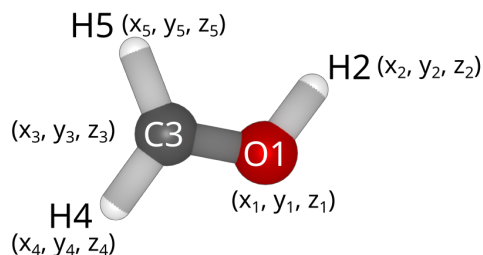


$$3N-6 = 9$$

- bond lengths, valence angles, and dihedrals instead of atomic positions (e.g. Z-matrix)

## Choice of coordinates

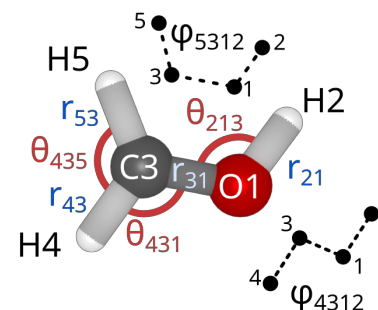
### Cartesian coordinates



$$3N = 15$$

- Each atomic position is specified by its x, y, and z coordinates.
- Advantage: Simplifies calculations of total energy and energy gradients.
- Disadvantage: Not ideal for geometry optimization due to strong coupling between coordinates.

### Internal coordinates



$$3N-6 = 9$$

- bond lengths, valence angles, and dihedrals instead of atomic positions (e.g. Z-matrix)
- Advantage: More suitable for geometry optimization.
- Disadvantage: choice of internal coordinates is not unique, back-conversion to Cartesian coordinates for energy and gradient computations

# Optimization of Molecular Structures

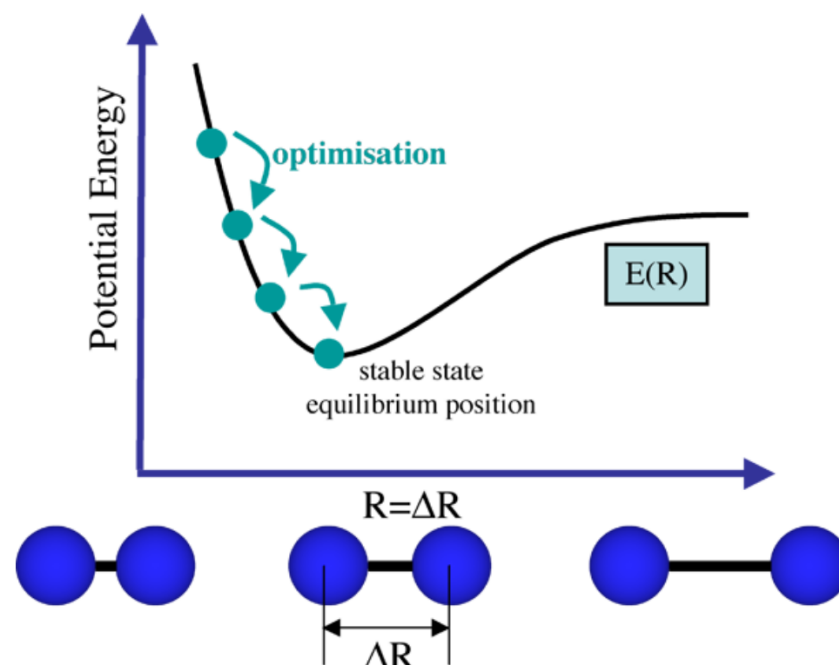
## Ingredients of structure optimization

### Structure Optimization

Structure optimization refers to the process of finding the **atomic coordinates** that **minimize** the **energy** of a molecular system, typically corresponding to a local energy minimum on the potential energy surface (PES). A local minimum represents an equilibrium molecular structure, where the first-order energy derivative vanishes, and the Hessian matrix has only positive eigenvalues.

Ingredients of structure optimization:

1. initial molecular coordinates
2. choice of coordinate system



# Optimization of Molecular Structures

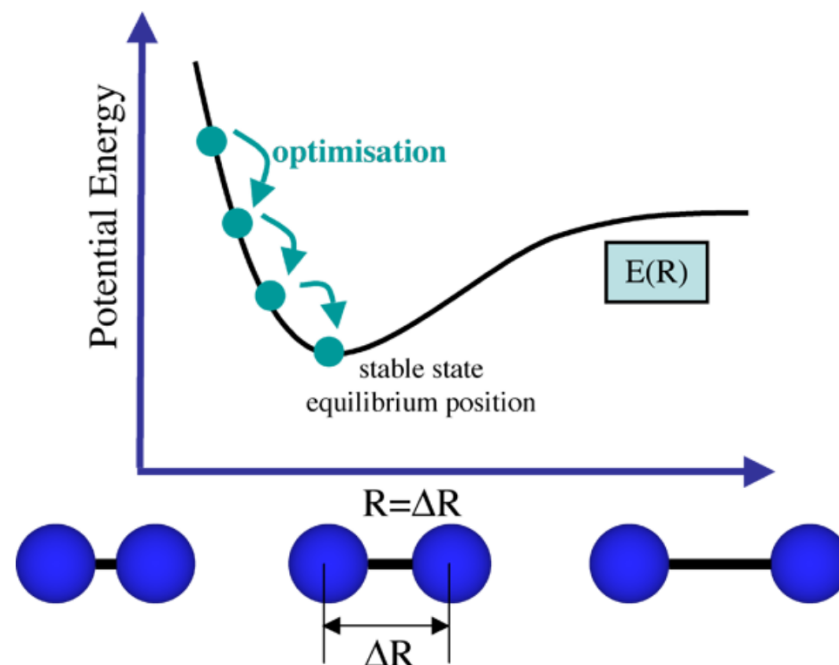
## Ingredients of structure optimization

### Structure Optimization

Structure optimization refers to the process of finding the **atomic coordinates** that **minimize** the **energy** of a molecular system, typically corresponding to a local energy minimum on the potential energy surface (PES). A local minimum represents an equilibrium molecular structure, where the first-order energy derivative vanishes, and the Hessian matrix has only positive eigenvalues.

Ingredients of structure optimization:

1. initial molecular coordinates
2. choice of coordinate system
3. energy at a specific geometry  $E(R)$





# Optimization of Molecular Structures

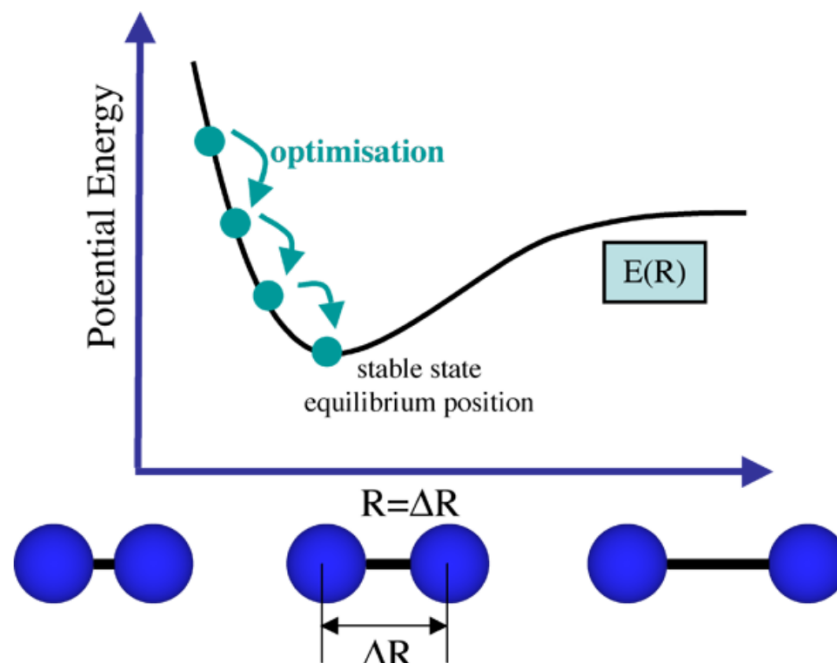
## Ingredients of structure optimization

### Structure Optimization

Structure optimization refers to the process of finding the **atomic coordinates** that **minimize** the **energy** of a molecular system, typically corresponding to a local energy minimum on the potential energy surface (PES). A local minimum represents an equilibrium molecular structure, where the first-order energy derivative vanishes, and the Hessian matrix has only positive eigenvalues.

Ingredients of structure optimization:

1. initial molecular coordinates
2. choice of coordinate system
3. energy at a specific geometry  $E(R)$
4. gradient  $g(R) = \nabla E(R)$



# Optimization of Molecular Structures

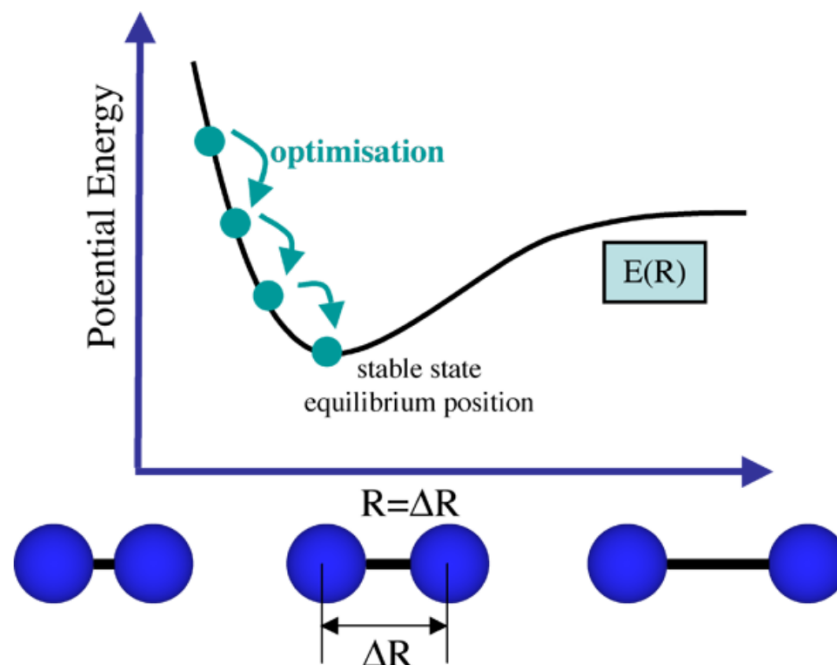
## Ingredients of structure optimization

### Structure Optimization

Structure optimization refers to the process of finding the **atomic coordinates** that **minimize** the **energy** of a molecular system, typically corresponding to a local energy minimum on the potential energy surface (PES). A local minimum represents an equilibrium molecular structure, where the first-order energy derivative vanishes, and the Hessian matrix has only positive eigenvalues.

Ingredients of structure optimization:

1. initial molecular coordinates
2. choice of coordinate system
3. energy at a specific geometry  $E(R)$
4. gradient  $g(R) = \nabla E(R)$
5. Hessian, and



# Optimization of Molecular Structures

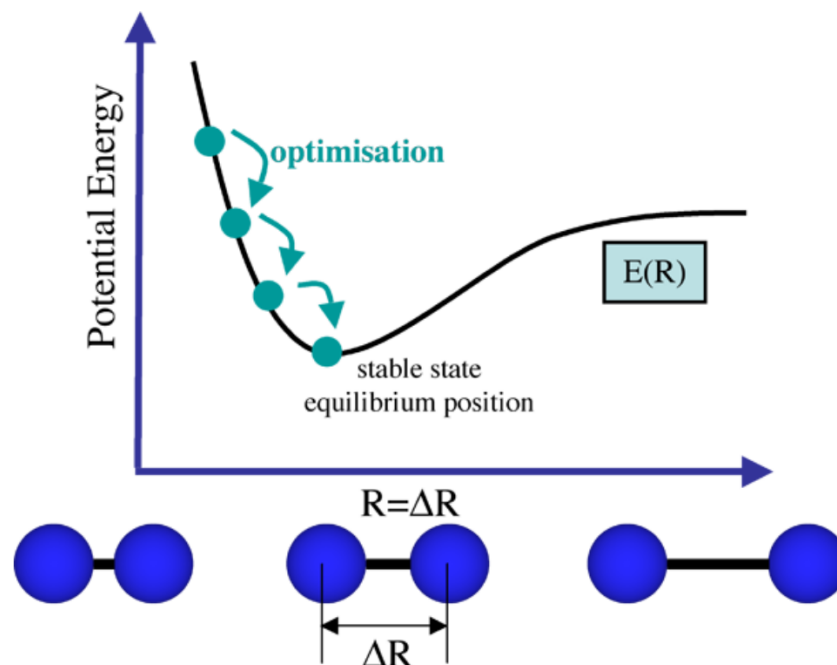
## Ingredients of structure optimization

### Structure Optimization

Structure optimization refers to the process of finding the **atomic coordinates** that **minimize** the **energy** of a molecular system, typically corresponding to a local energy minimum on the potential energy surface (PES). A local minimum represents an equilibrium molecular structure, where the first-order energy derivative vanishes, and the Hessian matrix has only positive eigenvalues.

Ingredients of structure optimization:

1. initial molecular coordinates
2. choice of coordinate system
3. energy at a specific geometry  $E(R)$
4. gradient  $g(R) = \nabla E(R)$
5. Hessian, and
6. procedure to update the coordinates and Hessian and move on the potential energy surface towards lower energy



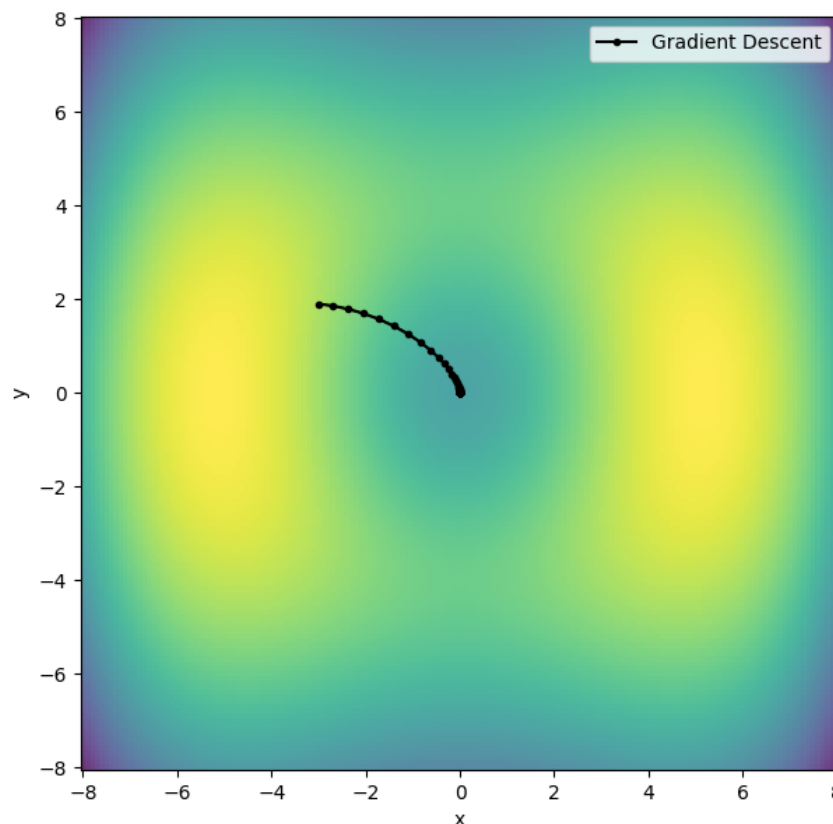
## Optimization algorithm

### Gradient Descent Algorithm

The simplest optimization procedure is to repeatedly take a step in the direction opposite to the local gradient:

$$\mathbf{R}_{i+1} = \mathbf{R}_i - k_i \cdot g(\mathbf{R}) \quad ,$$

where  $\mathbf{R}_{i+1}$  is the new coordinate and  $\mathbf{R}_i$  are the coordinates at the previous step  $i$ ,  $k_i$  is the step size and  $g(\mathbf{R})$  is the gradient. The step size can either be kept constant, or adjusted at each iteration, e.g. by the line search procedure.



## Optimization algorithm

### Conjugate Gradient Algorithm

An improved method over the gradient-descent approach is to use the “gradient history” (steps  $i$  and  $i - 1$ ) to determine the coordinates at step  $i + 1$ :

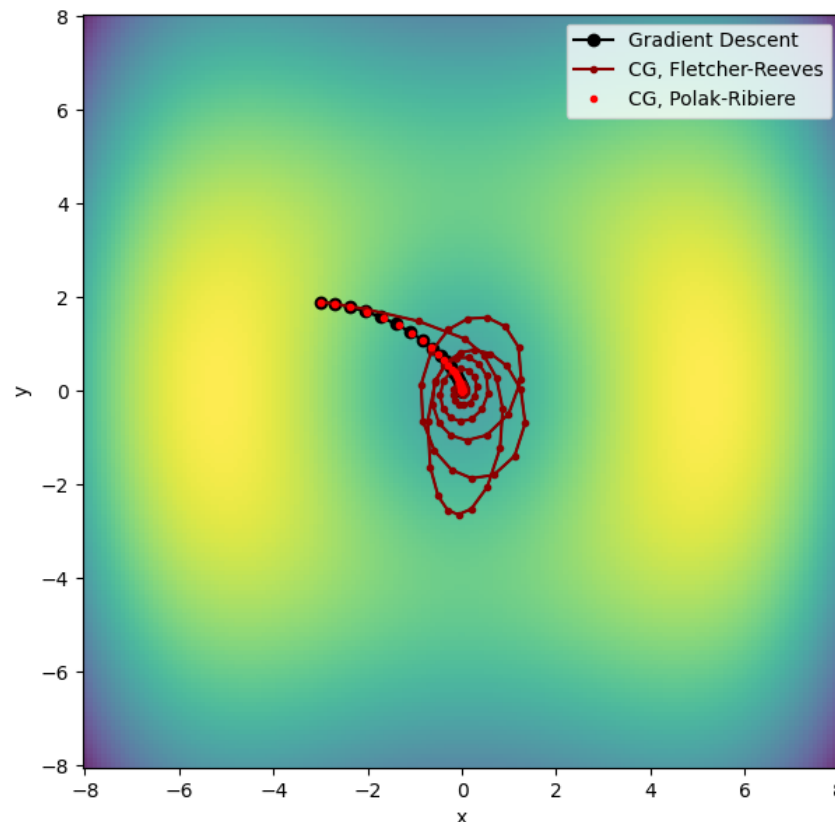
$$\mathbf{R}_{i+1} = \mathbf{R}_i - k_i \cdot \mathbf{h}_i ,$$

with

$$\mathbf{h}_i = g(\mathbf{R}_i) + \gamma_i \cdot \mathbf{h}_{i-1}$$

The function  $\gamma_i$  contains gradient information from steps  $i$  and  $i - 1$ , e.g. Fletcher-Reeves conjugate gradient method:

$$\gamma_i = \frac{|g(\mathbf{R}_i)|^2}{|g(\mathbf{R}_{i-1})|^2}$$



## Optimization algorithm

### Newton-Raphson Algorithm

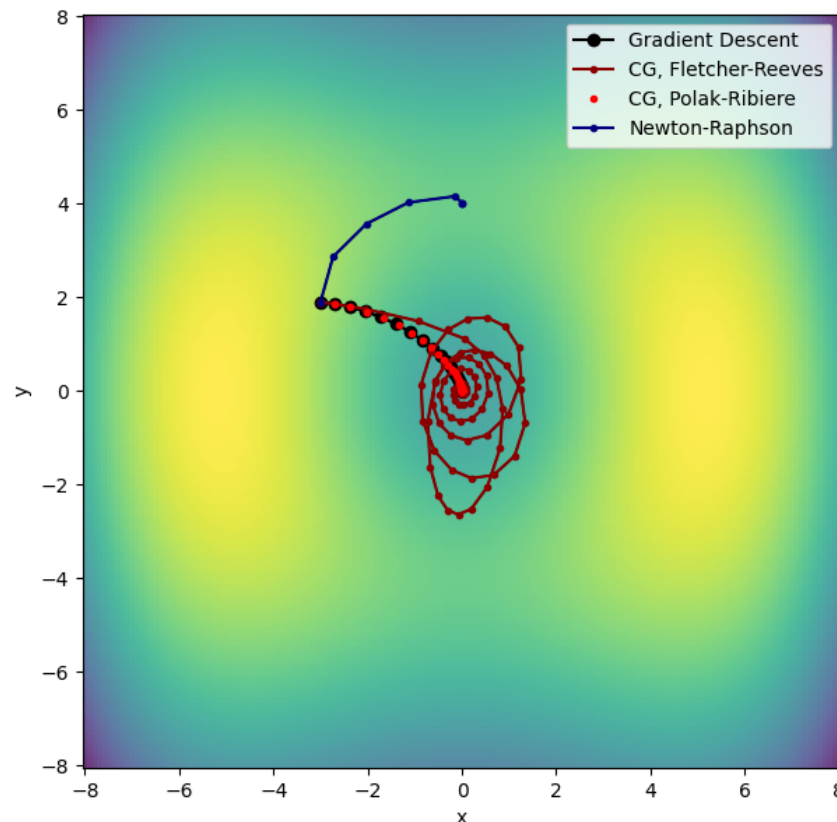
In this minimization method both, the first and second order energy derivatives (*i.e.* gradient and Hessian  $\mathbf{H}$ ) are used in determining the next step in conformation space.

This is based on a quadratic approximation for the local shape of the PES

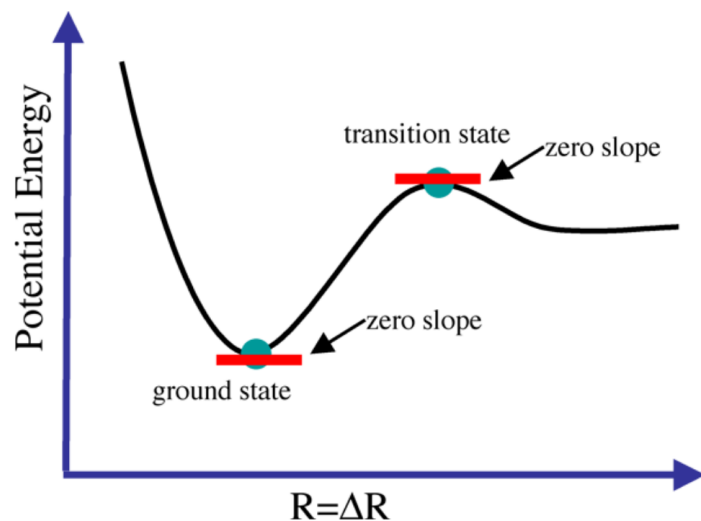
$$E(\mathbf{R} + \Delta\mathbf{R}) \approx E(\mathbf{R}) + g(\mathbf{R})\nabla\mathbf{R} + \frac{1}{2}\nabla\mathbf{R}^T\mathbf{H}\nabla\mathbf{R}$$

Here,  $\nabla\mathbf{R}$  is the Newton step used for updating the coordinates:

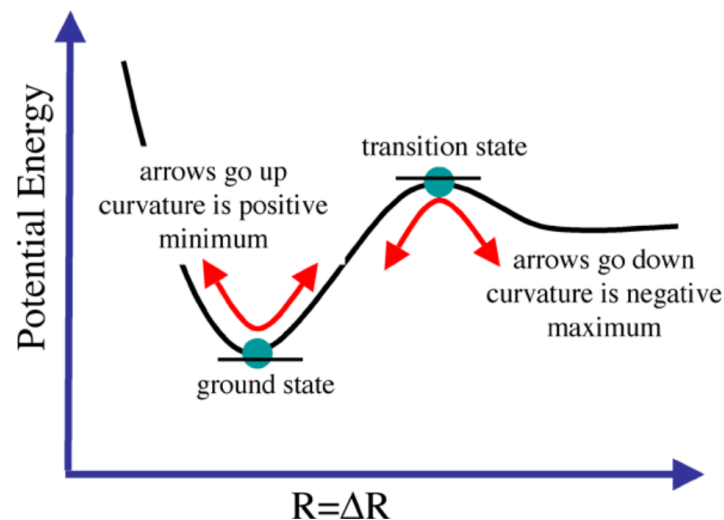
$$\nabla\mathbf{R} = -\mathbf{H}^{-1}g(\mathbf{R})\mathbf{R}_{i+1} = \mathbf{R}_i + \nabla\mathbf{R}$$



## Summary



Minima, transition states: geometries with zero-gradient



Minima: only positive values in Hessian  
transition states: 1 negative value in Hessian

### Ethanol

- optimize geometry (global minimum)
- scan internal coordinates

### Vinyl Alcohol

- optimize geometries of isomers (two local minimum geometries)
- scan coordinates between the two minima

### Ethylene Glycol

- optimize geometries of conformers (multiple local minima)
- scan coordinates between local minima
- interpolate coordinate between local minima