

# Geometry Optimization

## Energy

- Find most stable molecular geometry: Compare conformers
- Find transition state geometries: Identify reaction pathways

## Residuals

- Fitting experimental data: Model observations
- Potential fitting: Simplify calculations
- Machine learning: Surrogate models

## # Solution coefficients $\mathbf{x}$

- Molecular geometries
- Fitting coefficients
- Model coefficients

## # Scalar objective function $f$

- Energy
- Residual norm
- Here: smooth, i.e. differentiable function

$$f(x_1, x_2, \dots, x_n) = f(\mathbf{x}) = y \quad (18)$$

## # Domain $X$

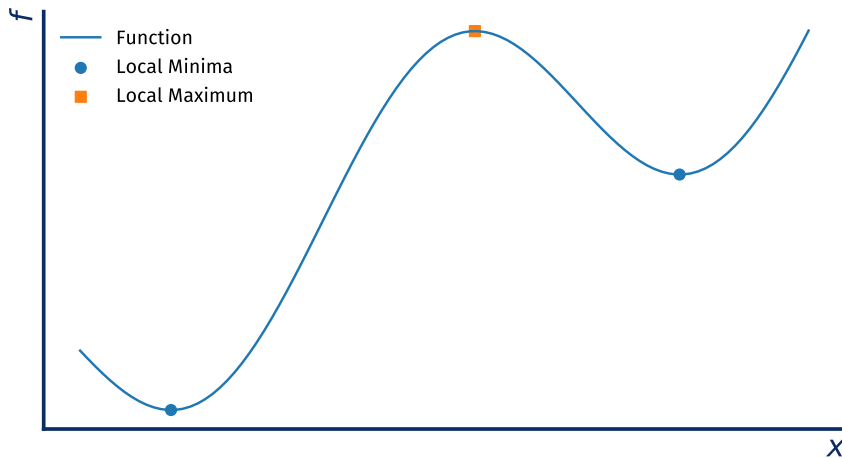
- Valid parameter range
- Any solution within accepted

## # Target $\mathbf{x}_0$

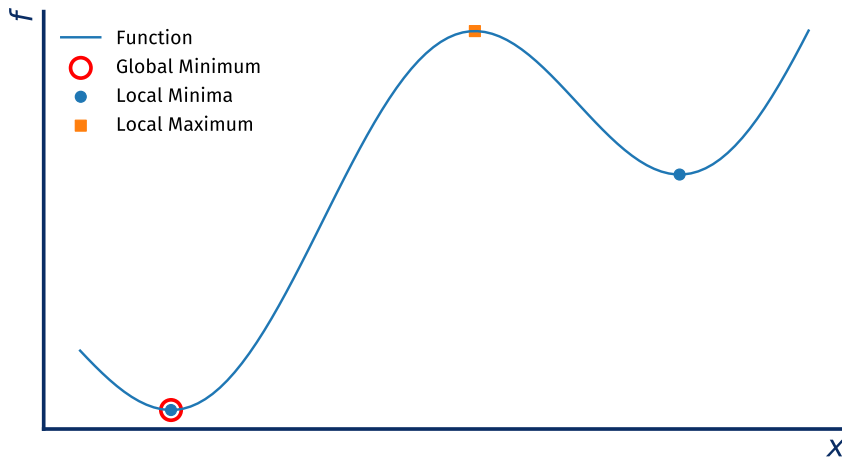
- Maximise or minimise  $y$  (over domain)

$$\begin{aligned} \mathbf{x}_0 &\equiv \arg \min_{\mathbf{x} \in X} f(\mathbf{x}) \\ &= \{\mathbf{x} \mid \mathbf{x}, \mathbf{y} \in X : f(\mathbf{x}) \leq f(\mathbf{y})\} \end{aligned} \quad (19)$$

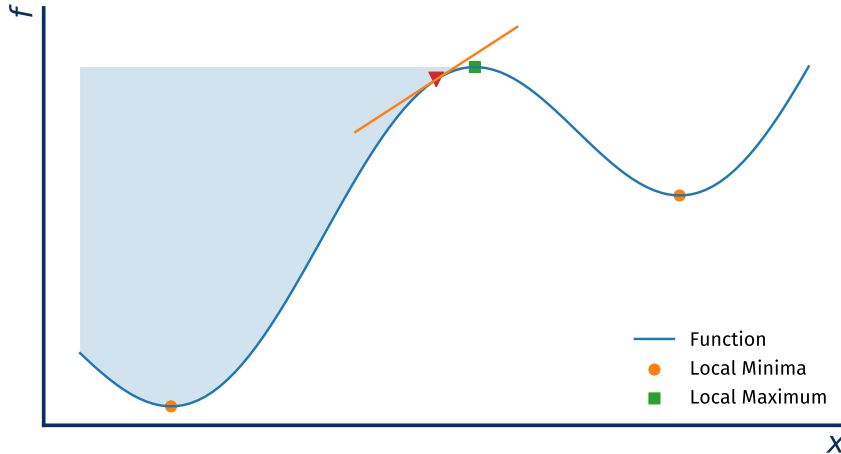
$$\exists \epsilon > 0 : \forall y \in [x_0 - \epsilon, x_0 + \epsilon] : f(x_0) \leq f(y) \quad (20)$$



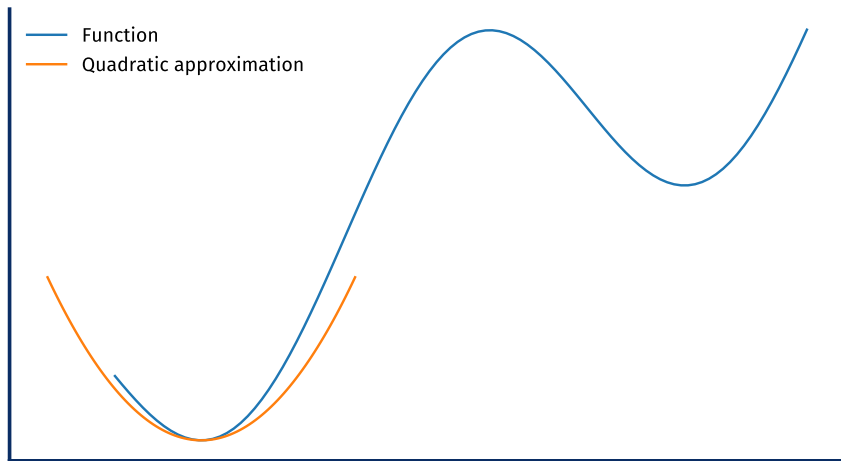
$$\forall y \in X : f(x_0) \leq f(y) \quad (21)$$

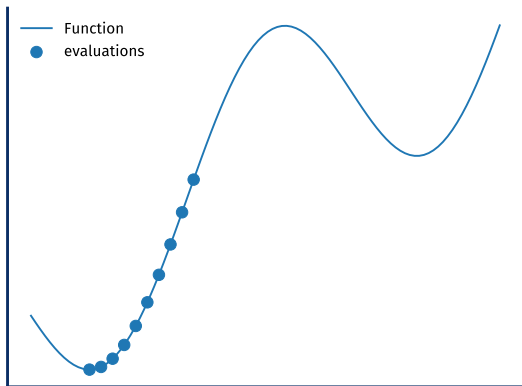


All values that if the gradient is followed reach a given minimum.



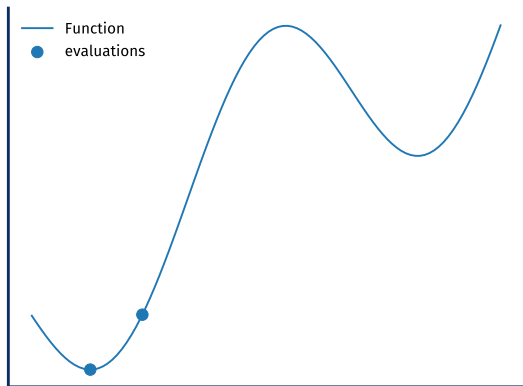
All values where a Taylor series expansion up to second order around the minimum is a *good* approximation.





## ↻ Iterative

- Edging closer to the minimum
- Continue until close enough



## ↴ Direct

- One-step optimization
- Analytical expression, no gradients



## ↓ Pure strategies

- Follow gradient and/or Hessian: (Quasi-)Newton methods
  - Transition states: eigenmode following
- Reduce dimensionality: Subspace methods
- (Quasi-)randomly pick points: Stochastic optimisation
- Regularly pick points: Grid refinement

## ↯ Hybrid

- Problem specific
- Typically global optimization
- E.g. stochastic first, then Newton

Series notation for iterative approaches

$$\{a_n\} \quad ; \quad \lim_{n \rightarrow \infty} = x_0 \quad (22)$$

## Cartesian coordinates inefficient

- Convergence rate slow
- Physical intuition: collective motions
- Tiny steps
- Numerical instability

## Issues

- Separability of internal motions
- Condition number of Hessian matrix (ratio of smallest and largest eigenvalue)
- Handling of constraints and symmetries (typical physical constraints)

## ↻ Spurious degrees of freedom

- 3 translational modes:  $\mathbf{R} = \frac{1}{M} \sum_I m_I \mathbf{r}_I$
- 3 rotational modes

## ⚠ Poor conditioning

- Large eigenvalue spread in Hessian matrix
- Coupling between bond stretching and molecular rotation

## ↻ Example: Dimer

- Embedding dimensions:  $2 \cdot 3$
- Actual dimensionality:  $2 \cdot 3 - 5$  (linear molecule)
- Internal coordinates: 1

Hessian eigenvalues:

$$\lambda_{\text{translation}} = \lambda_{\text{rotation}} = 0$$

$$\lambda_{\text{vibration}} \gg 0$$

## ≡ Natural molecular descriptors

- Bond lengths:  $d_{IJ} = |\mathbf{r}_I - \mathbf{r}_J|$
- Bond angles:  $\theta_{IJK} = \arccos \frac{(\mathbf{r}_I - \mathbf{r}_J) \cdot (\mathbf{r}_K - \mathbf{r}_J)}{d_{IJ}d_{JK}}$
- Dihedral angles:  $\phi_{IJKL}$  (torsion around JK bond)

## ✓ Advantages for optimization

- Direct chemical interpretation
- Natural constraint handling
- Better conditioned Hessian matrices
- Efficient sampling of conformational space

Internal coordinates:

$$\mathbf{q} = \{d_{IJ}, \dots, \theta_{IJK}, \dots, \phi_{IJKL} \dots\}$$

## Overcompleteness

- Minimal coordinate set can have singularities
- Avoids linear dependencies near planar/linear configurations
- More robust, easier to automate

## Complete vs. minimal sets

- Minimal: exactly  $3N - 6$  coordinates
- Complete: all possible bonds, angles, dihedrals
- Redundant:  $M > 3N - 6$  coordinates

## ↔ Coordinate transformation problem

- Energy gradient available in Cartesian coordinates:  $\mathbf{g}_x = \nabla_x E$
- Need gradient in internal coordinates:  $\mathbf{g}_q = \nabla_q E$
- Chain rule application required

$$\frac{\partial E}{\partial q_i} = \sum_{j=1}^{3N} \frac{\partial E}{\partial x_j} \frac{\partial x_j}{\partial q_i} \quad (23)$$

$$\mathbf{g}_q = \mathbf{B}^+ \mathbf{g}_x \quad (24)$$

Pseudo-inverse

## □ Wilson B-matrix properties

- Dimensions:  $M \times 3N$  where  $M$  = number of internal coordinates
- For redundant coordinates:  $M > 3N - 6$
- Rank deficient:  $\text{rank}(\mathbf{B}) = 3N - 6$

$$\mathbf{B}_{ij} = \frac{\partial q_i}{\partial x_j} \quad (25)$$

Singular value decomposition approach

$$\mathbf{B} = \mathbf{U}\mathbf{\Sigma}\mathbf{V}^T$$

where  $\mathbf{\Sigma}$  contains singular values

$$\sigma_1 \geq \sigma_2 \geq \dots \geq \sigma_r > 0$$

$$\mathbf{B}^+ = \mathbf{V}\mathbf{\Sigma}^+\mathbf{U}^T \quad (26)$$

pseudo-inverse

$$\Sigma_{ii}^+ = \begin{cases} \sigma_i^{-1} & \text{if } \sigma_i > \epsilon \\ 0 & \text{if } \sigma_i \leq \epsilon \end{cases} \quad (27)$$

threshold

## ↓ Optimization in projected space

- Eliminates redundant degrees of freedom
- Ensures progress along physically meaningful directions
- Maintains numerical stability

## ✓ Advantages of SVD approach

- Automatic rank determination
- Numerical robustness
- Handles near-linear dependencies gracefully
- Preserves maximum information content

## Concepts

- Relevant points are extrema on the potential energy surface
- Internal coordinates more accessible
- Requires gradient evaluation in most cases: will be expensive