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Cagliari / Sardinia / Italy

Visualization of Biomolecular Structures: State of the Art

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Introduction

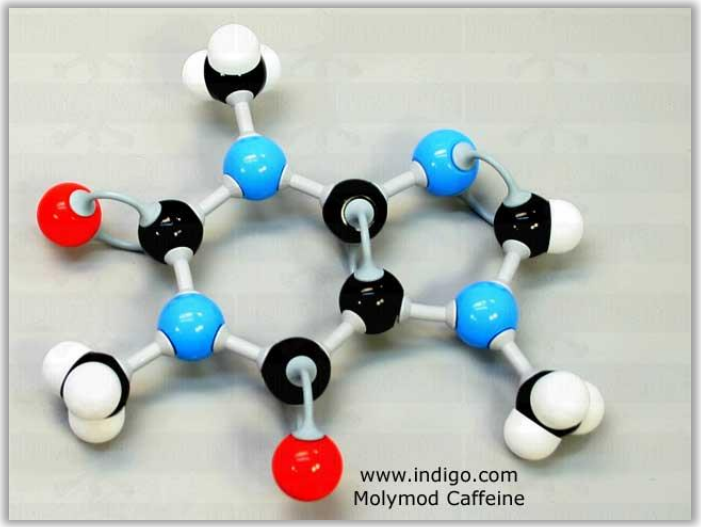
- Molecular visualization is one of the oldest branches of data visualization
  - Builds up on pre-computer era depictions and models of molecules
- *Molecular visualization is a vast and diverse field of research*

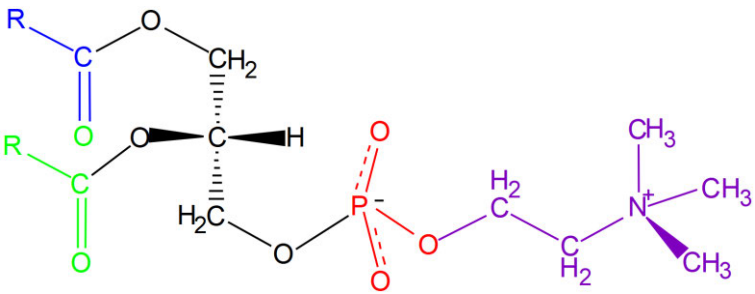
→ This STAR focuses on
  - **Interactive 3D Visualization** of
  - **Biomolecules** (DNA, proteins, lipids etc.) described by
  - **Classical Models** (no quantum effects, atoms depicted by hard spheres)

Biomolecules 101

- Molecules
  - Atoms (117 chemical element)
    - Protons and electrons
  - Bonds (e.g., covalent, disulfide, hydrogen)

- Small molecules & ions
  - Lipids (membranes)
  - Ligands/metabolites
  - Solvent molecules (e.g., water)
  - etc.

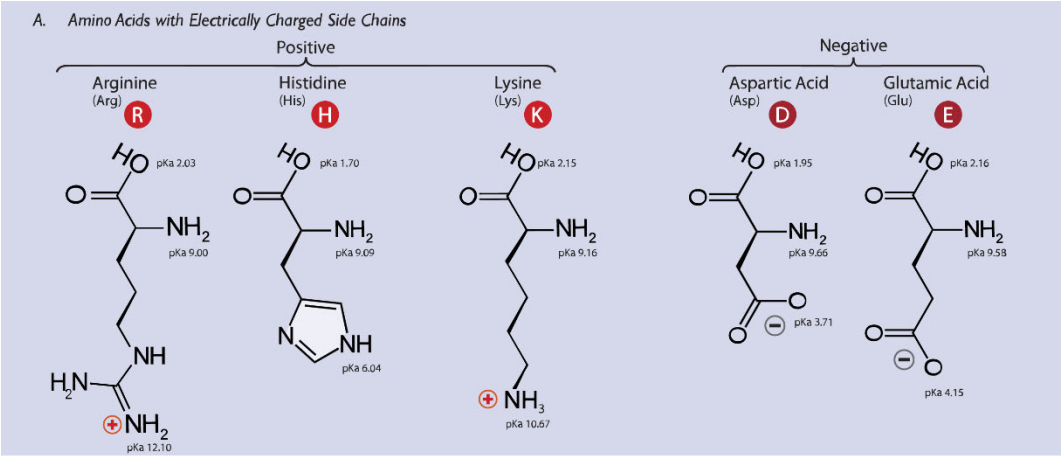




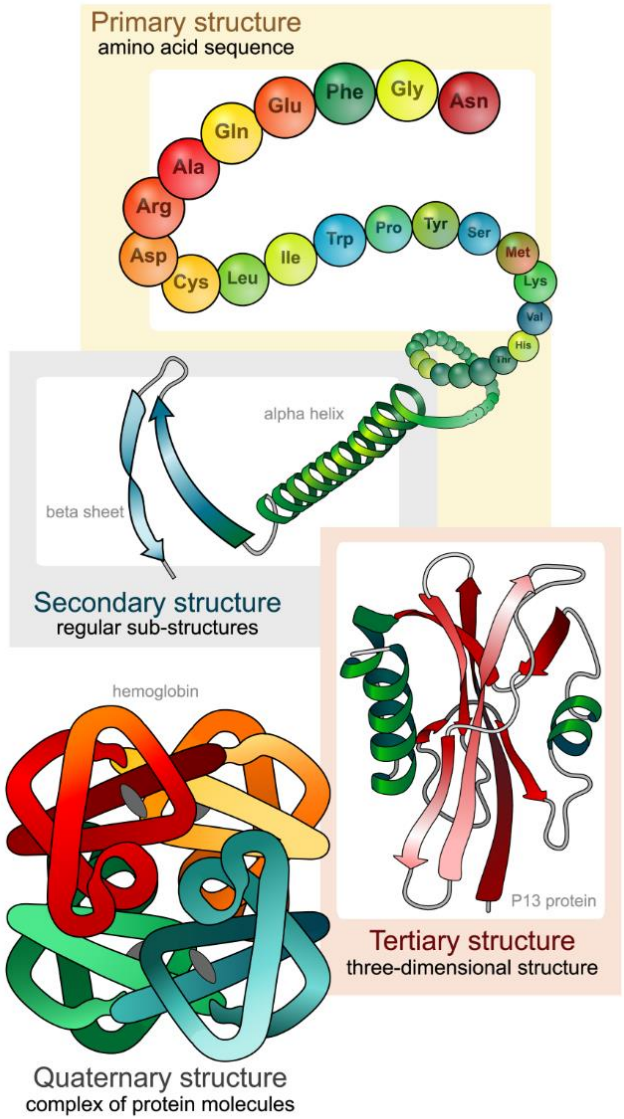
http://en.wikipedia.org/wiki/Phospholipid

Biomolecules 101

- Proteins
  - Building blocks of the „machinery of life“
  - Consists of amino acids
    - One or more linear chains of amino acids that form a functional complex
  - Secondary Structure (helix, sheet, turn, coil)



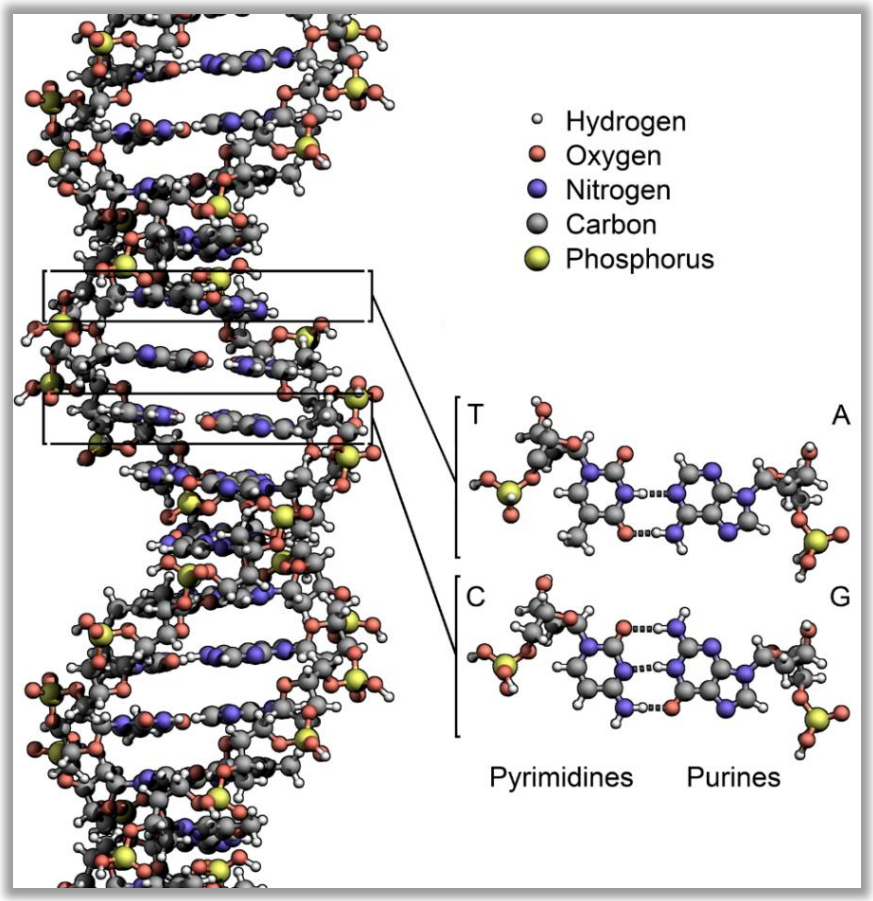
http://en.wikipedia.org/wiki/Amino_acid



http://en.wikipedia.org/wiki/Protein_structure

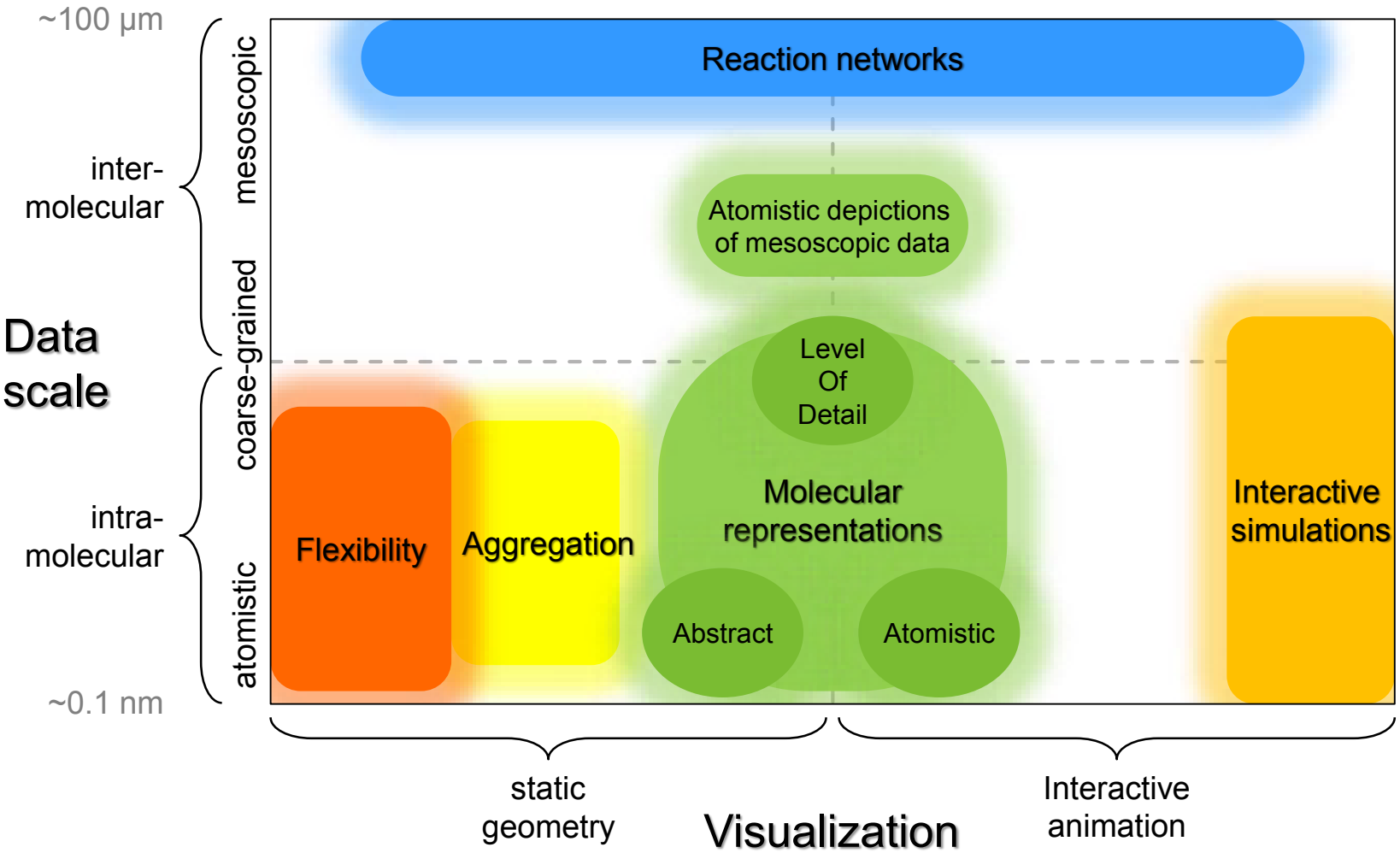
Biomolecules 101

- DNA & RNA
  - DNA stores the “genetic code”
    - Blueprint for proteins
  - Chain of nucleotides
    - Sugar backbone (Desoxy-/Ribose)
    - Phosphate
    - Nucleobase
      - cytosine, guanine, adenine, thymine/uracil)
    - 3 nucleotides encode 1 amino acid



http://en.wikipedia.org/wiki/DNA

Taxonomy


~100 µm
inter-
molecular
mesoscopic
coarse-grained
Data
scale
intra-
molecular
atomistic
~0.1 nm
Reaction networks
Atomistic depictions
of mesoscopic data
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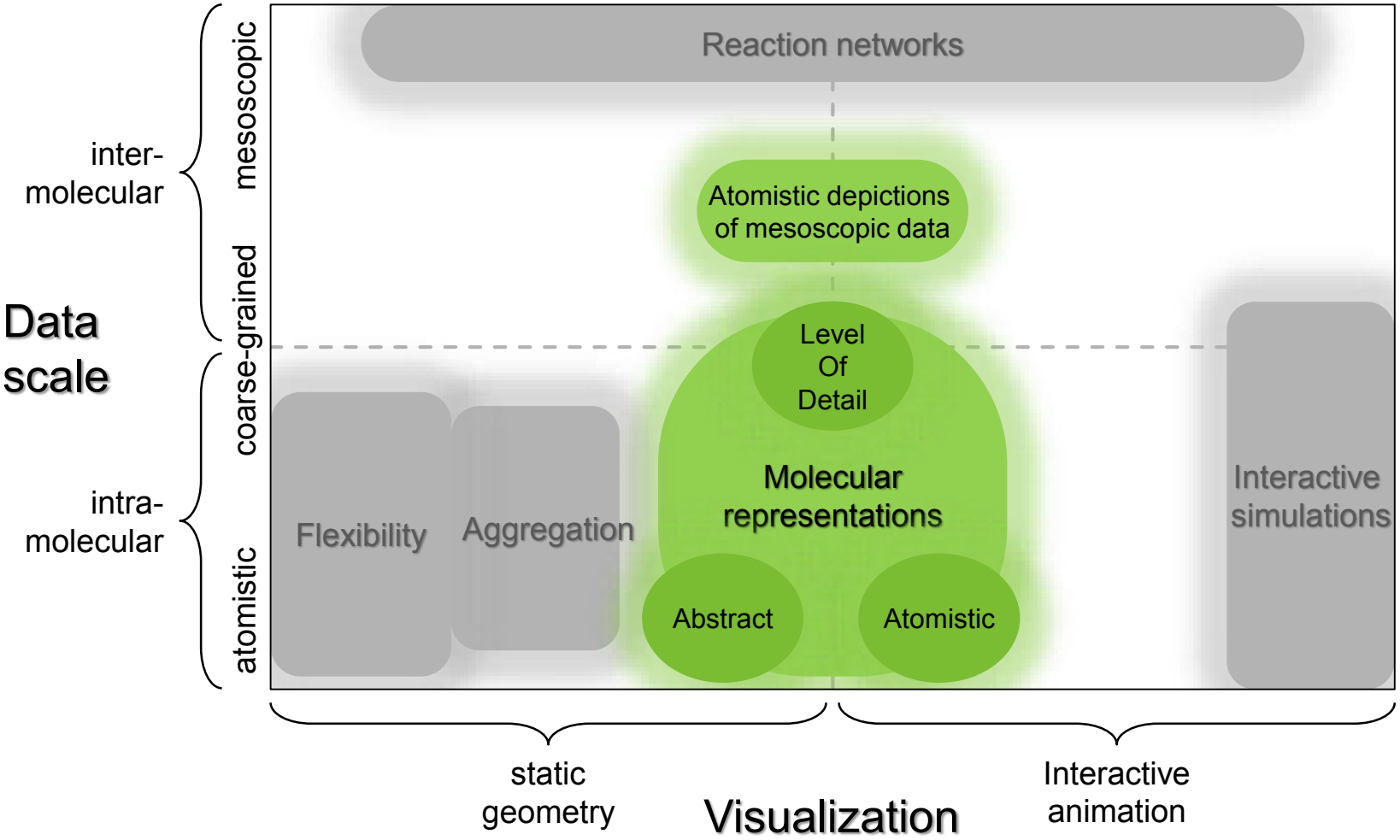
Taxonomy


Data scale
inter-molecular
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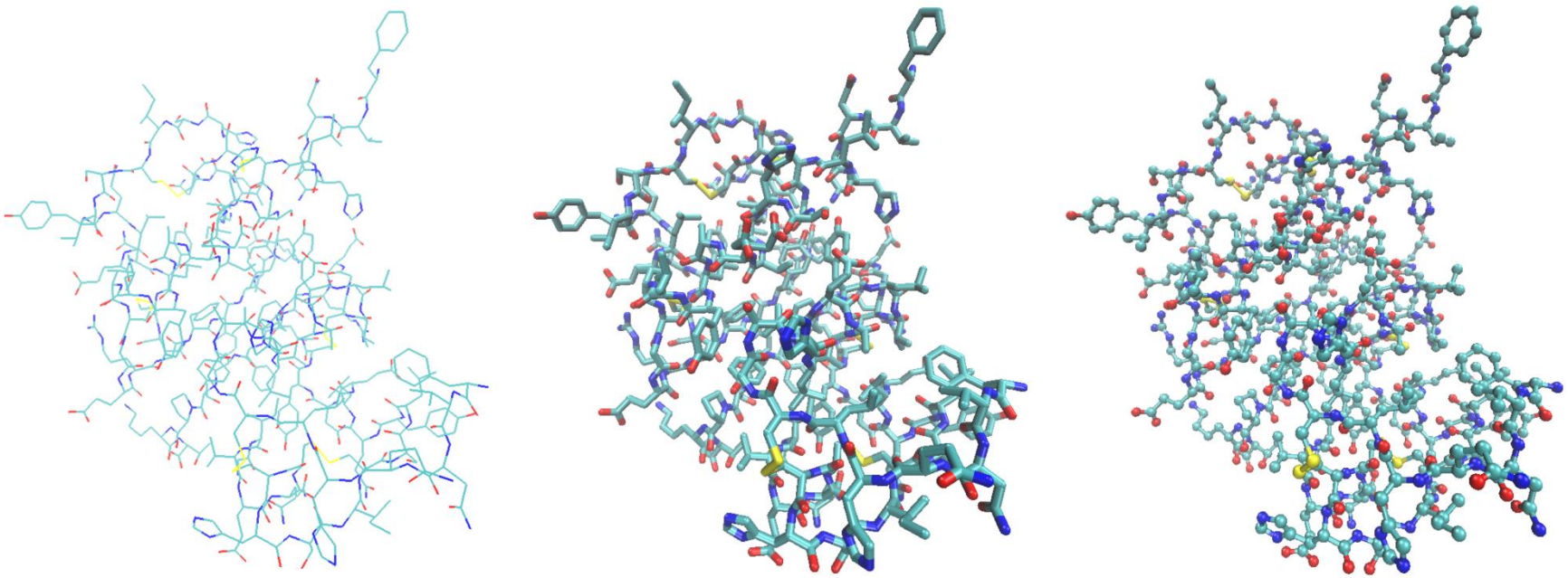
Molecular Representation Models

- Atomistic Representations
  - Bond-centric Models
  - Surface Models
- Abstract and Illustrative Representations
  - Representations of Molecular Architecture
  - Surface Abstractions
- Structural Level of Detail

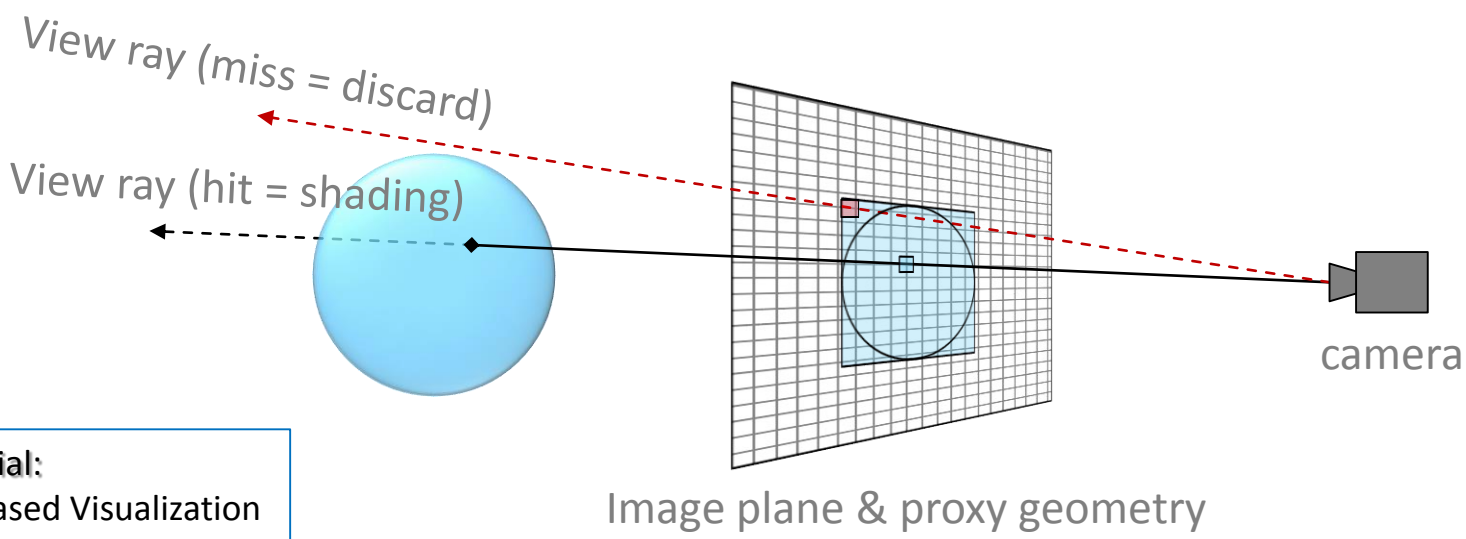
Atomistic Representations

- Molecular models that show the positon of the atoms
- Bond-centric Models
  - Bonds define the topology of the molecule
  - Lines, Stick, Ball-and-Stick → spheres and cylinders



GPU-based Glyph Ray Casting

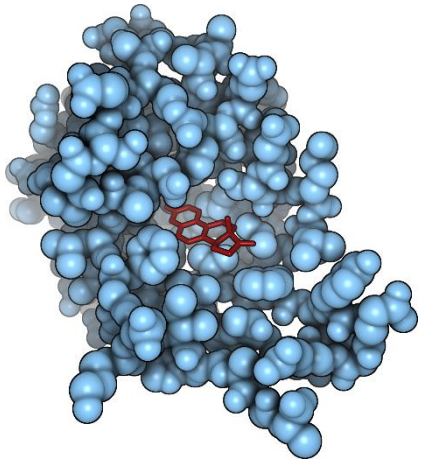
- State-of-the-art for rendering implicit objects
  - Upload implicit description of object to GPU
  - Proxy geometry that covers the object in Vertex/Geometry Shader
  - Object/ray intersection in Fragment Shader
    - Analytical solutions for low polynomial order (≤4) → spheres, cylinders, tori,…



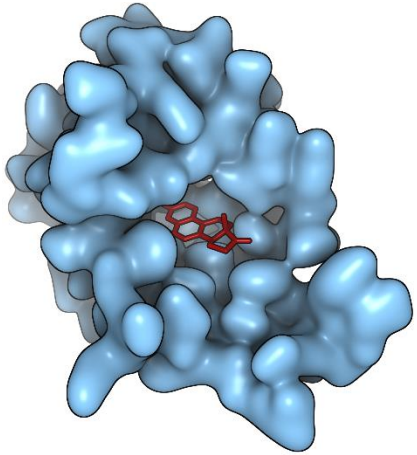
IEEE Vis 2015 Tutorial:
„Interactive GPU-based Visualization of Large Dynamic Particle Data“

Molecular Surfaces

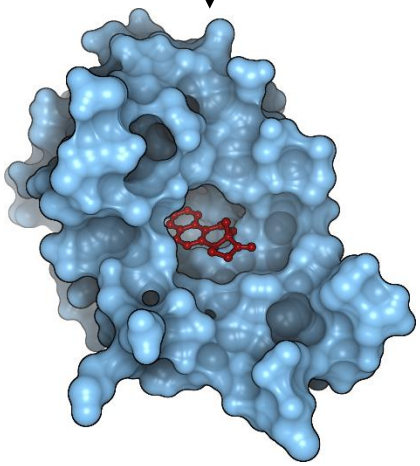
- Show molecular properties
- Depict boundary



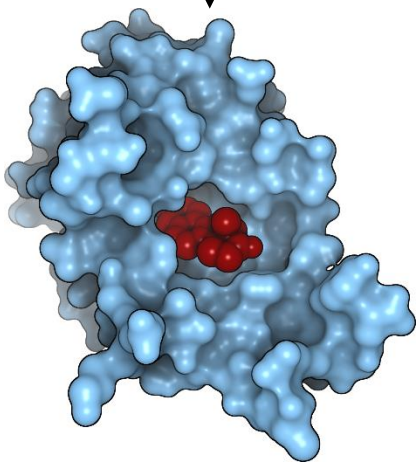
van der Waals Surface



Gaussian Surface (Metaballs)



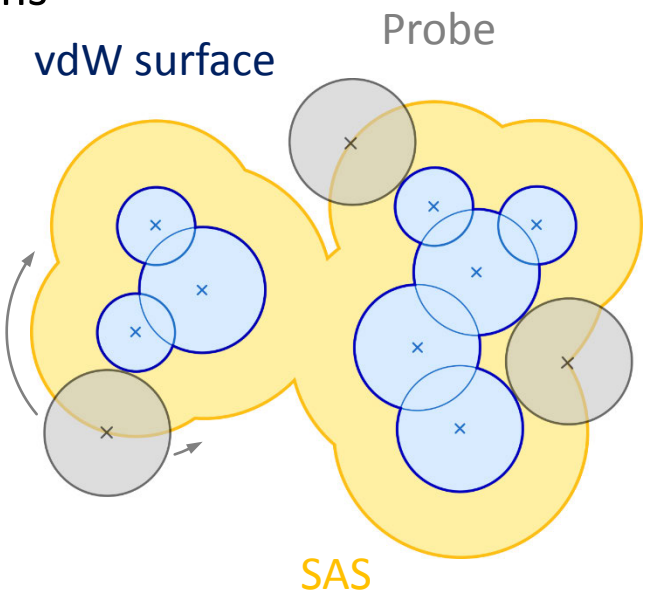
Solvent Excluded Surface



Ligand Excluded Surface

Van der Waals and Solvent Accessible Surface

- Van der Waals (vdW) surface
  - vdW radius: distance between non-bonded atoms
  - Molecular volume
  - Does not consider ligands or solvent molecules
- Solvent Accessible Surface (SAS)
  - Surface with respect to a certain solvent radius
    - Interior not reachable by solvent
  - Theory: Rolling probe (radius r_p)
  - Practice: Inflation of vdW radius by r_p
- Rendering via GPU ray casting



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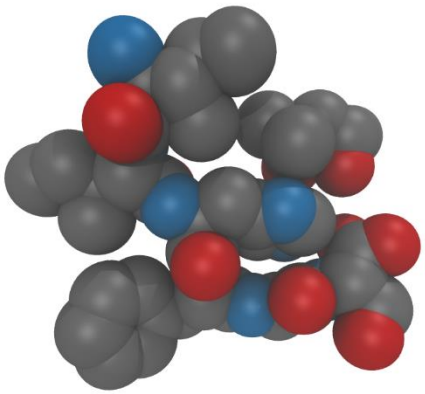

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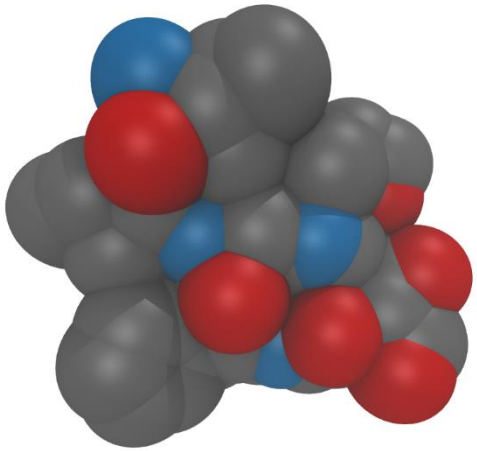
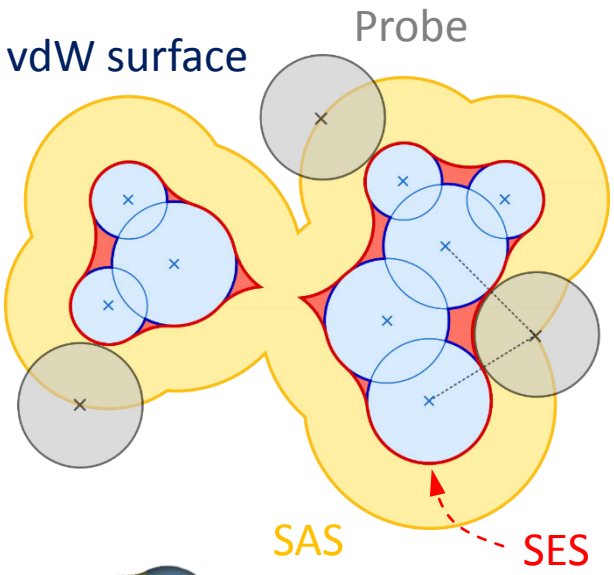


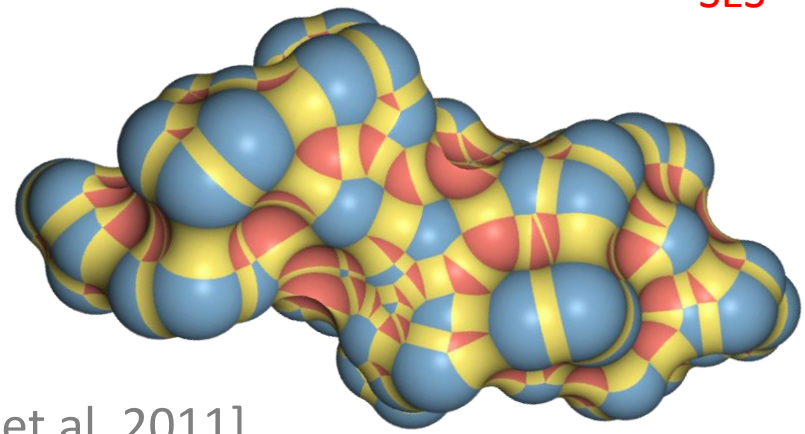
SAS

- Rendering via GPU ray casting

Solvent Excluded Surface – Definition

- Defined by rolling probe of radius r_p
  - Probe surface traces out SES
- Smooth, tight surface
  - Boundary with respect to solvent
  - No inflation (molecular volume is preserved)
- Three types of patches
  - Concave spherical triangles
  - Convex spherical patches
  - Saddle-shaped toroidal patches
- Parallel computation
  - Interactive for 100k atoms
  - CPU [Lindow et al. 2010] or GPU [Krone et al. 2011]





Solvent Excluded Surface – Rendering

- GPU ray casting of patches
- Implicit description [Parulek et al. 2012]
  - Direct ray casting via sphere tracing
  - Computationally expensive

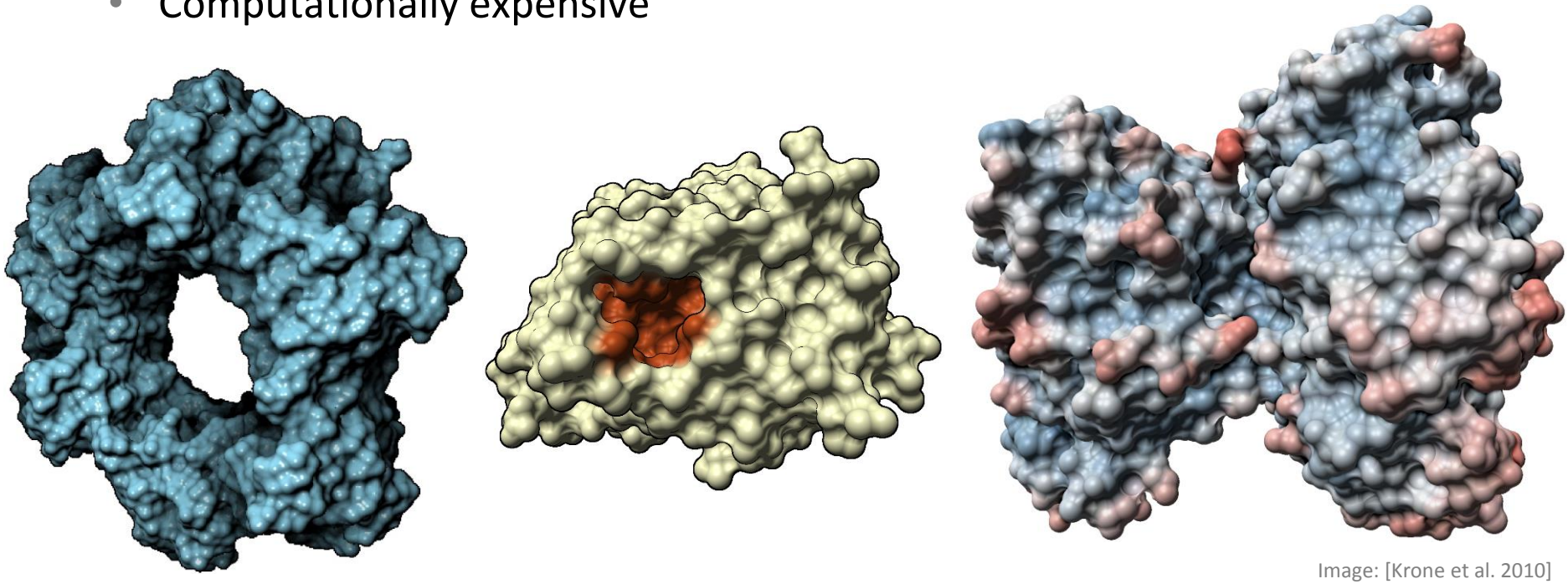
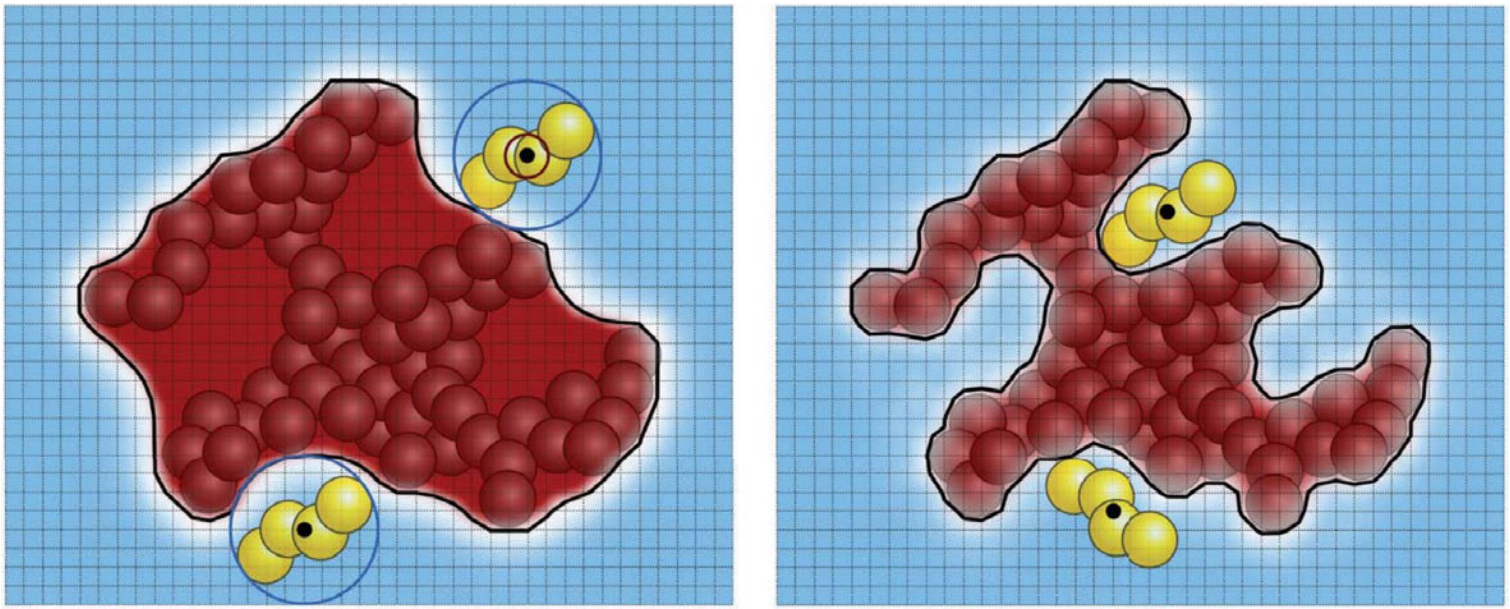


Image: [Krone et al. 2010]

Ligand Excluded Surface – Definition & Rendering

- Recent extension of the SES [Lindow et al. 2014]
  - Shows a more accurate contact surface with respect to a specific ligand
- No analytic computation (yet?)
  - Computationally expensive, grid-based sampling method



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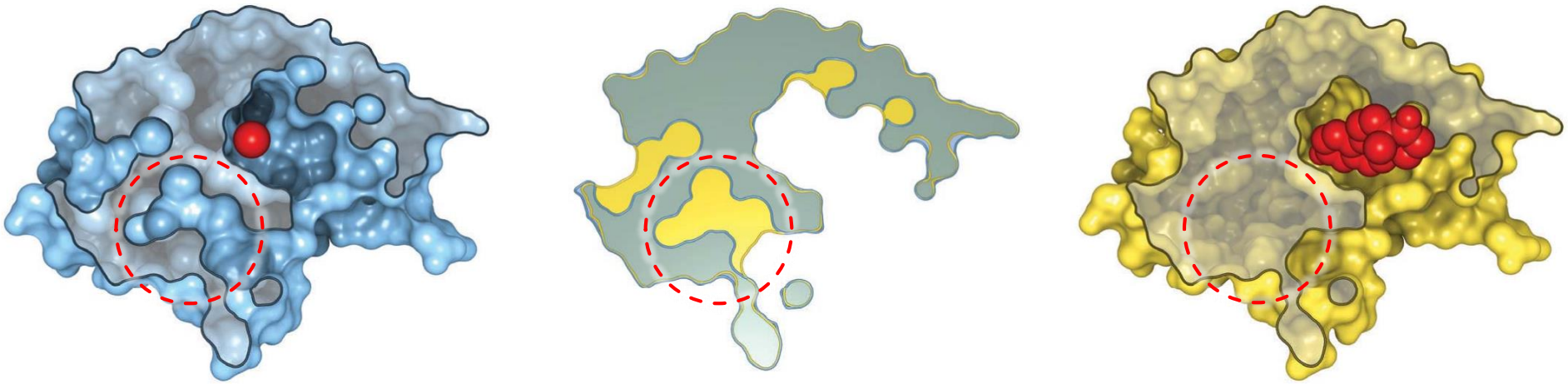
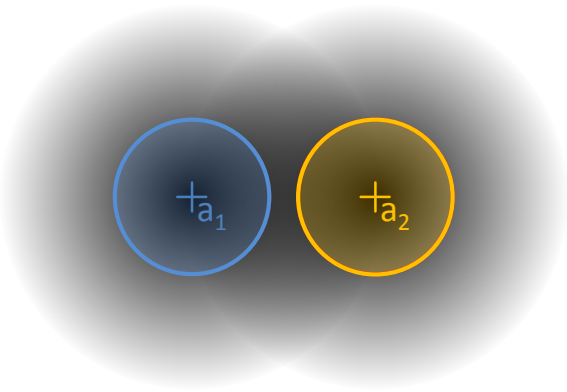


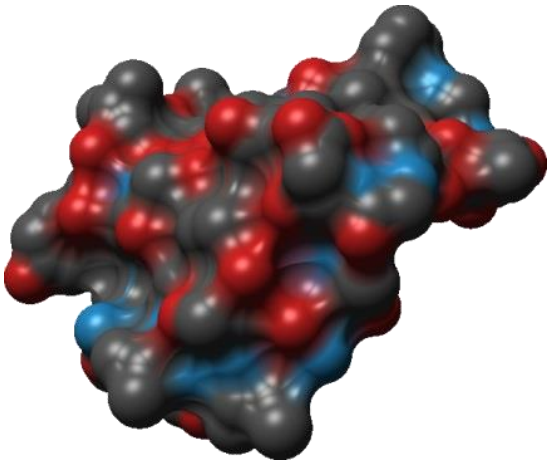
Solvent Excluded Surface → Difference ← Ligand Excluded Surface

Gaussian Surfaces – Definition

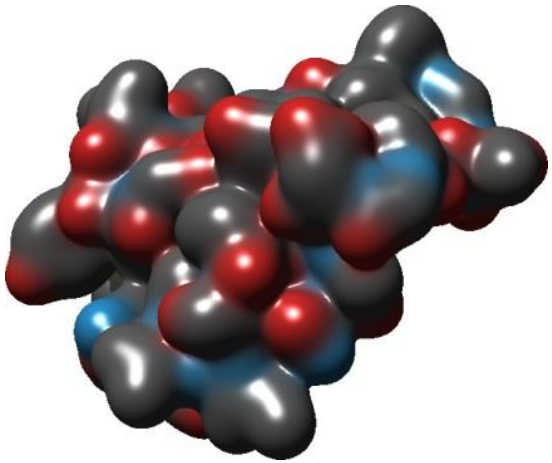
- Defined in 1982 by Jim Blinn (aka Metaballs/Convolution Surfaces)
  - Sum of Gaussian radial basis function for each atom (⇒ density field in $\mathbb{R}^3$)
  - Model electron density
  - Isosurface can approximate SES (surface shape and surface area)



Two atoms with radial symmetric Gaussian density kernels



SES

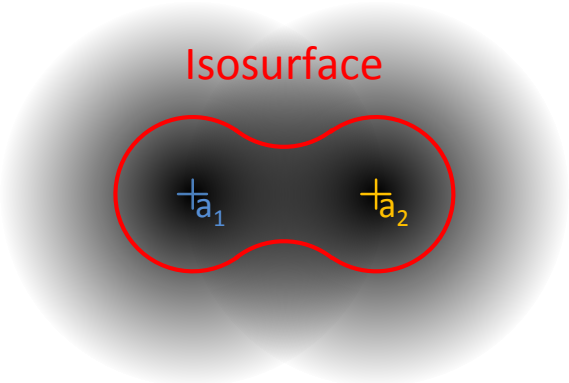


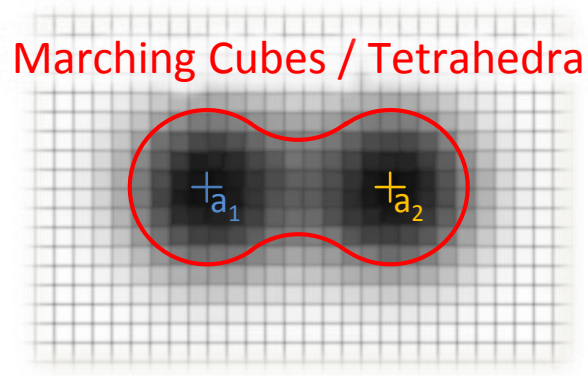
Gaussian surface

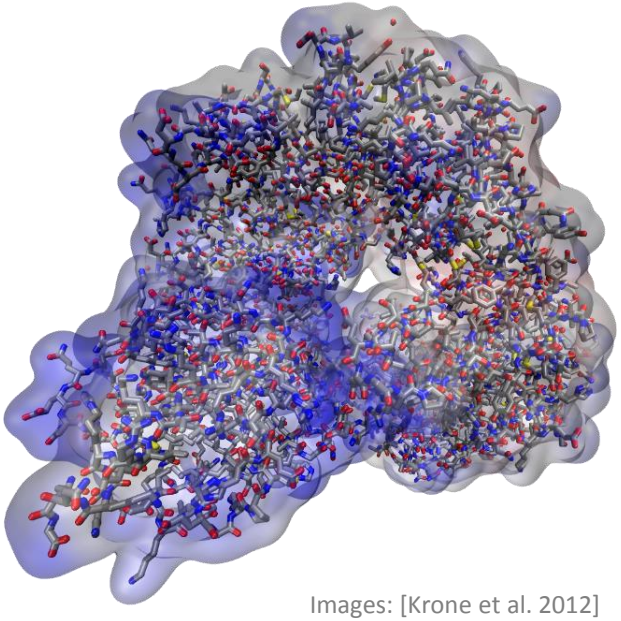
Images: [Krone et al. 2012]

Gaussian Surfaces – Rendering

- Interactive Rendering
  - Direct ray casting using depth peeling (~1M atoms) [Kanamori et al. 2008]
  - Grid-based sampling of the density (GPU-parallelized: ~10M atoms)
    - Isosurface extraction via Volume Ray Marching or Marching Cubes/Tetrahedra



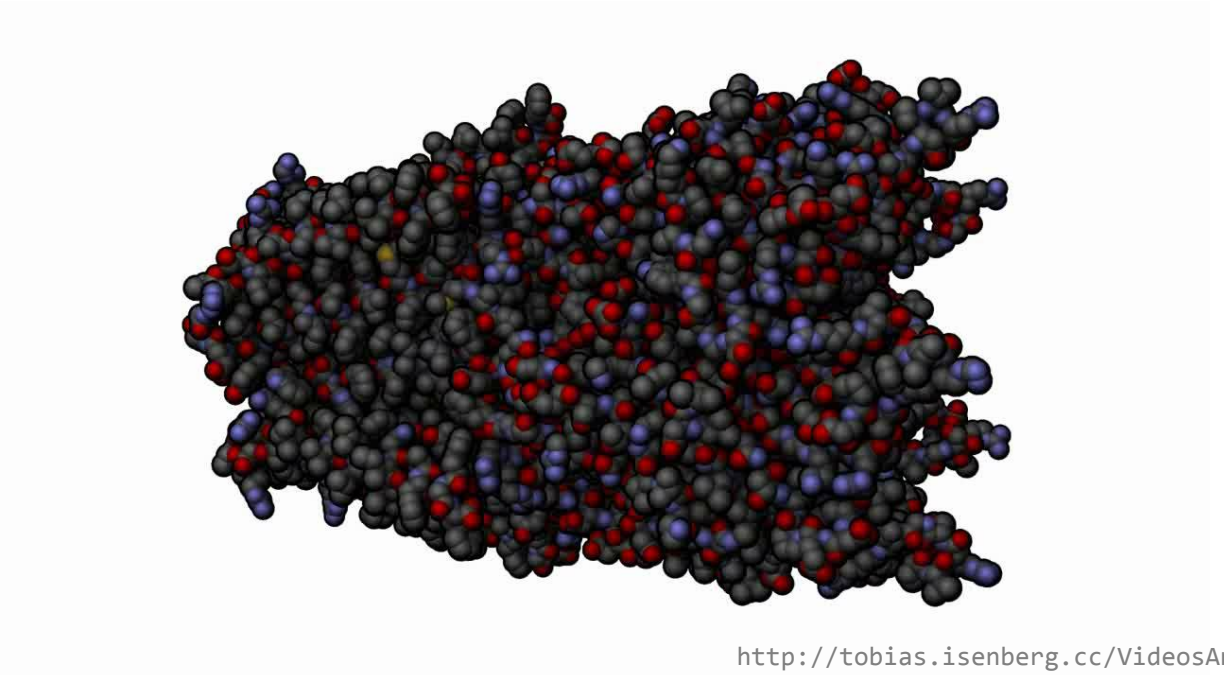




Images: [Krone et al. 2012]

Abstract and Illustrative Representations

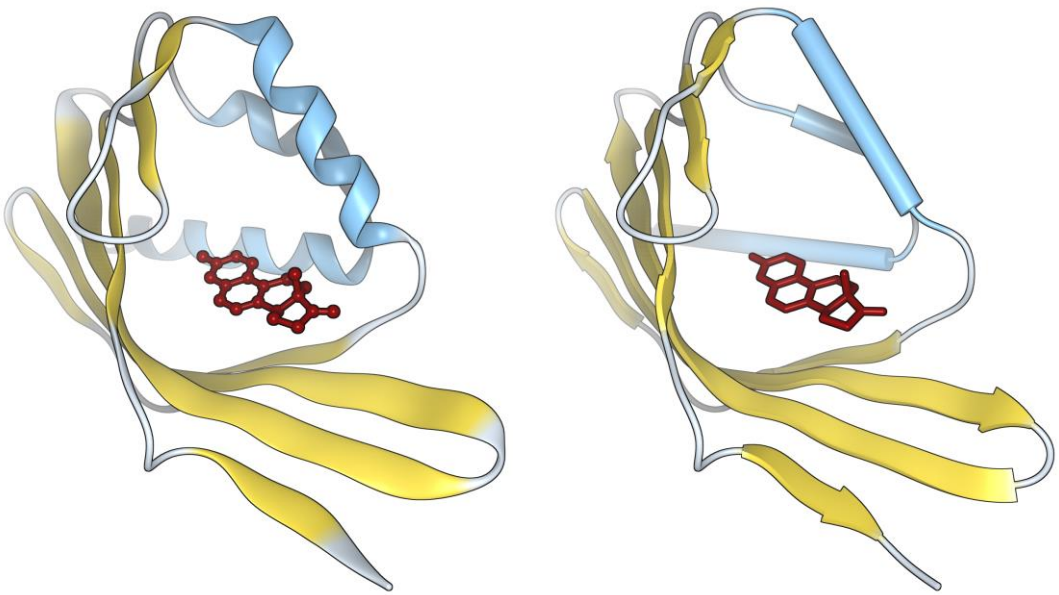
- Representations of Molecular Architecture
  - Show functional structure (derived from atom positions)
  - Cartoon Representation for DNA and proteins
    - Seamless transition [van der Zwan et al. 2011]

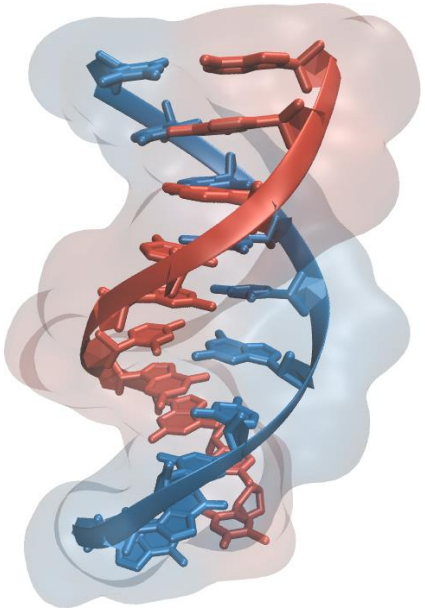


http://tobias.isenberg.cc/VideosAndDemos/Zwan2011IMV

Abstract and Illustrative Representations

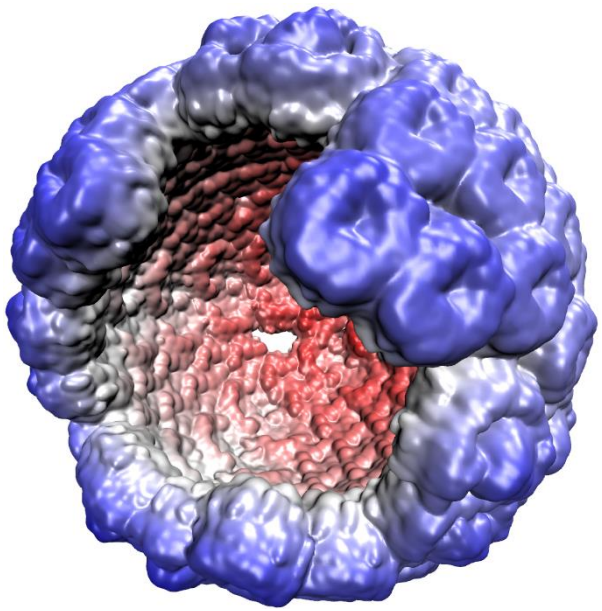
- Cartoon Rendering
  - Complex shapes → no ray casting
  - GPU-acceleration polygonal rendering
    - Vertex shader [Wahle et al. 2011]
    - Geometry shader [Krone et al. 2008]

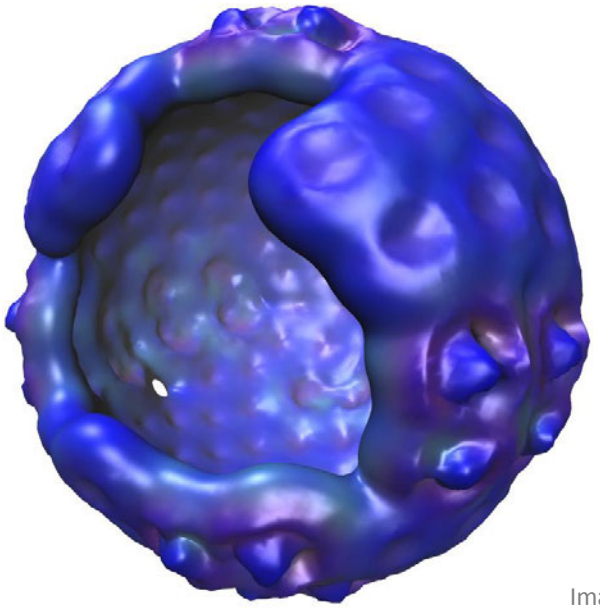




Abstract and Illustrative Representations

- Surface Abstractions
  - Coarsening of Gaussian surfaces (LoD, bounding spheres) [Krone at al. 2012]
  - Smoothing of high-frequency surfaces like SES [Cipriano, Gleicher 2007]
  - Mapping of molecular surface to a sphere (e.g., [Rahi, Sharp 2014])





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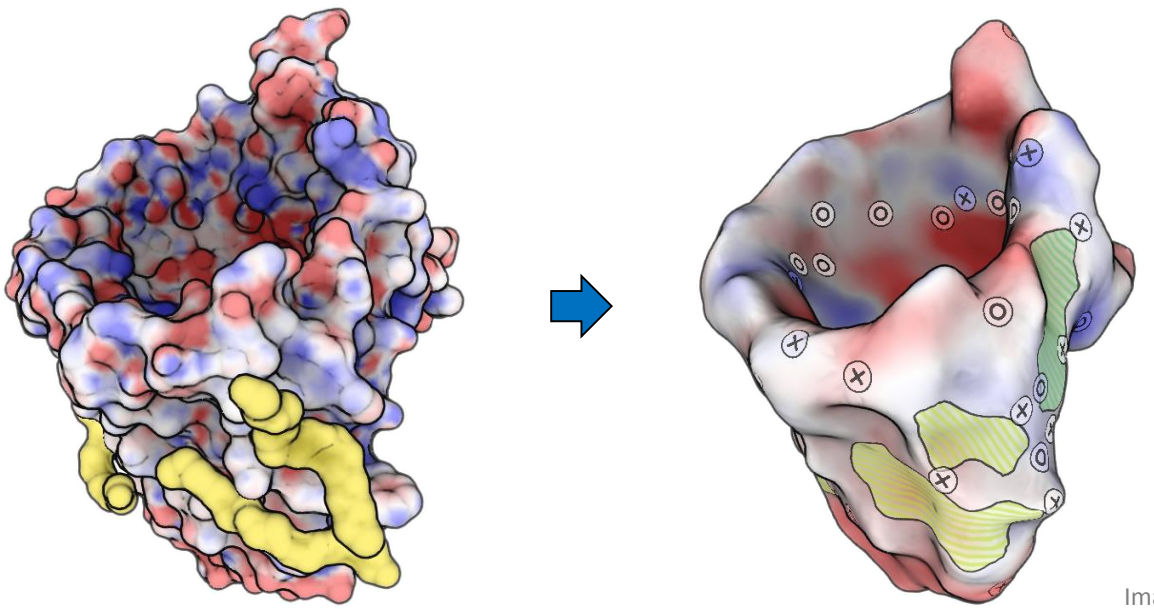

Images: [Cipriano, Gleicher 2007]

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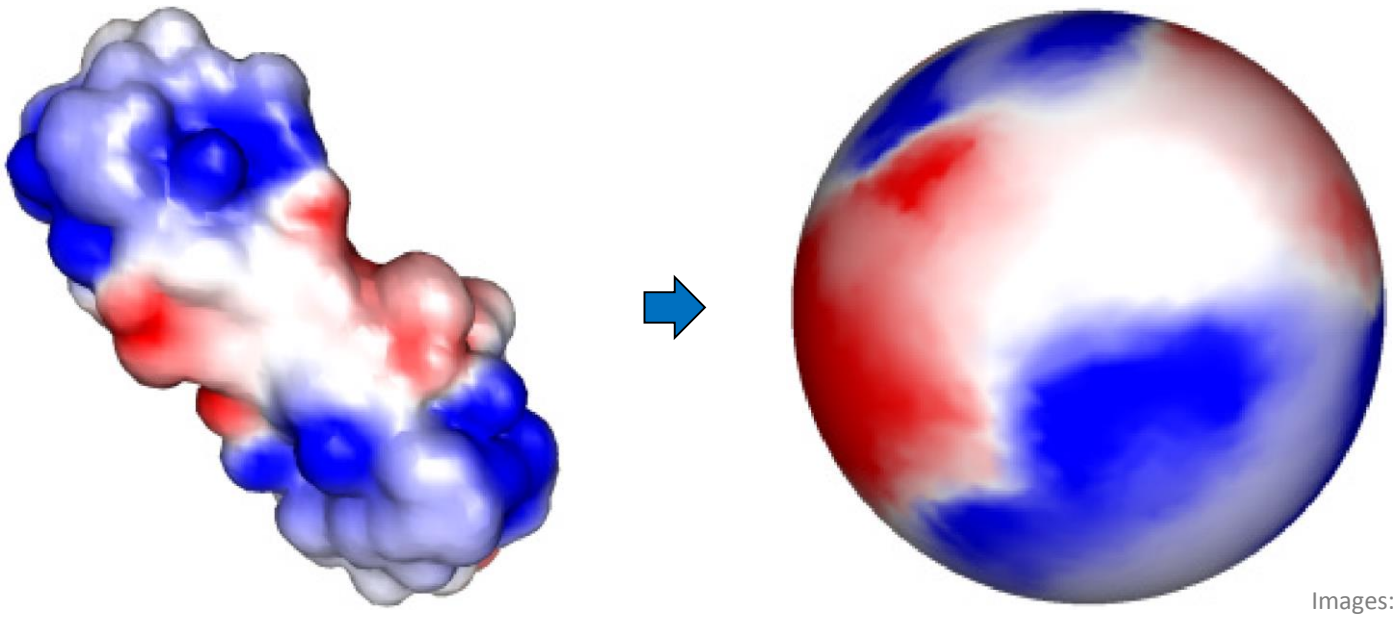
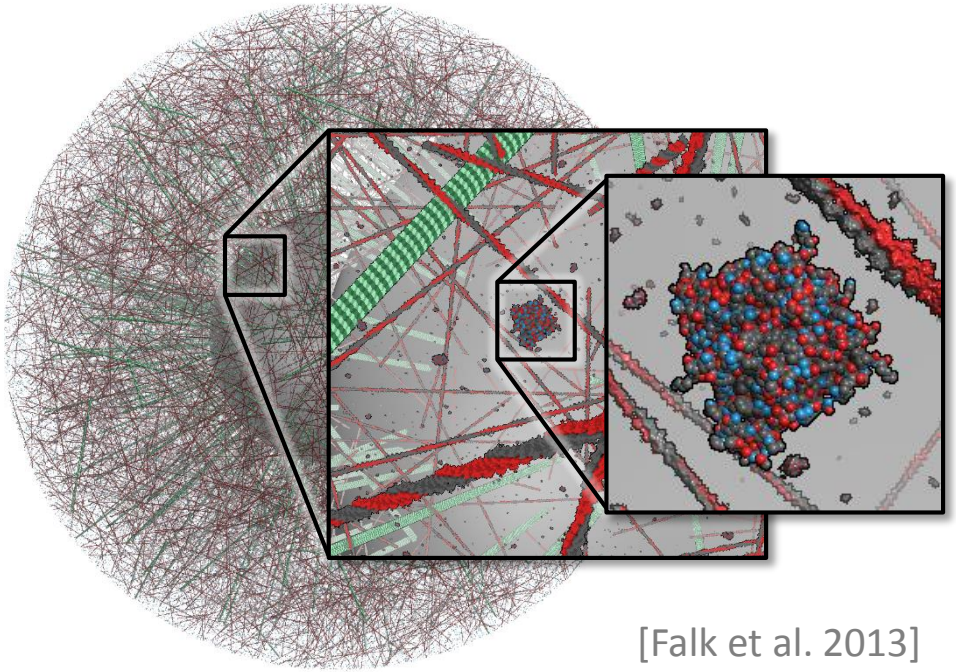


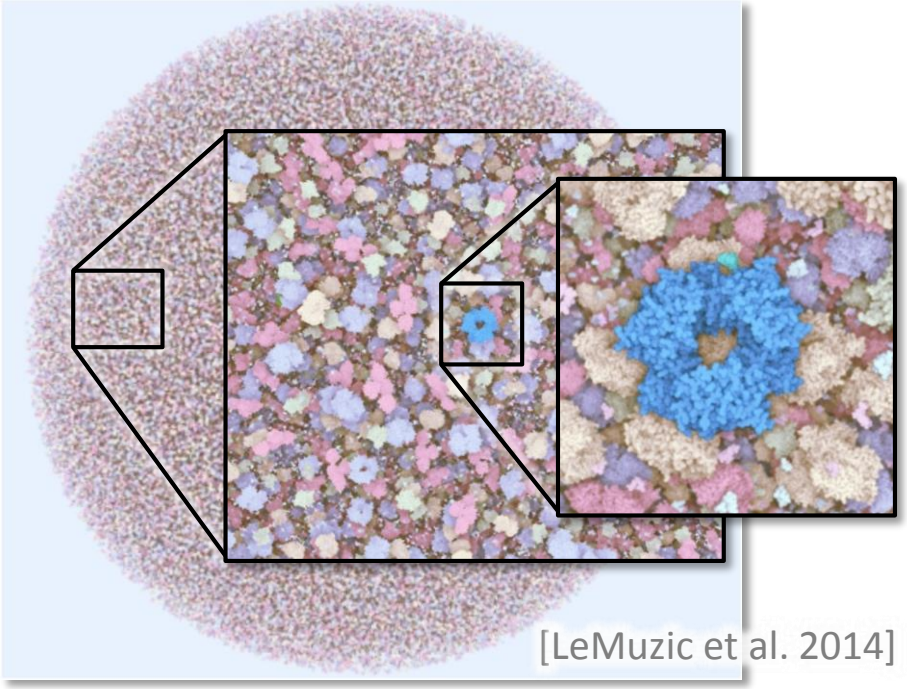
Images: [Rahi, Sharp 2014]

Structural Level of Detail

- Derive all-atom representation from coarse-grained simulations
  - Cellular environment → Many instances of the same molecules
  - Special GPU-accelerated rendering methods
  - Interactive rendering of up to 10 billion particles



[Falk et al. 2013]



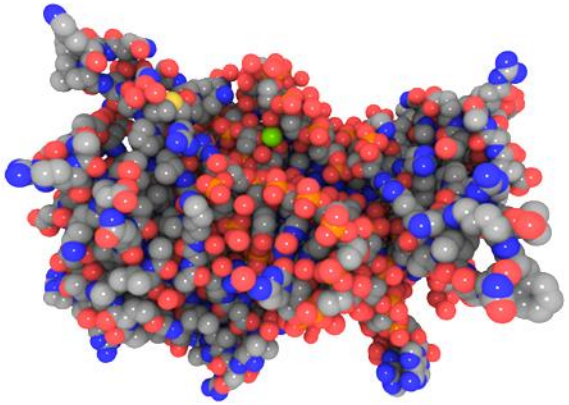
[LeMuzic et al. 2014]

Molecular Rendering

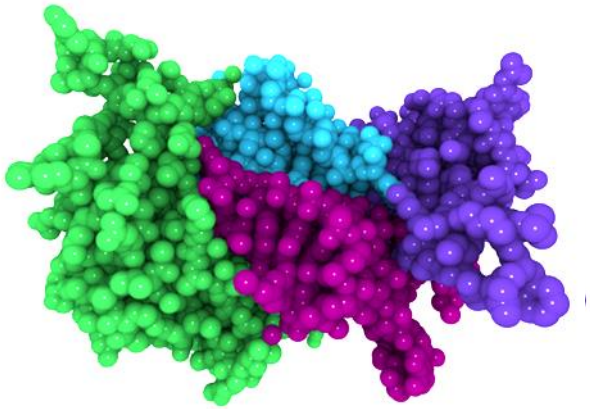
- Enhances
  - Image quality
  - Perception of geometric shapes and depth complexity
- Achieved by
  - Shading
  - Depth cues
- Computable for dynamic data in real-time

Color

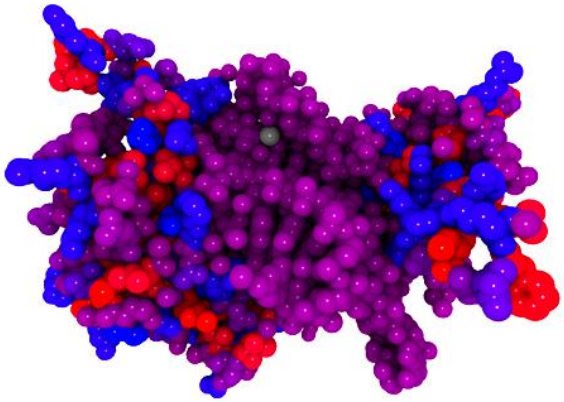
type of atoms



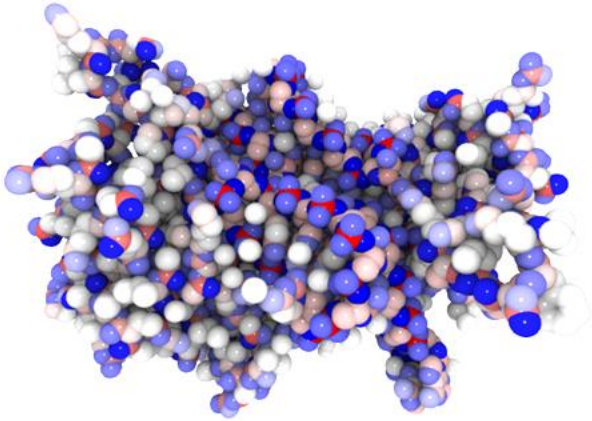
chains



hydrophobicity

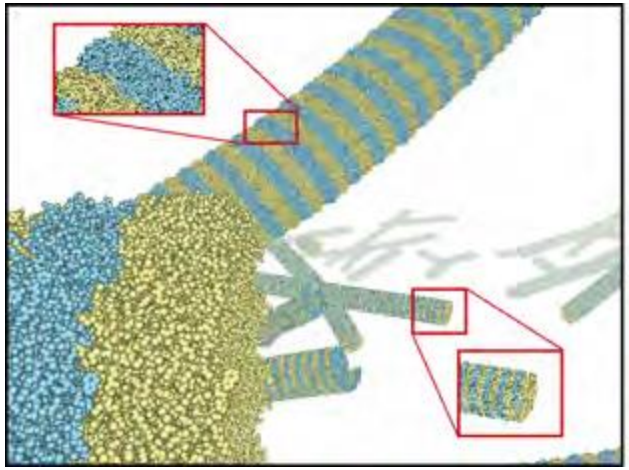


partial charge

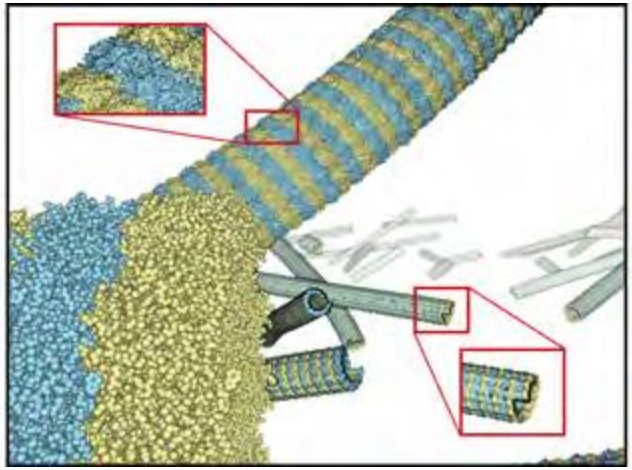


Illumination

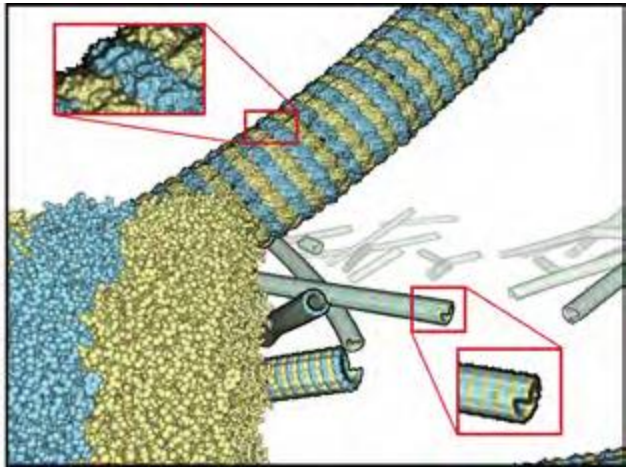
- Phong and Blinn-Phong
  - Specular highlights create artifacts
- Normal correction scheme based on deferred shading



analytically computed normals



deferred shading [Grottel et al. 2010]

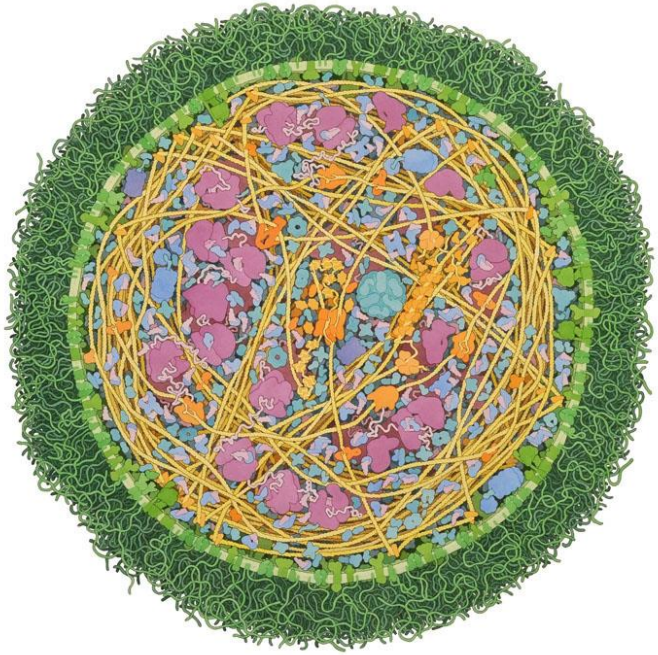


deferred shading [Lindow et al. 2012]

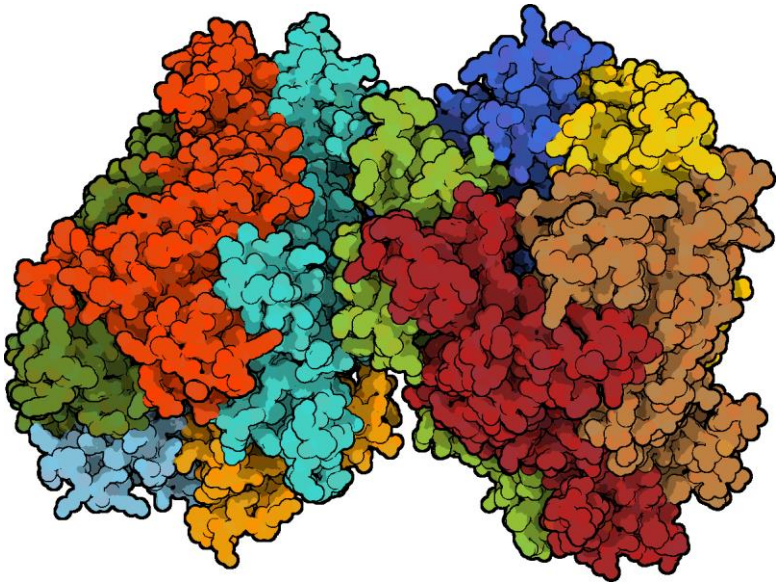
Images: [Lindow et al. 2012]

Cel Shading

- Artistic or non-photorealistic renderings with a comic-like look
- Resembles hand-drawn illustrations by David Goodsell



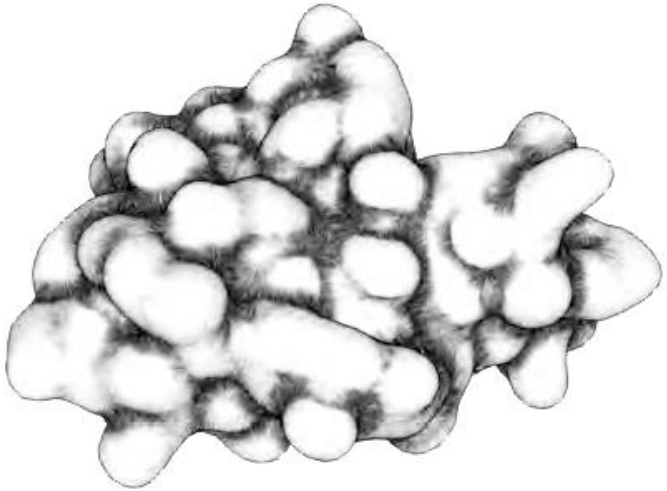
Mycoplasma cell
[Goodsell]



B-Raf protein rendered in MegaMol
[Grottel et al. 2015]

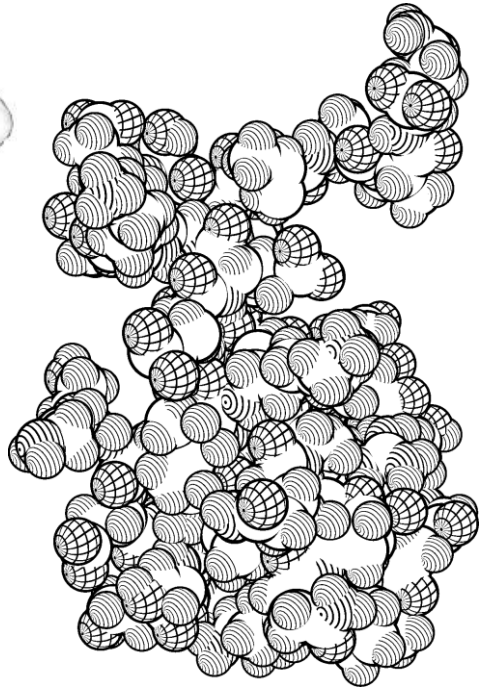
Feature lines and hatching

[van der Zwan et al. 2011]



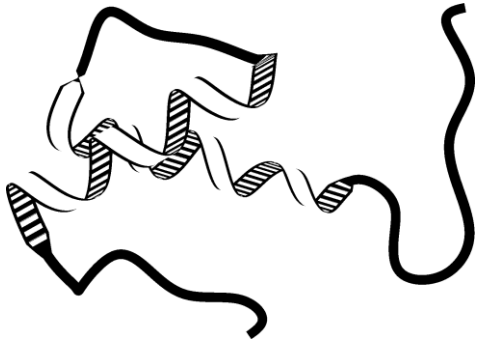
molecular surfaces

[Lawonn et al. 2014]

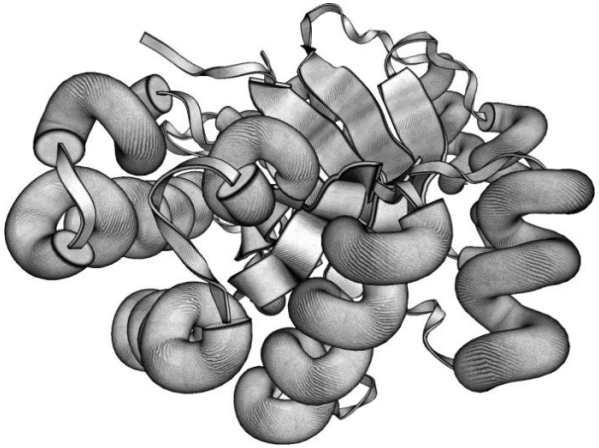


space filling models

[van der Zwan et al. 2011]



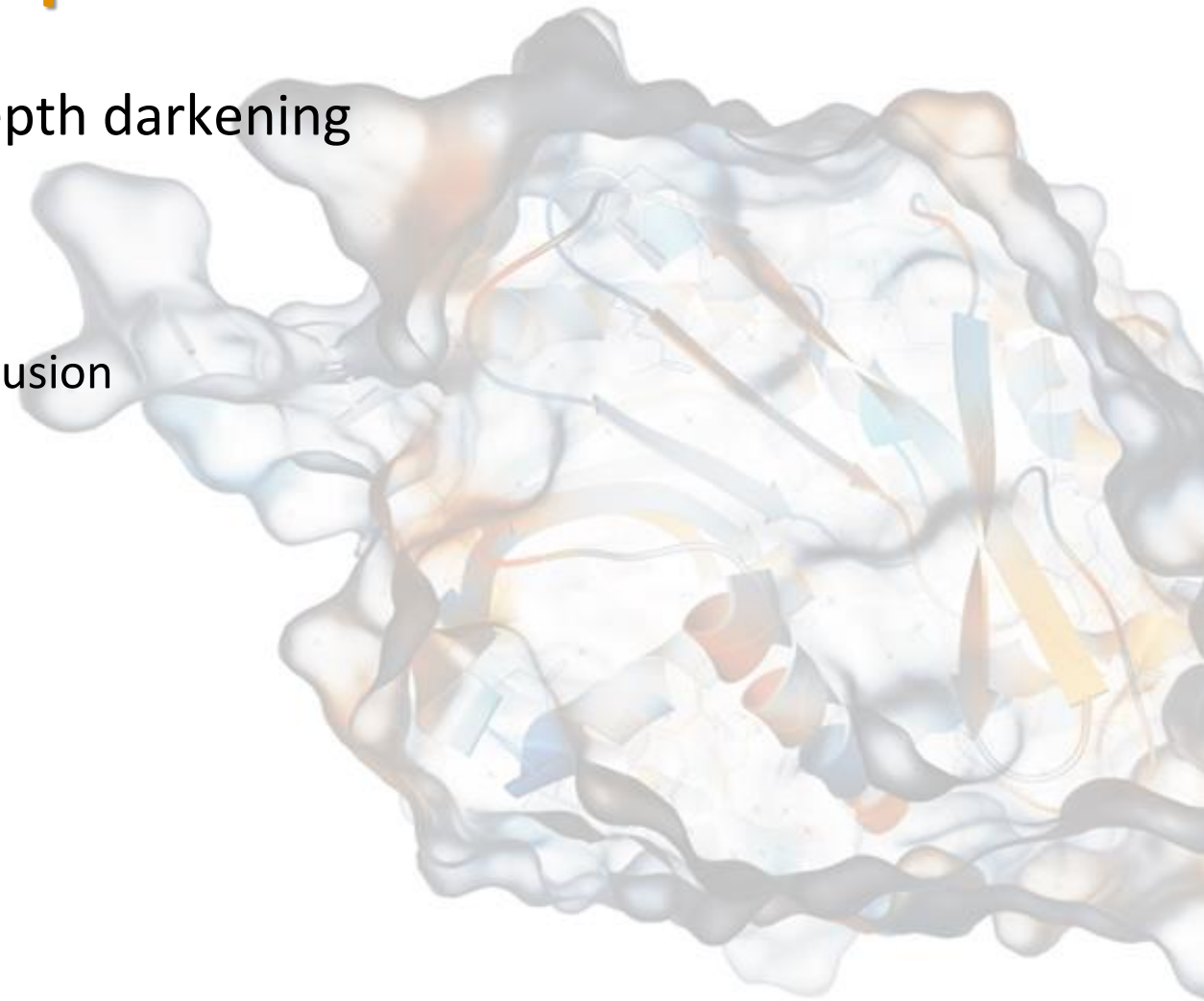
cartoon representations



[Weber 2009]

Depth Cue Techniques

- Sihouettes, halos, depth darkening
- Ambient Occlusion
  - Real-time Ambient Occlusion
- Depth of Field



Ordinal Depth Cues

- **Silhouettes**

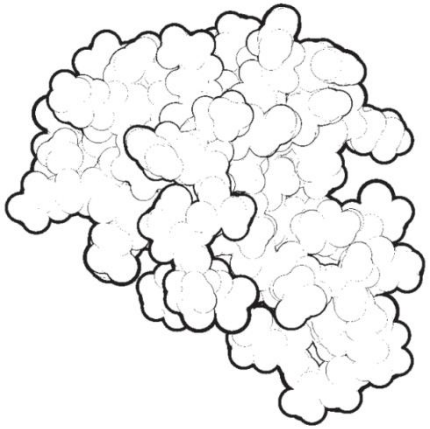
  Computed in image space in postprocessing

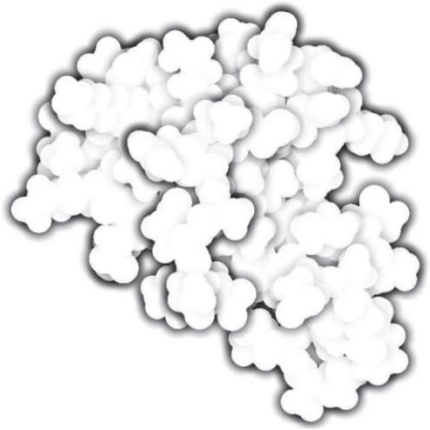
- **Halos**

  Extended from the object boundaries

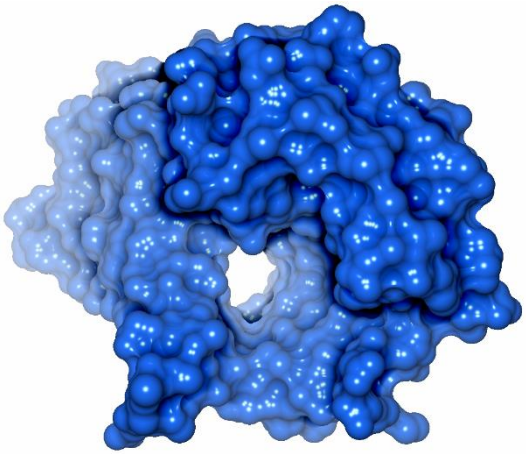
- **Depth darkening**

  Visually separates distant overlapping objects





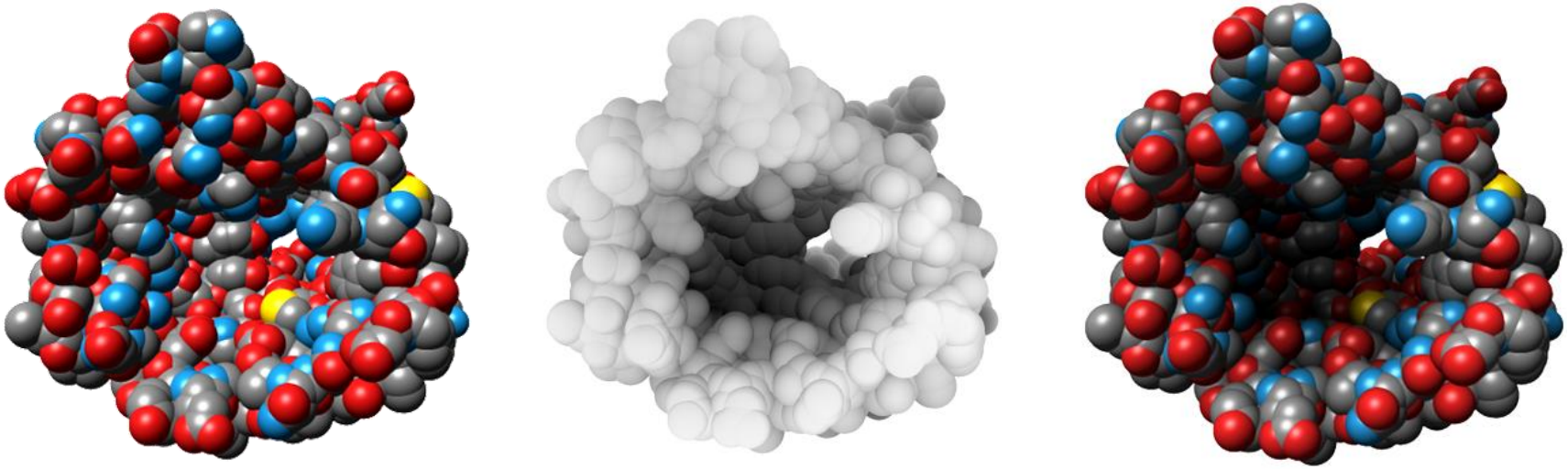
[Tarini et al. 2006]



[Krone et al. 2009]

Relative Depth Cues – Ambient Occlusion

- Mimicking the transport of diffuse light between objects
- Local shadowing, increases depth perception

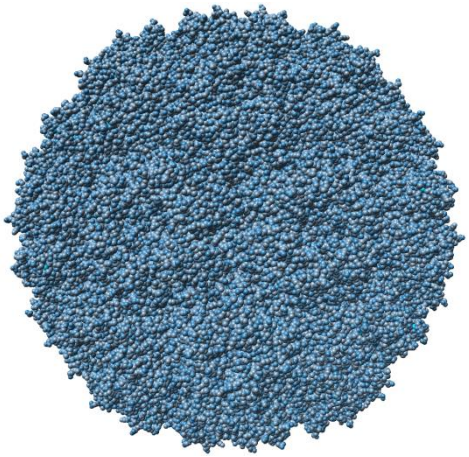


Local lighting | Ambient Occlusion | Combined

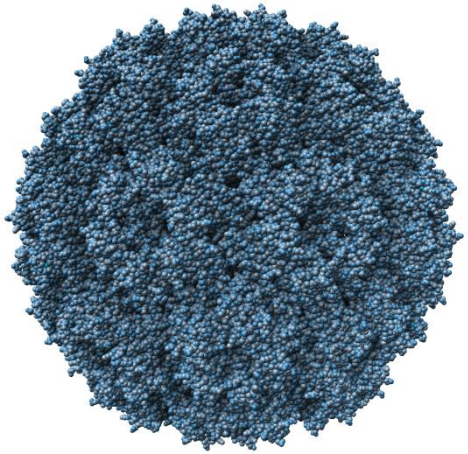
- Computationally expensive, accelerated approaches developed

Real-time Ambient Occlusion

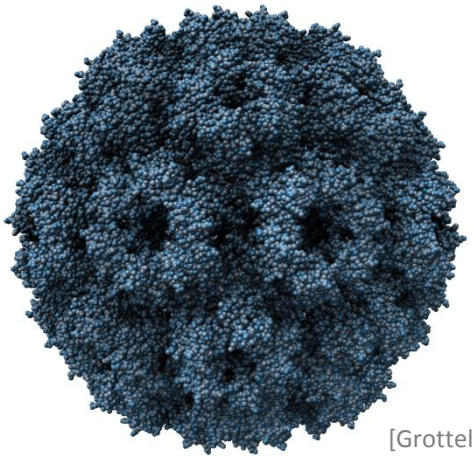
- Screen-Space Ambient Occlusion
  - Image space technique, approximates the effects in postprocessing
  - Considers the visible neighborhood of fragments
- Object-Space Ambient Occlusion
  - Considers the entire local neighborhood of atoms



Local lighting



Screen Space AO
[Kajalin 2009]

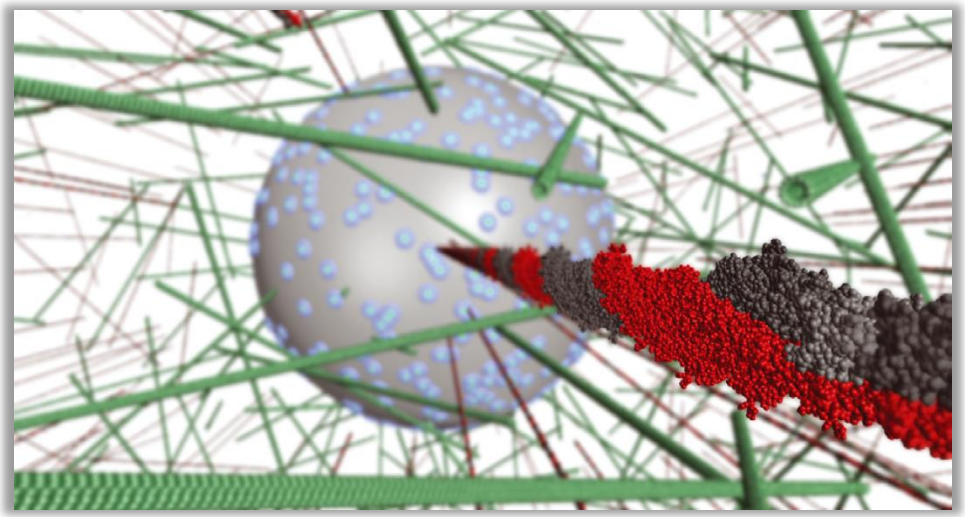


Object Space AO
[Grottel et al. 2012]

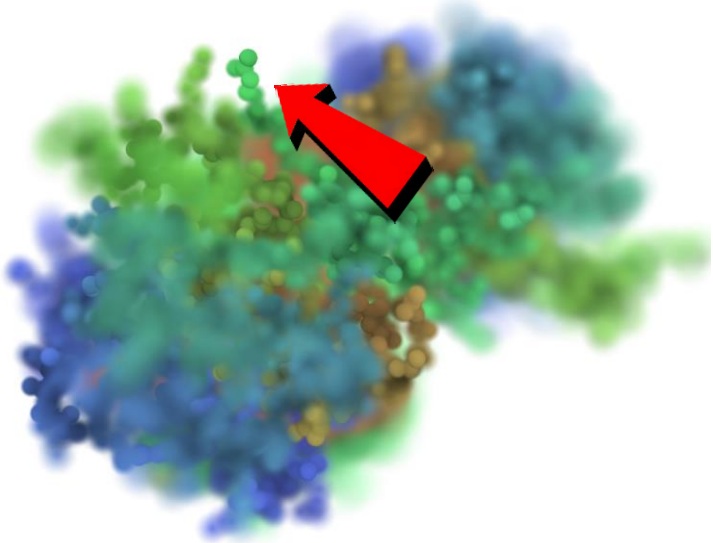
Images:
[Grottel et al. 2012]

Depth of Field

- Separating foreground from background
- Image-space and object-space based approaches
- Draw the attention to a specific region or semantic properties

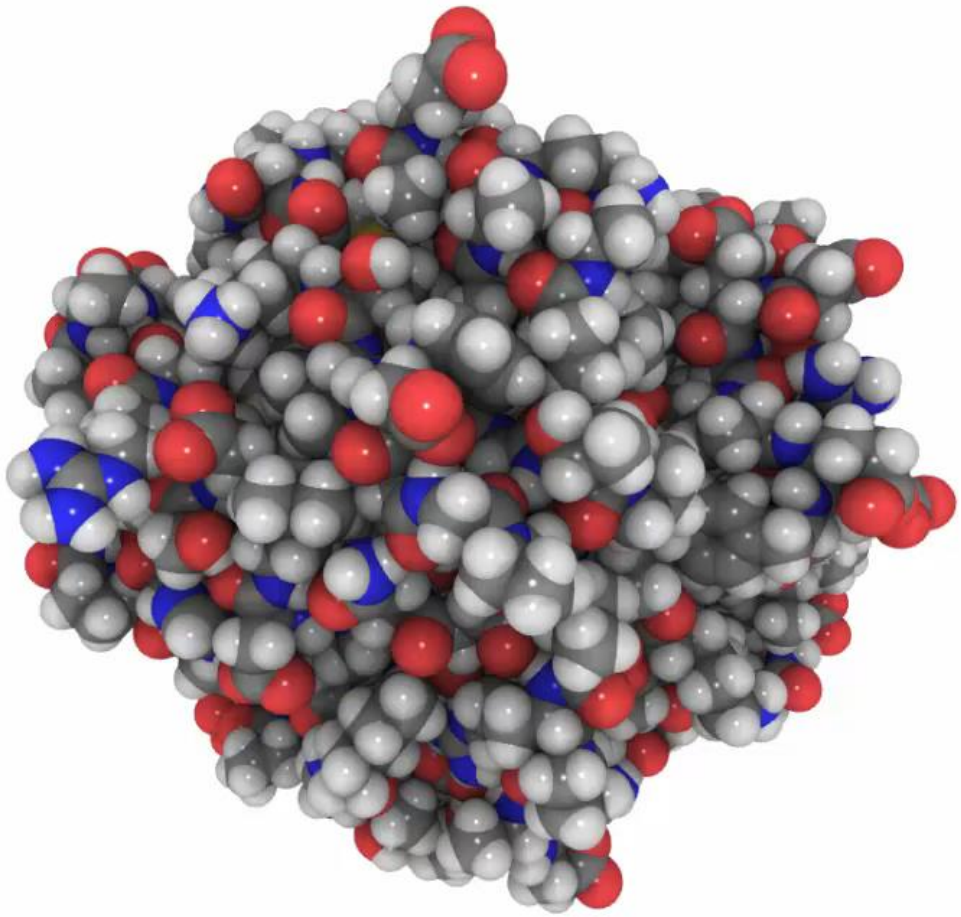


Region-based
[Falk et al. 2013]

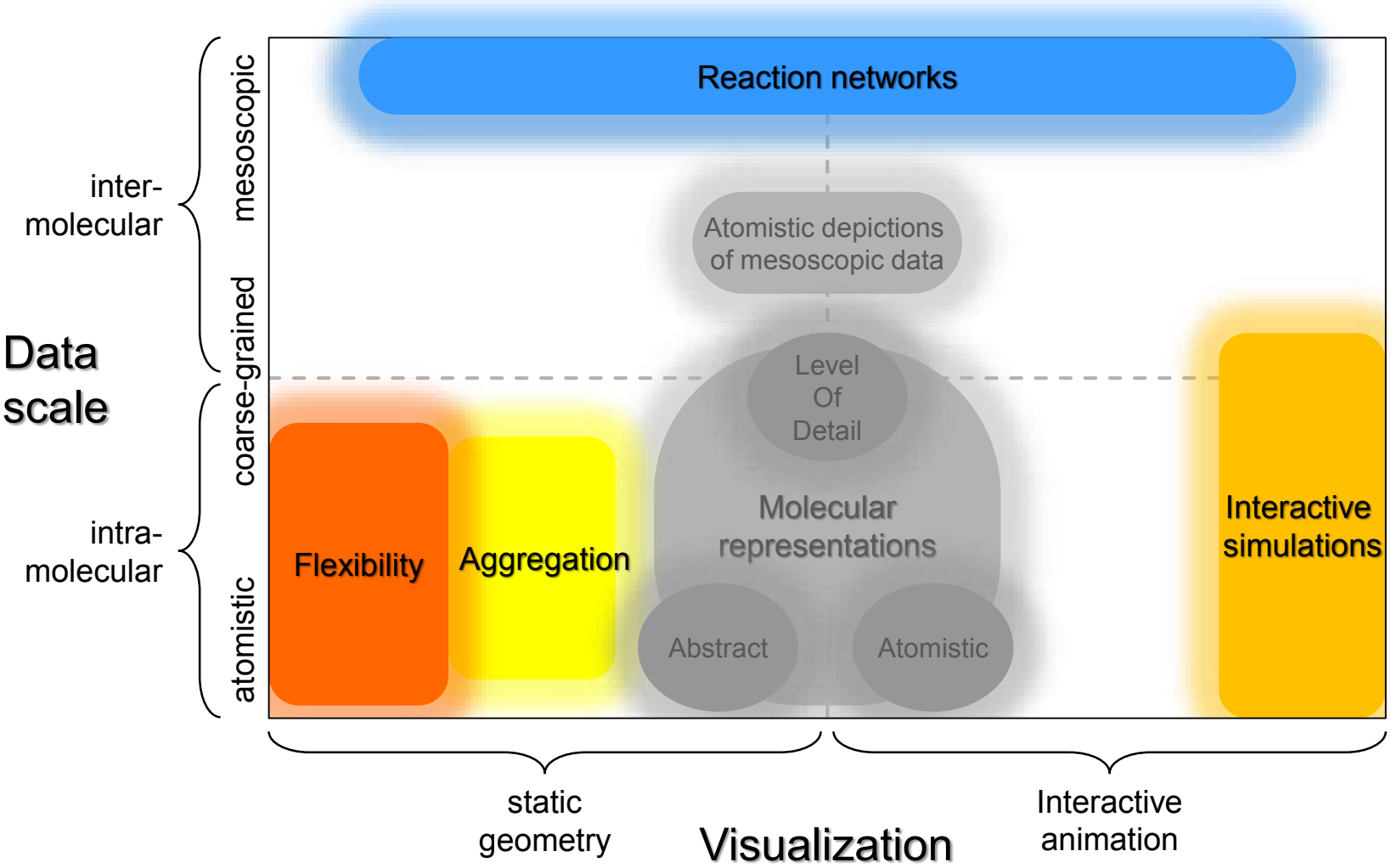


Semantic-based
[Kottravel et al. 2015]

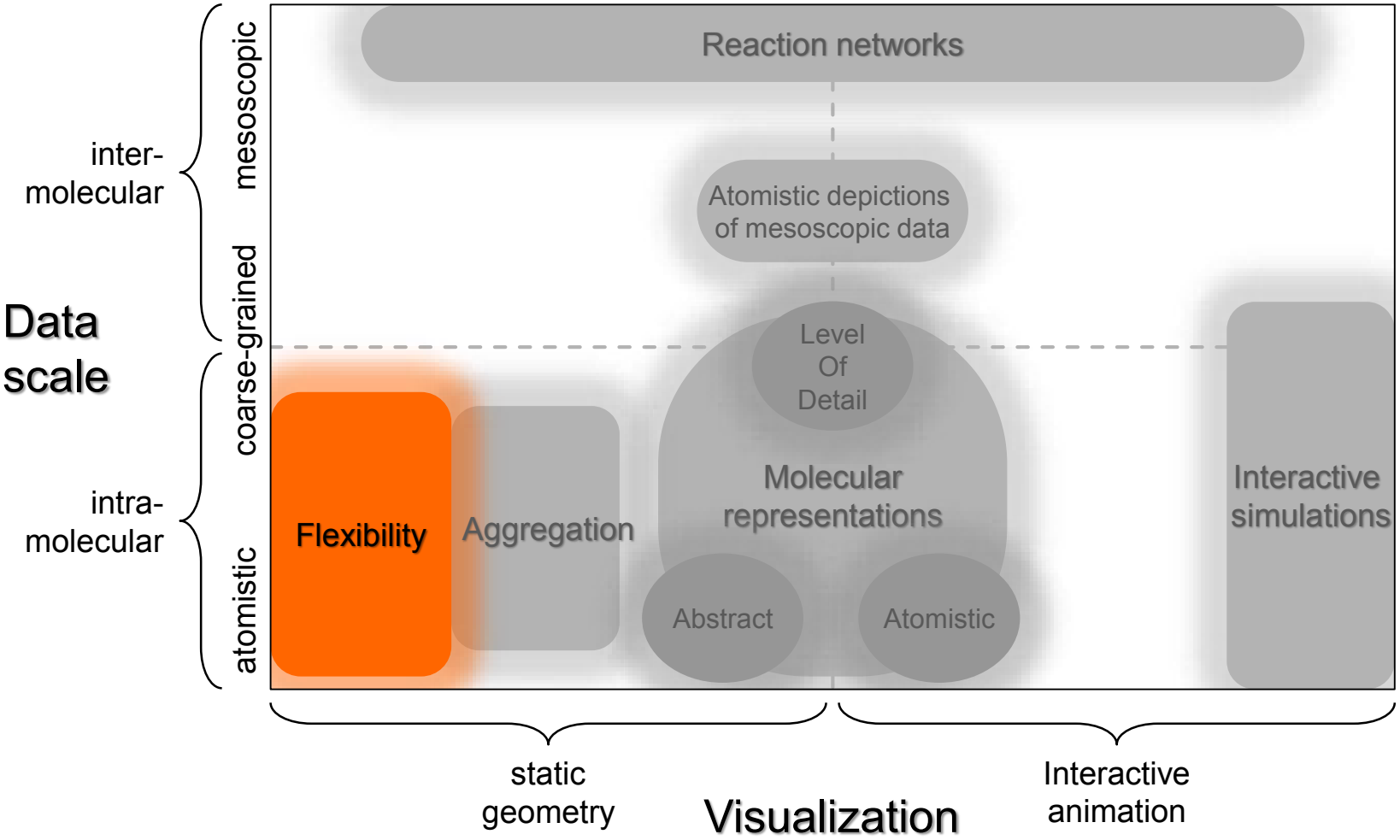
Visualization of Molecular Dynamics



Visualization of Molecular Dynamics

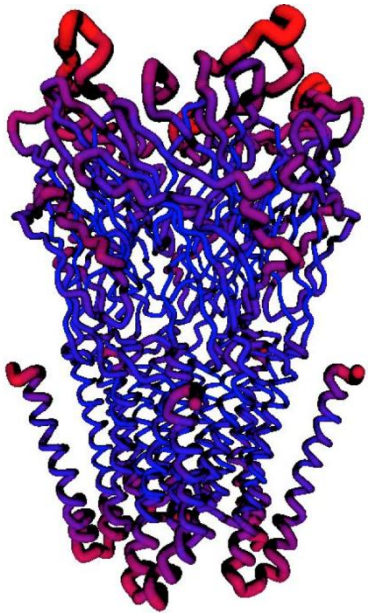


Taxonomy

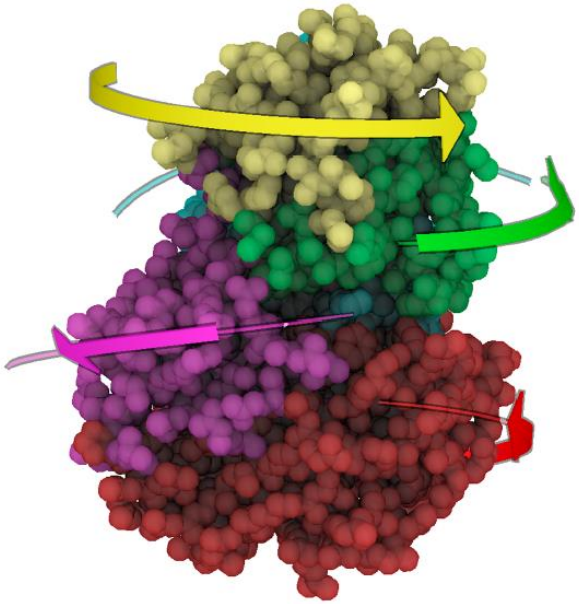

Data scale
inter-molecular
intra-molecular
mesoscopic
coarse-grained
atomistic
Reaction networks
Atomistic depictions of mesoscopic data
Level Of Detail
Molecular representations
Abstract
Atomistic
Flexibility
Aggregation
Interactive simulations
static geometry
Visualization
Interactive animation

Visualization of Flexibility

- Probability distribution depicting the varying molecular conformations

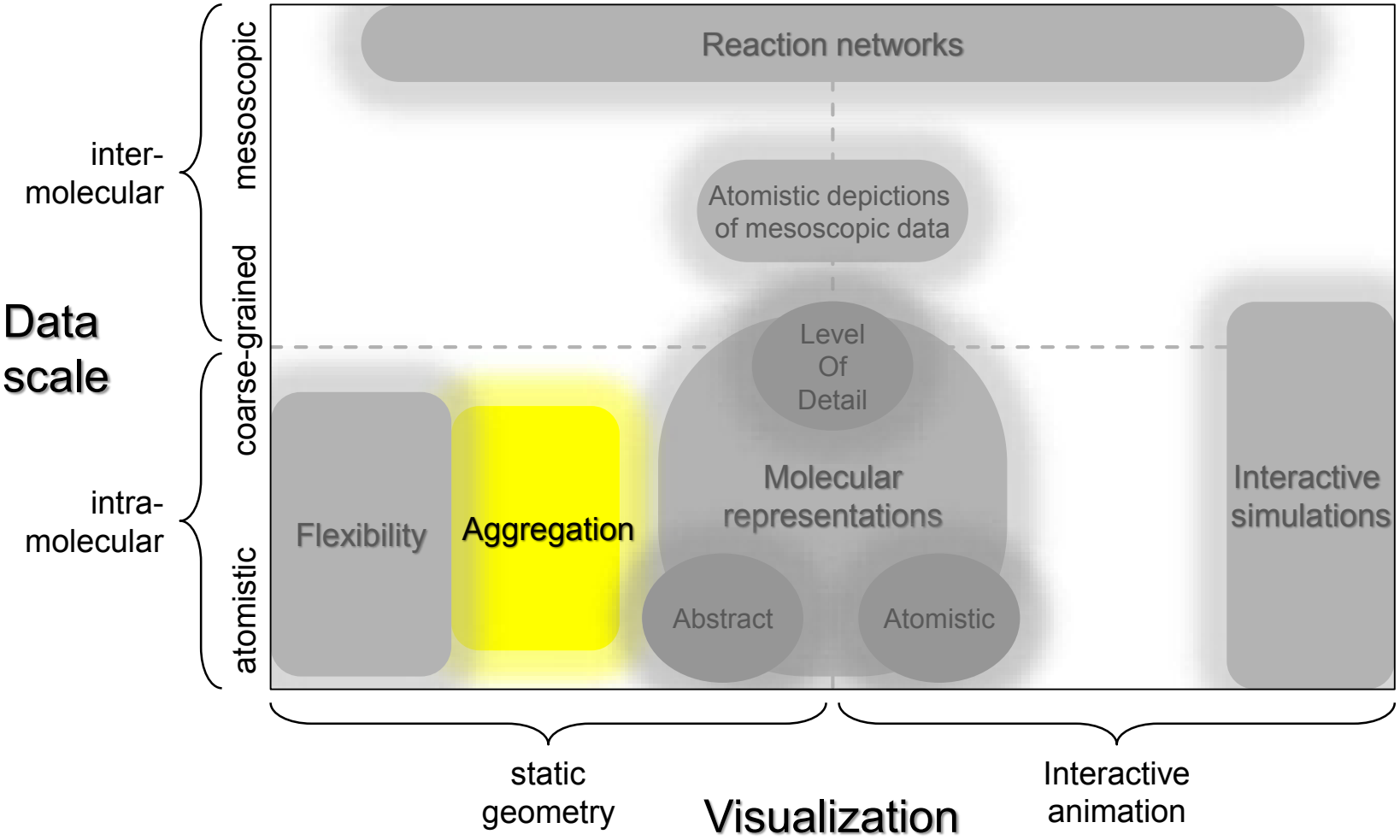


Modulated tube
[Lv et al. 2013]



Normal Mode Analysis
[Bryden et al. 2012]

Taxonomy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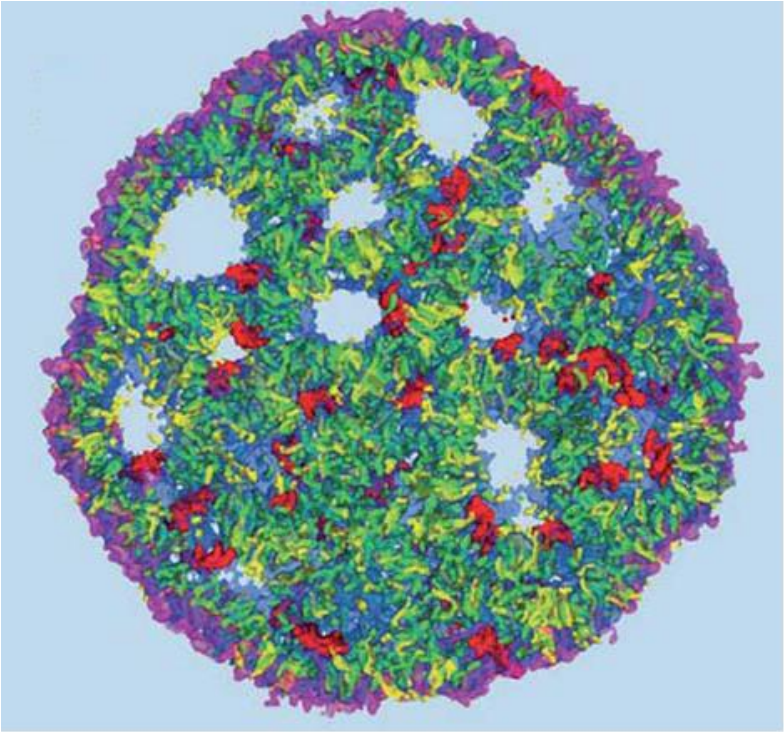
static geometry
Visualization
Interactive animation

Aggregation

- **Spatial**

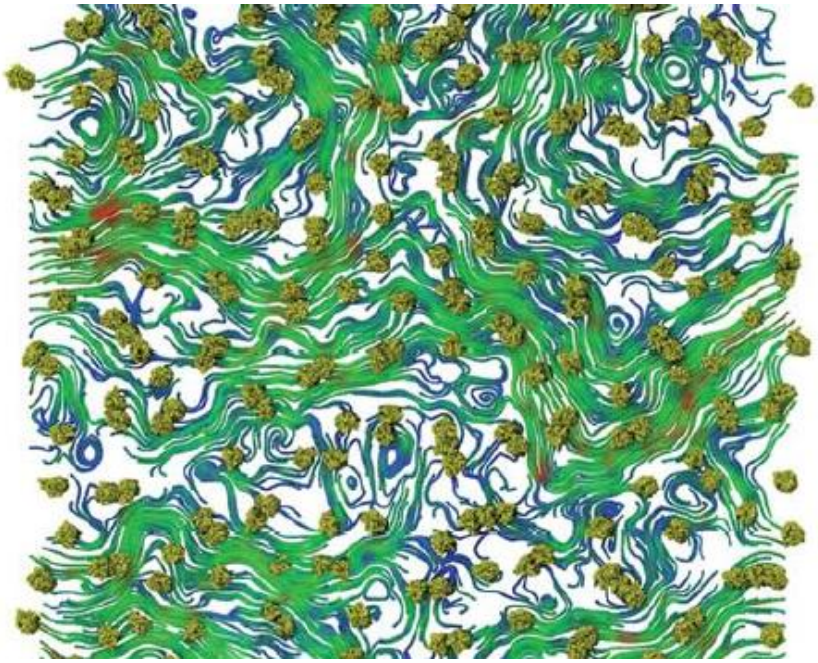
  Aggregating atom densities using property grids



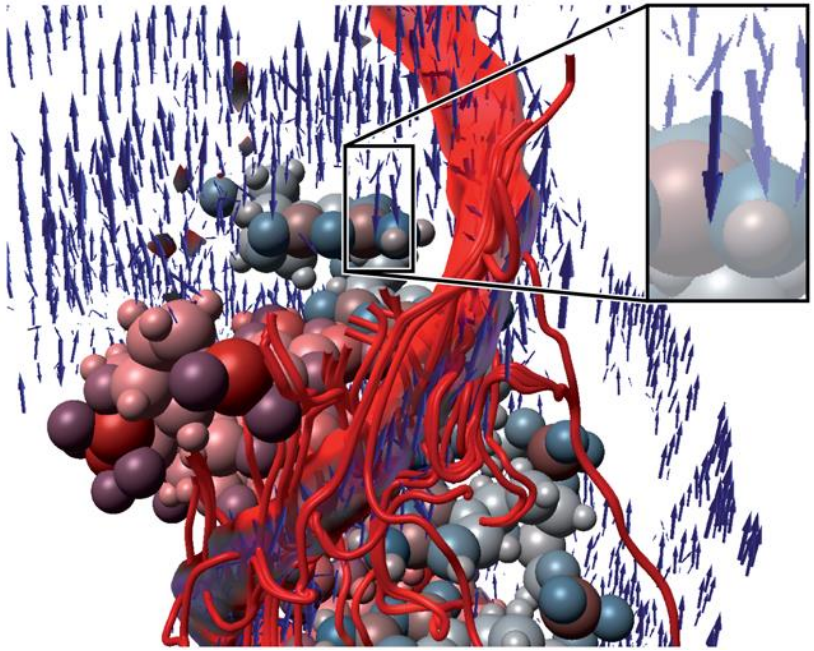
[Rozmanov et al. 2014]

Aggregation

- **Temporal**
  - Aggregated diffusional motion
  - Combination of temporal and spatial aggregation

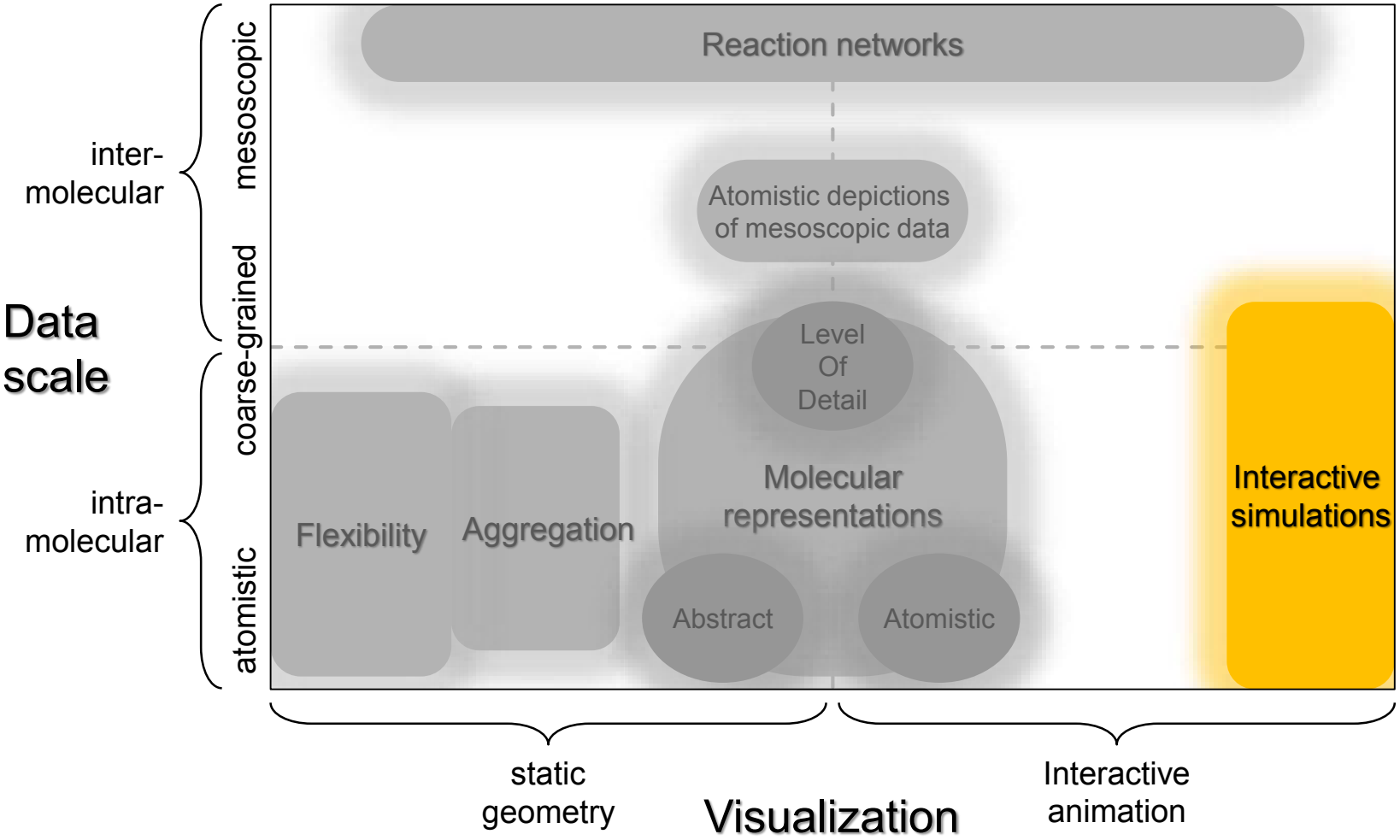


[Chavent et al. 2014]



[Ertl et al. 2014]

Taxonomy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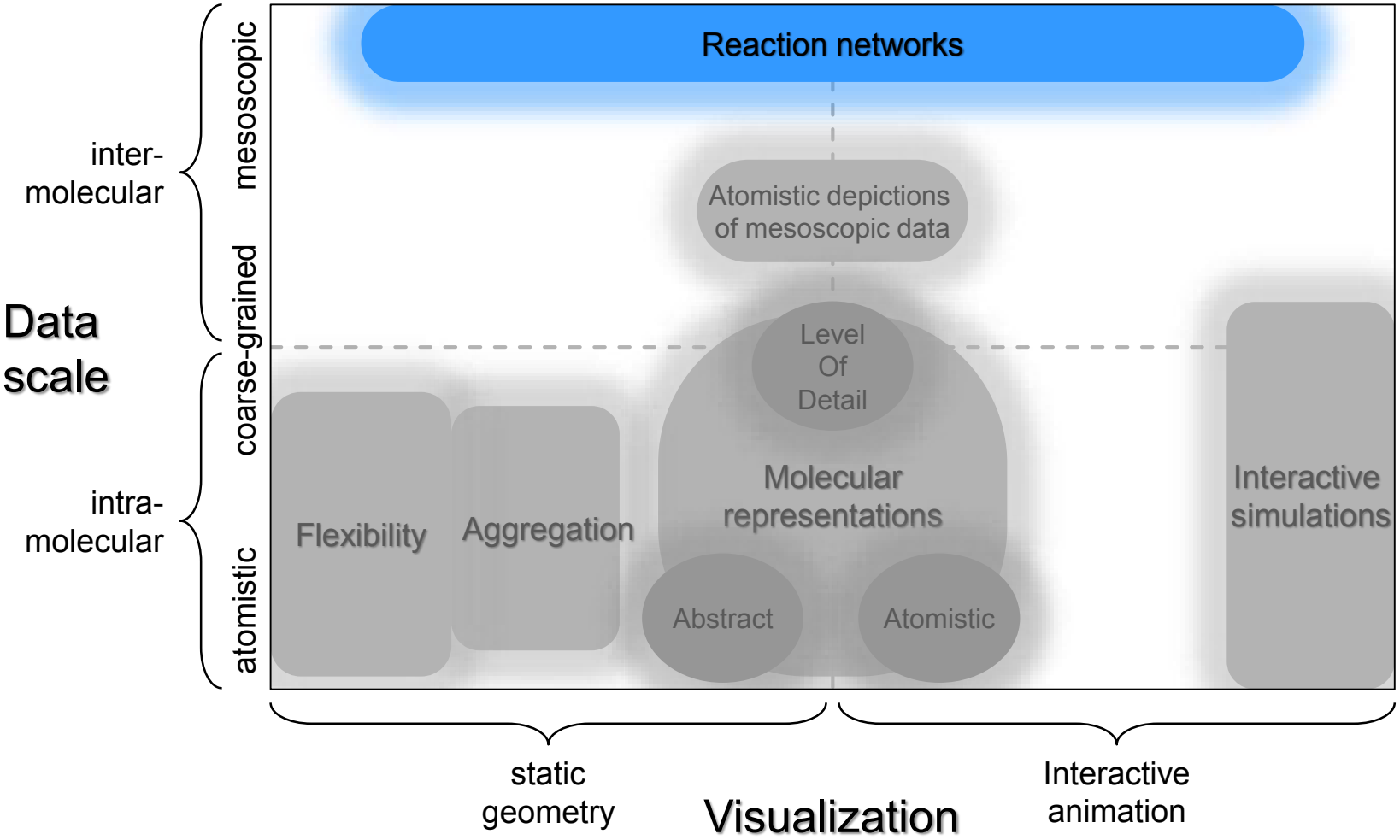
Interactive Simulations

- Visualization has to be interactive → simulation performance has to be the limiting factor
- Haptic rendering – 1000 Hz refresh rates
- Cheaper and better hardware → haptic steering is very attractive

  Applied to systems with more than 1 million atoms

[Dreher et al. 2013]

Taxonomy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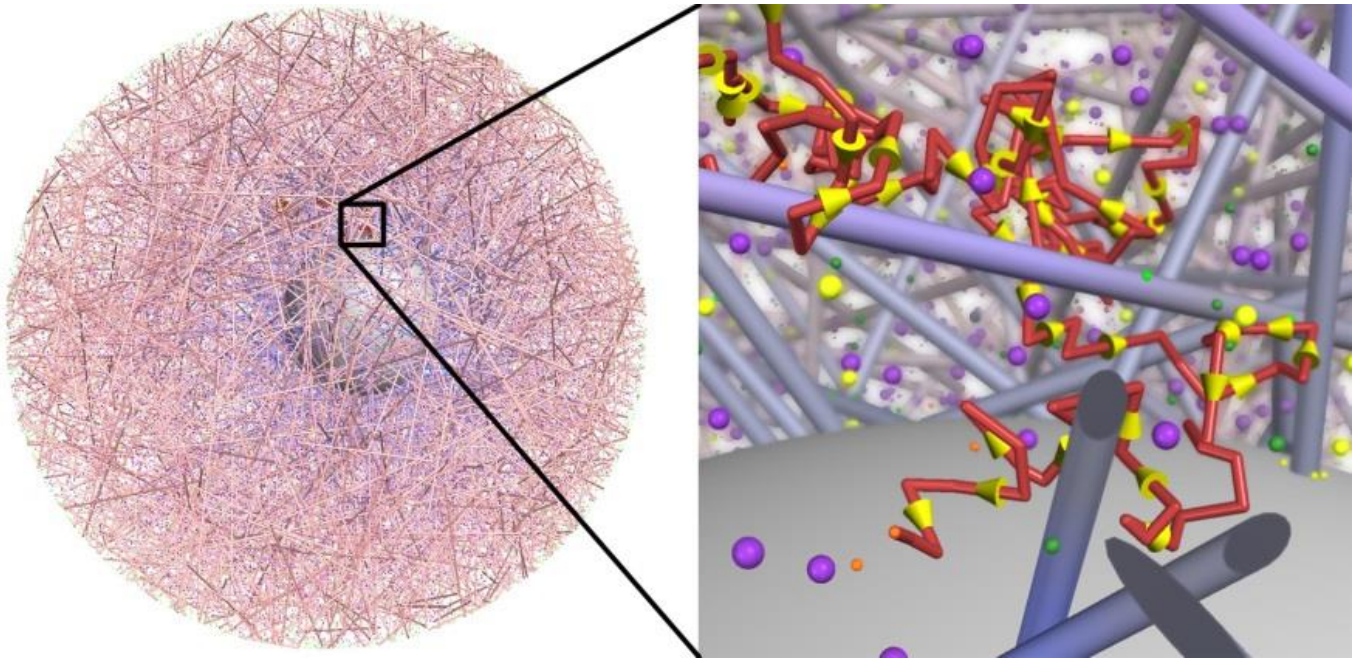
Visualization

Visualization of Molecular Reactions

- Several existing tools for the visualization of reaction networks
- Particle simulations are very crowded

Methods visually emphasizing interesting aspects of simulations



particle trajectory [Falk et al. 2009]

Visualization of Molecular Reactions

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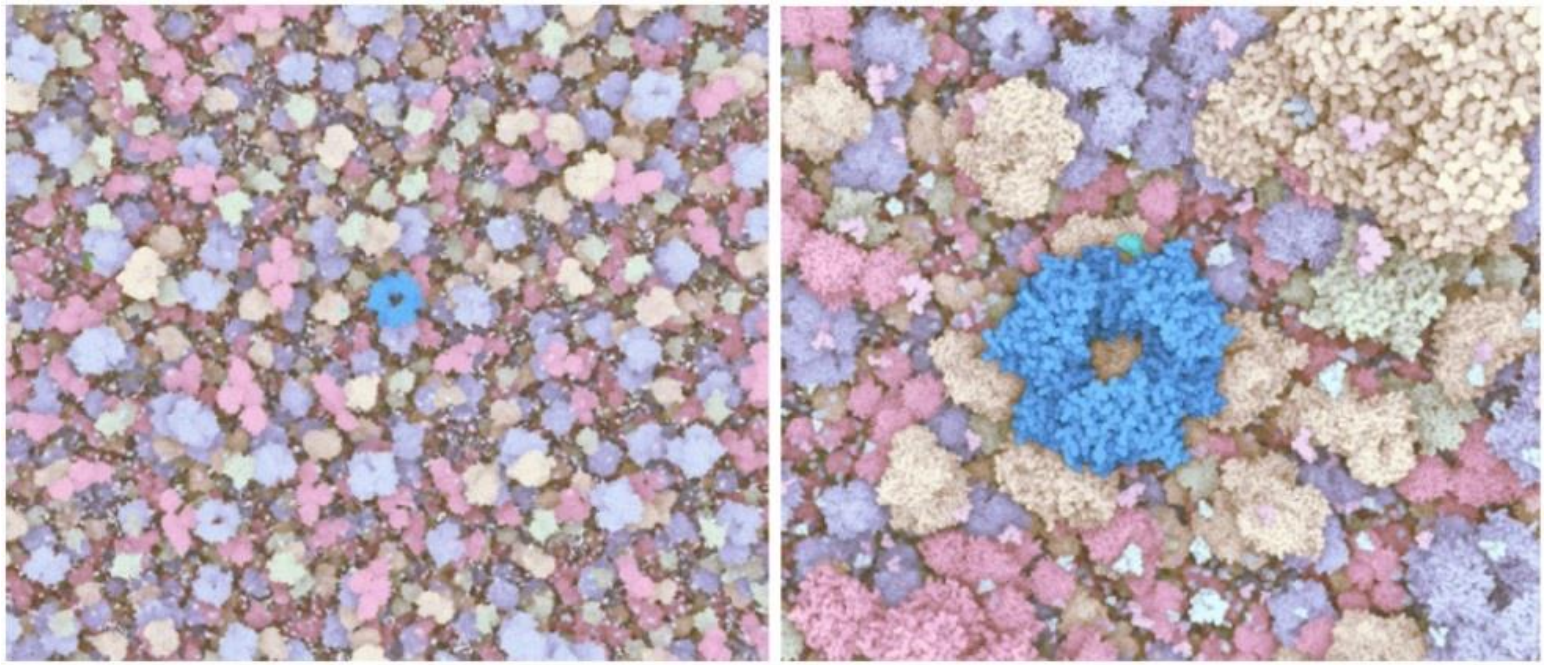
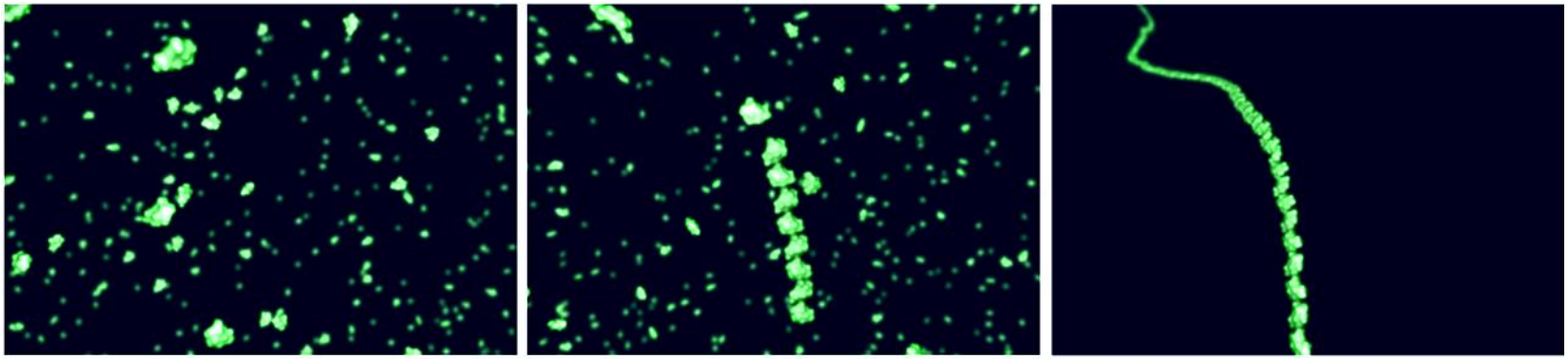


focus on reactions [Le Muzic et al. 2014]

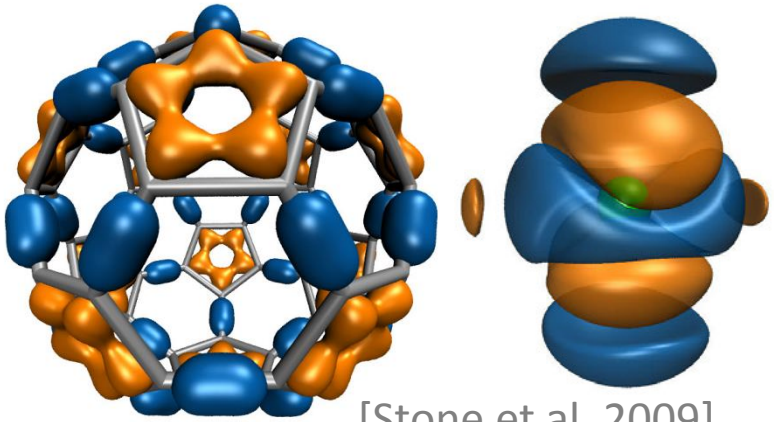
Visualization of Molecular Reactions

- Visualization of polymerization

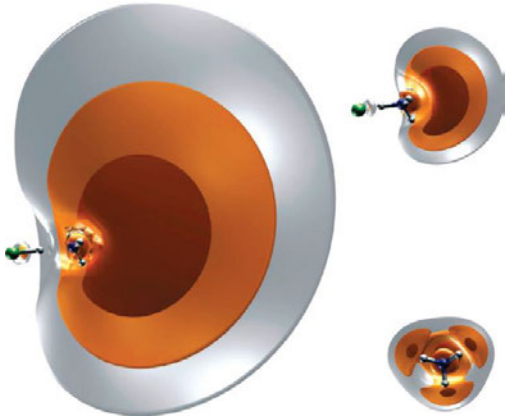
[Kolesár et al. 2014]



- Visualization of molecular orbitals, electron densities, bonds



[Stone et al. 2009]



[Haranczyk, Gutowski 2008]

Molecular Visualization Systems

- Most commonly used and robust systems incorporating the mentioned techniques
- Categorization into three groups

Molecular Visualization Systems

- Most commonly used and robust systems incorporating the mentioned techniques
- Categorization into three groups
  - Freely available systems

Molecular Visualization Systems

- Most commonly used and robust systems incorporating the mentioned techniques
- Categorization into three groups
  - Freely available systems
  - Open-source prototype tools

VMD Visual Molecular Dynamics

PyMOL

CAVER ANALYST

YASARA

UCSF Chimera

MegaMol™

QuteMol

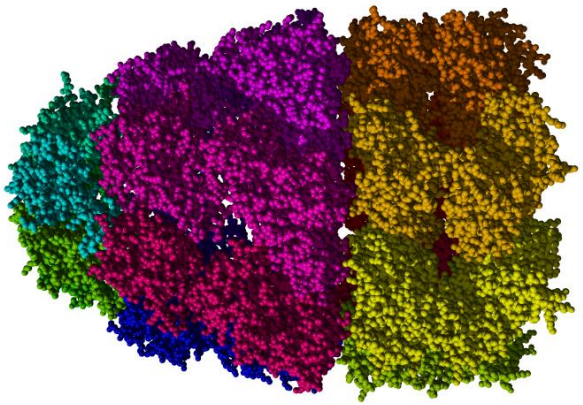
UnityMol

Molecular Visualization Systems

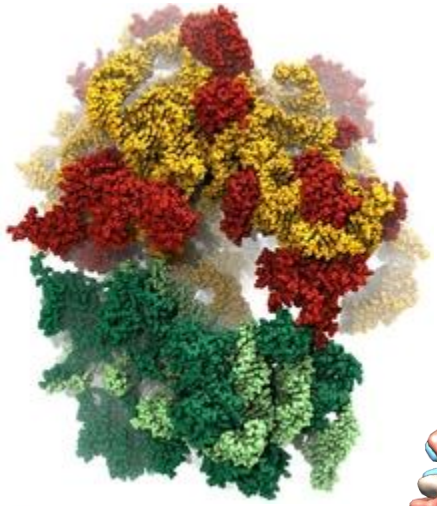
- Most commonly used and robust systems incorporating the mentioned techniques
- Categorization into three groups
  - Freely available systems
  - Open-source prototype tools
  - Commercial systems

Freely Available Complex Systems

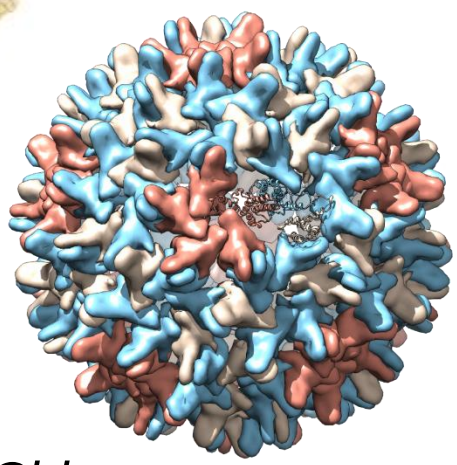
Comprehensive and popular tools



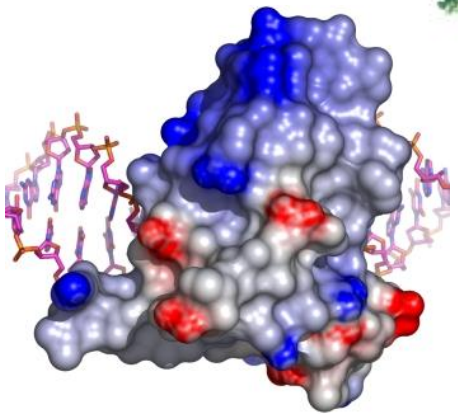
YASARA View



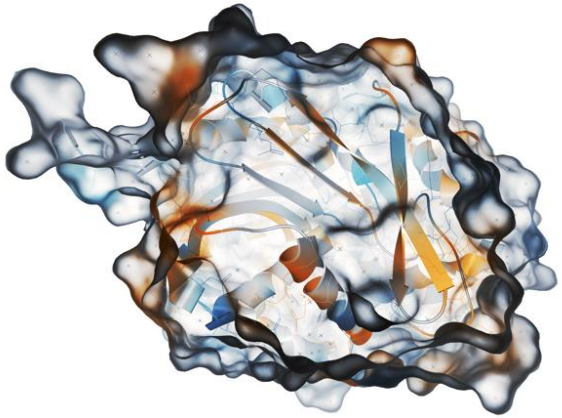
VMD



Chimera



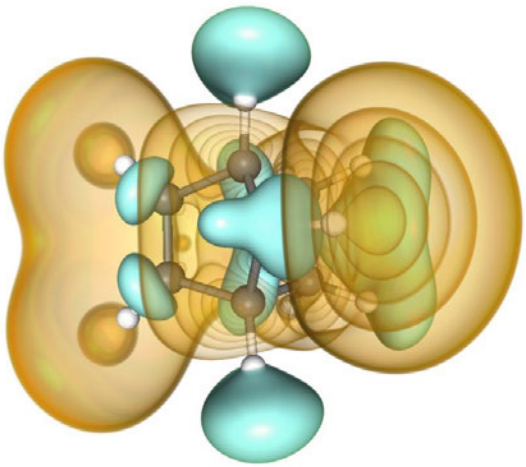
PyMol



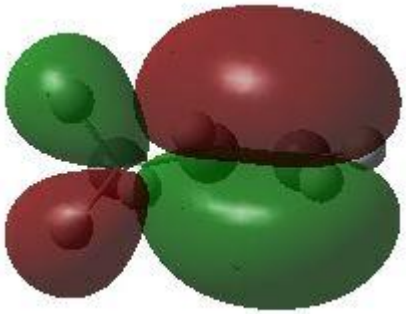
CAVER Analyst

Freely Available Specialized Systems

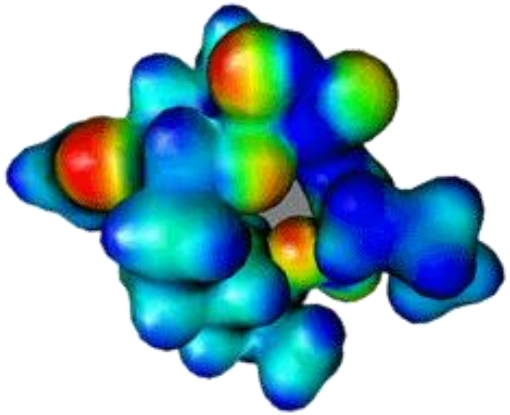
Stand-alone tools for visualization of physico-chemical properties



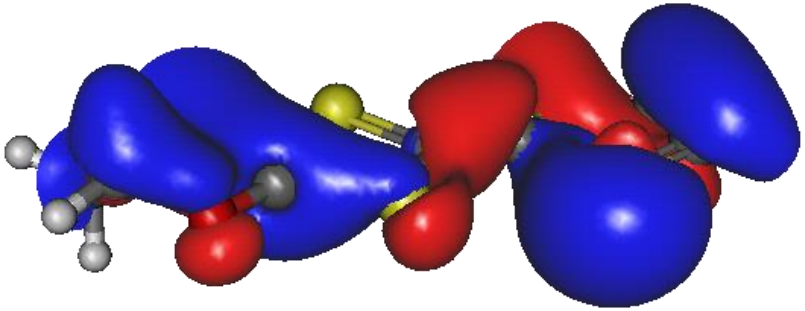
Molekel



GaussView



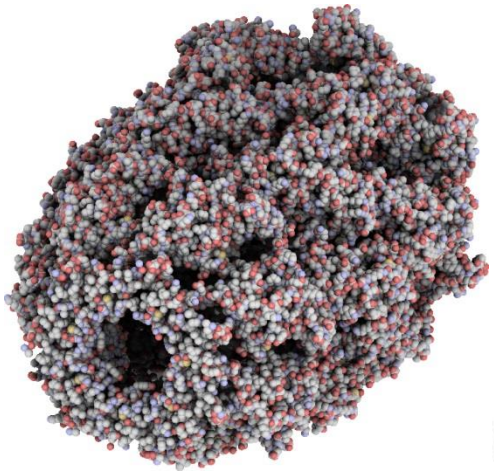
Molden package



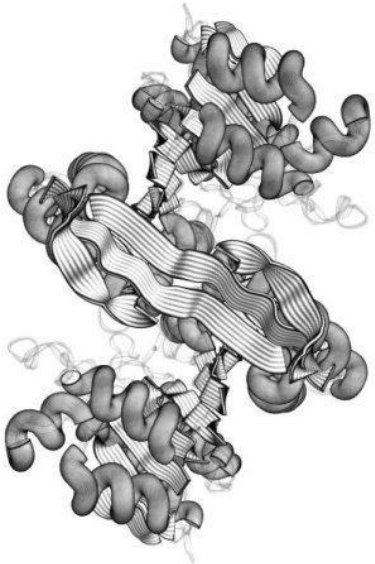
Gabedit

Open-Source Prototype Tools

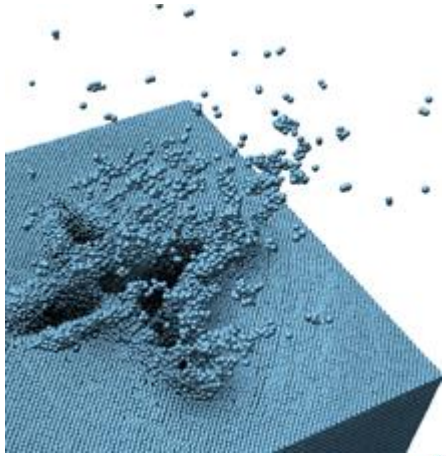
Focus on very efficient implementation



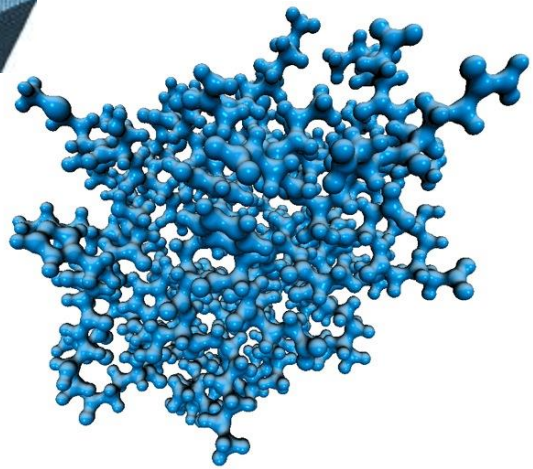
QuteMol



ProteinShader



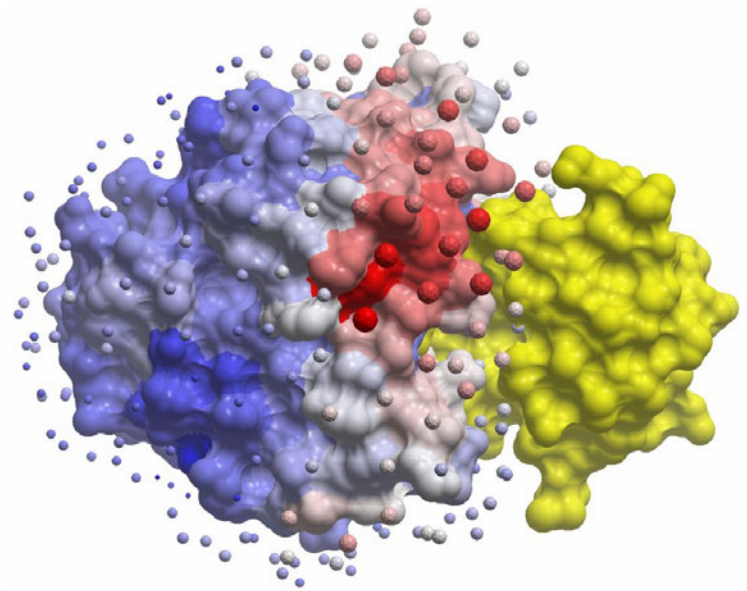
MegaMol



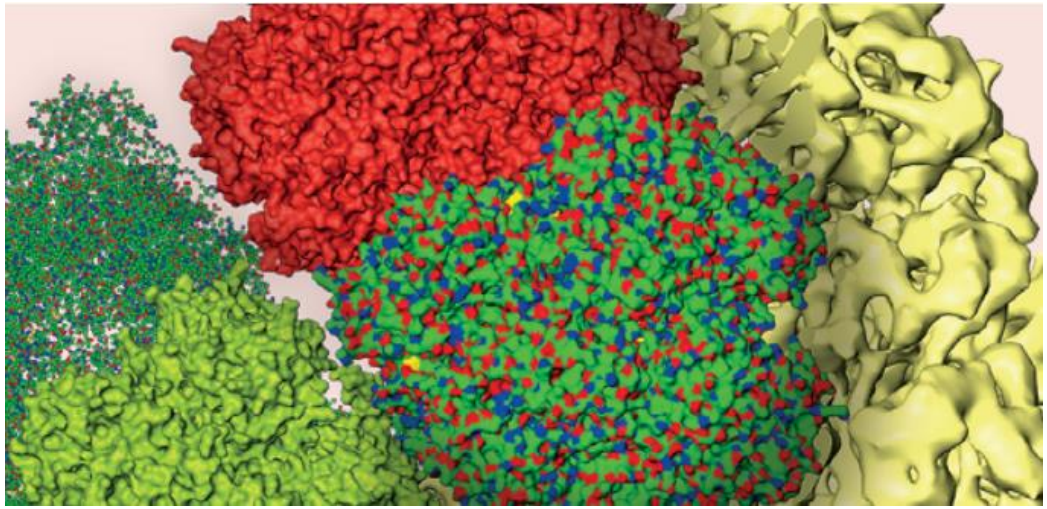
UnityMol

Commercial Systems

Classical representations, iso-surfaces, volume rendering



MolSoft ICM-Pro



Amira

Future Challenges

- Recent trend is to use GPU based rendering and computations
  - Programmable GPUs and multi-core GPUs enable parallelization
- Increasing amount of captured data sets in terms of particle numbers and time steps
- Complexity of data will require new visual representations
  - Visual analysis
- Quantum mechanics simulations will require novel visualization methods
- Interactive ray tracing
- Visual language for biomolecules

Conclusion

- Different representations coming from a diverse field of molecular biology
- There is not one best representation but rather many possible ones, each one best suited for a specific task

Thank you for your Attention

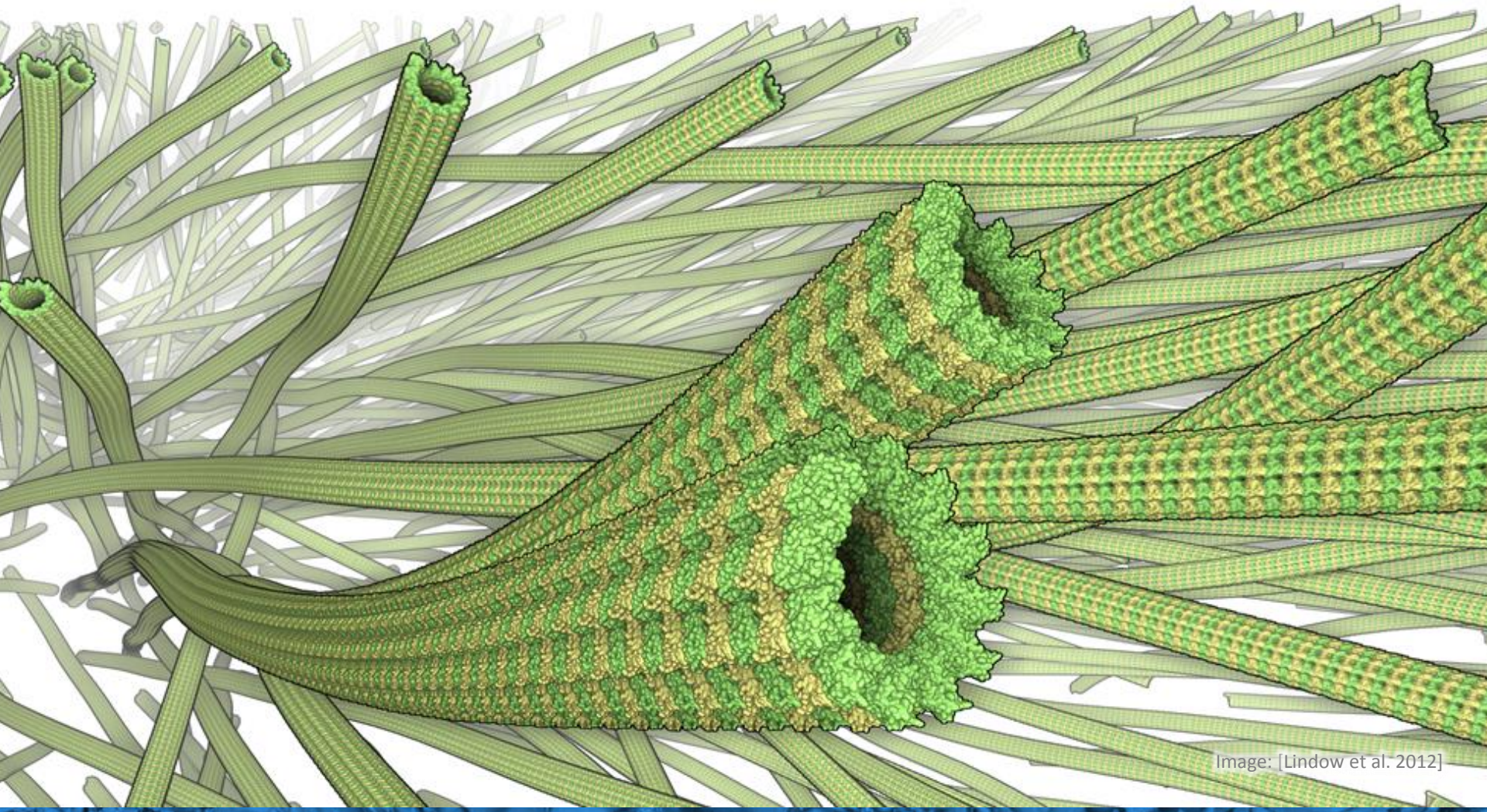


Image: [Lindow et al. 2012]

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