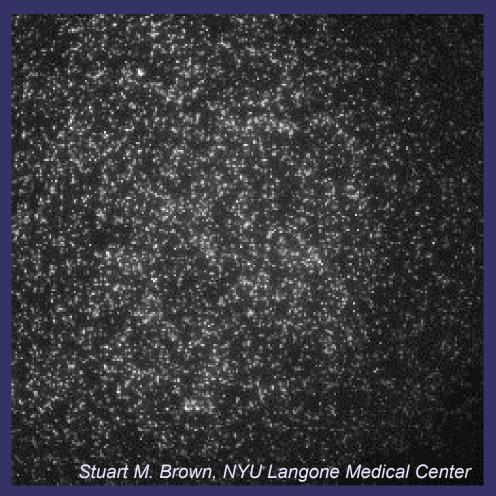


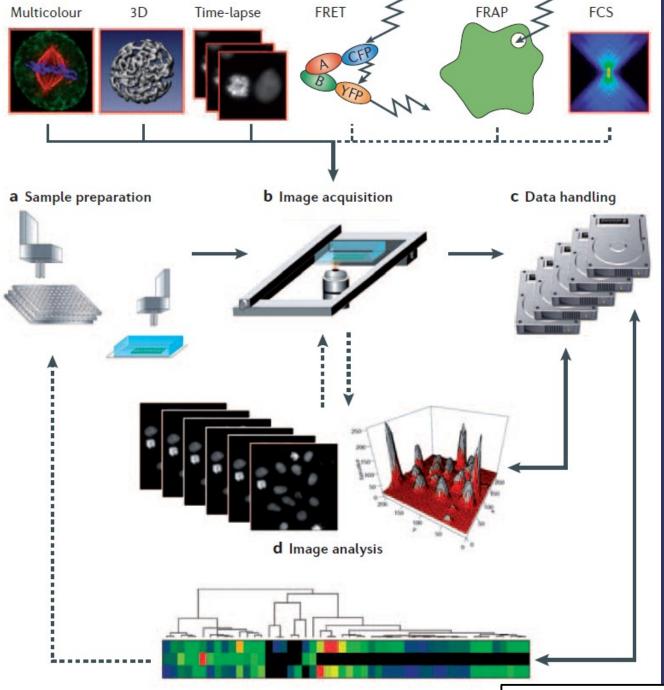
#### Agenda

- Biological data deluge
- Data mass and comprehension
- Comprehension by 3D modeling
- Modeling DNA is required
- MicroMégas is of great help

#### Biological data deluge

Modern sequencers: One human genome every 14 minutes, 1-2 TB of raw data



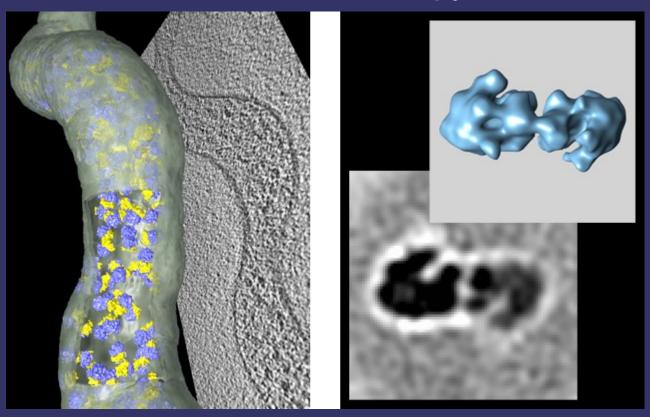


# Biological data deluge

- Fluorescence microscopy:
  - Basis of numerous experiments
  - Acquisition of millions images per run
  - Generates several tens of terabytes

# Biological data deluge

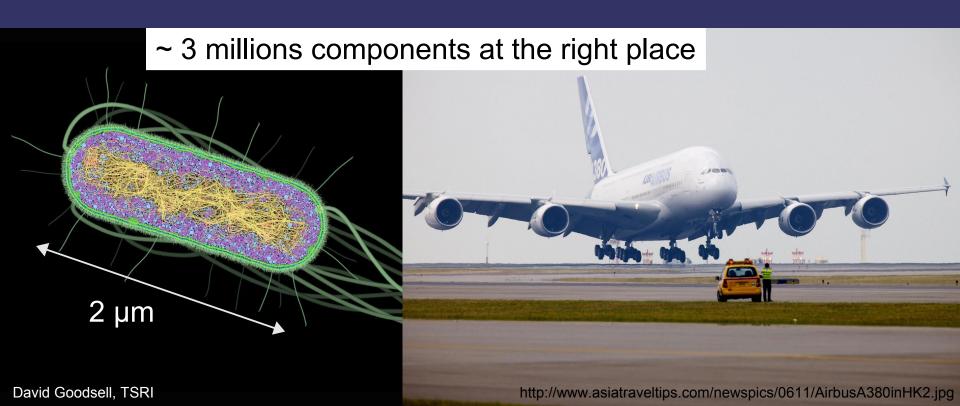
#### Electron microscopy



Julio.Ortiz, Max Planck Institute of Biochemistry

#### Data mass and comprehension

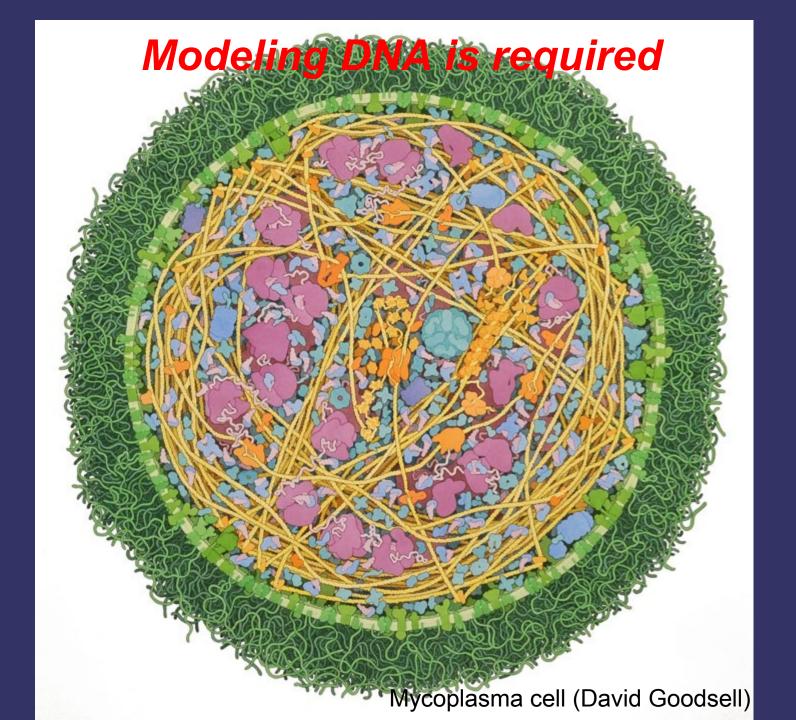
- 50 years used to dissect cells
- Time is come to re-assemble the disconnected parts



### Comprehension by 3D modeling

- 3D modeling is being adopted
- 3D software borrowed from "Hollywood"
- Need a career time to be learned

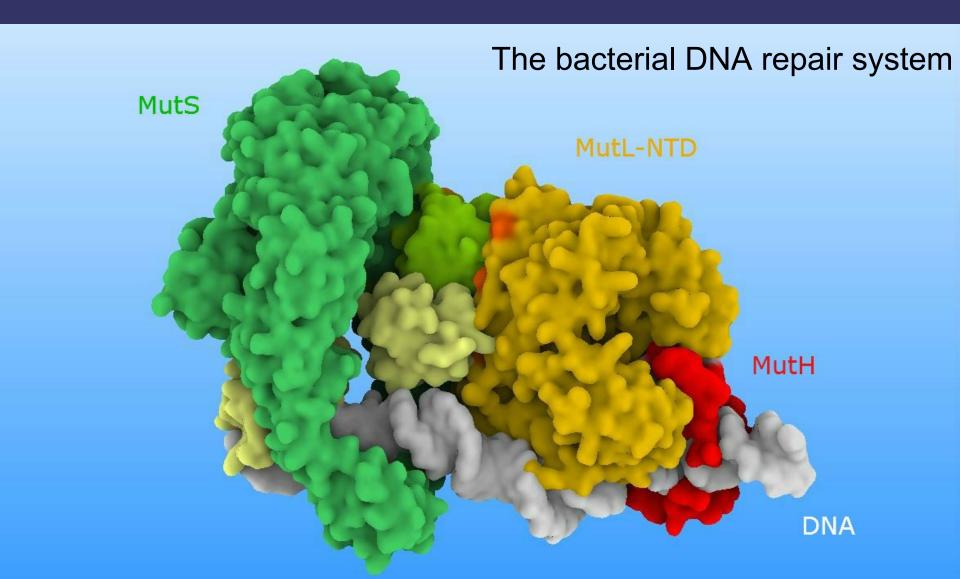




#### Modeling DNA is required

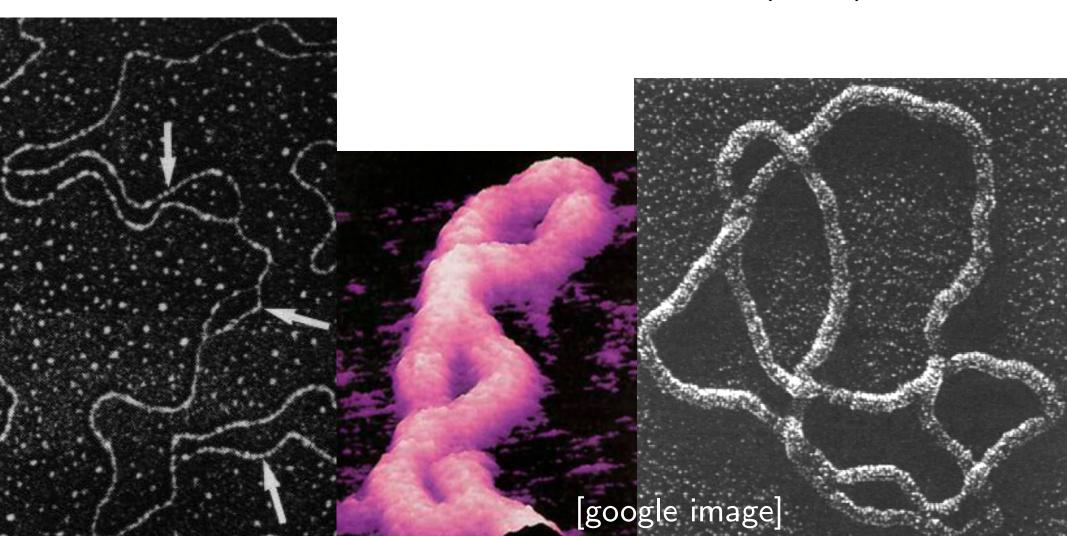
- Standard molecular tools and webservices:
  - Lack of intuitivity
  - Very basic modeling functions
- The opensource and intuitive MicroMégas plugin overcomes this situation

# MicroMégas is of great help



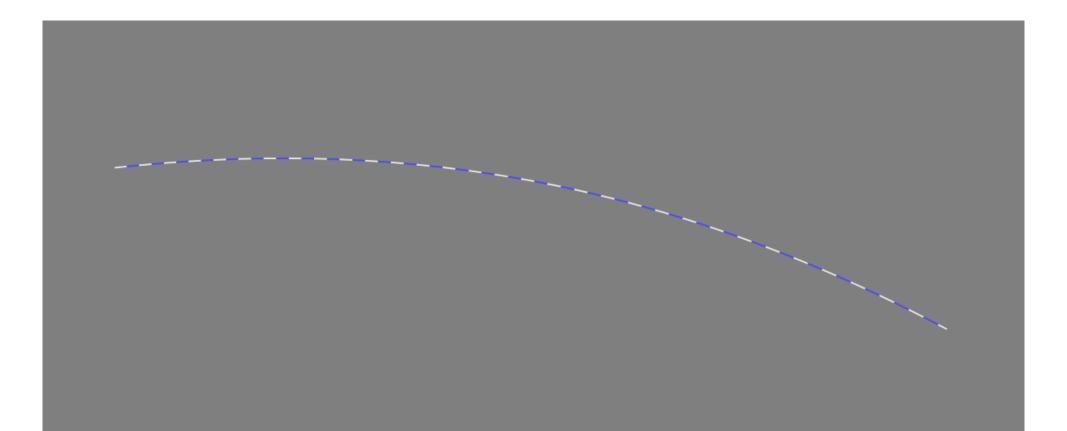
Naive view of DNA is good for low-level modeling:

- string-like structure
- helical shape
- long sequence of very similar "base pairs" (ACGT)



Computer graphicists translate this structure to:

• a curve

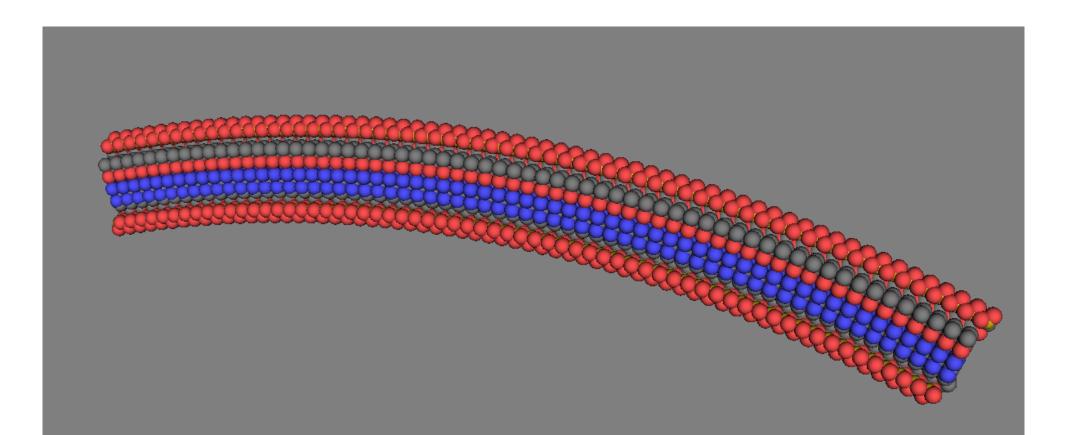


Computer graphicists translate this structure to:

- a curve
- a uniform sampling of orthonormal frames

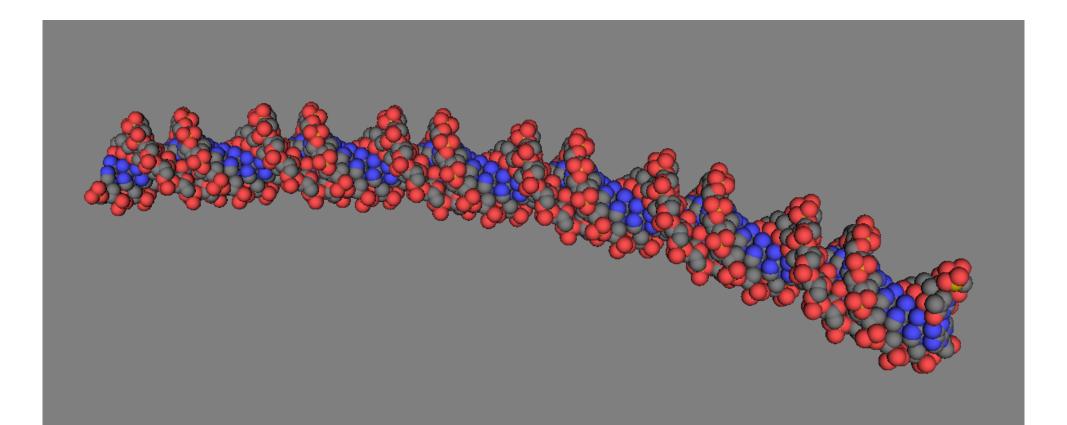
Computer graphicists translate this structure to:

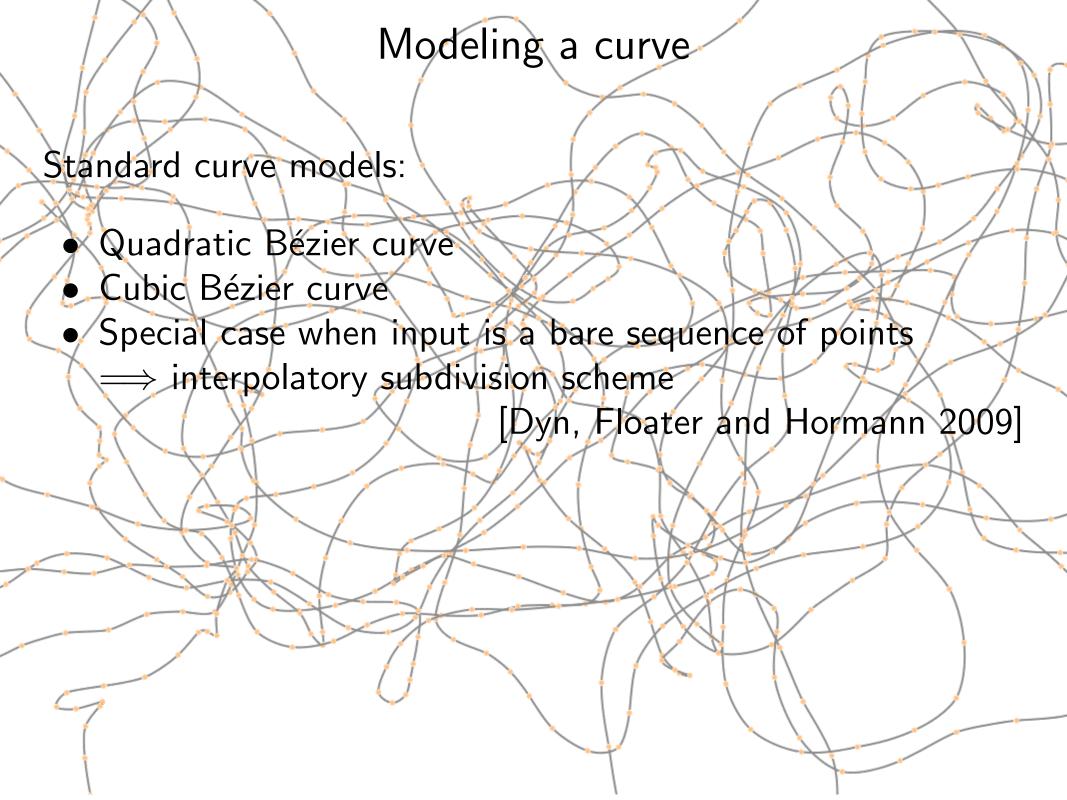
- a curve
- a uniform sampling of orthonormal frames
- instancing of base pairs



Computer graphicists translate this structure to:

- a curve
- a uniform sampling of orthonormal frames
- instancing of base pairs
- with twisting: rotation around the tangent vector





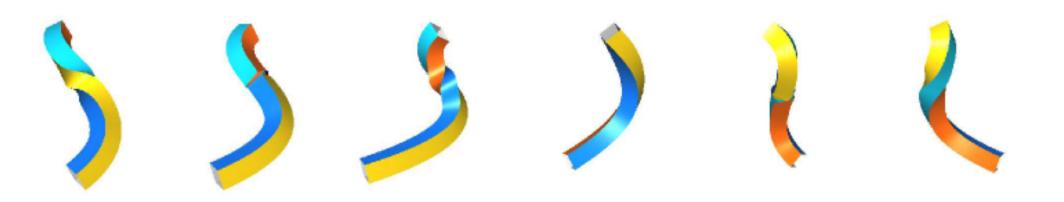
# Uniform sampling

Generating a uniform sampling with tangent is easy Generating a normal at each sample point is difficult

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We want a continuous frame that minimizes torsion E.g. the Frénet-Serret frame is not continuous

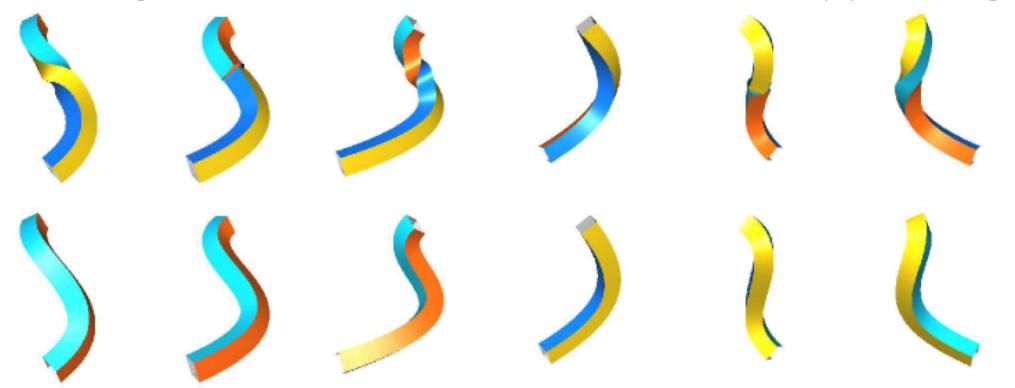


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Generating a uniform sampling with tangent is easy Generating a normal at each sample point is difficult

We want a continuous frame that minimizes torsion E.g. the Frénet-Serret frame is not continuous

Recent technique: very fast and very good approximation: [Rotation Minimizing Frames, ACM ToG 27(1):2, 2008]



Use OpenGL to instantiate a 3D model of a base-pair in each frame along the curve:

- Setup GL transform matrix
- One call to glDrawArrays to draw one base pair

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A base-pair has  $\approx 40$  atoms. We setup GLSL programs so that:

- input = array of atoms {center, radius, color}
- geometry shader builds a quad in front of the atom
- pixel shader compute intersection of ray & atom (a sphere)

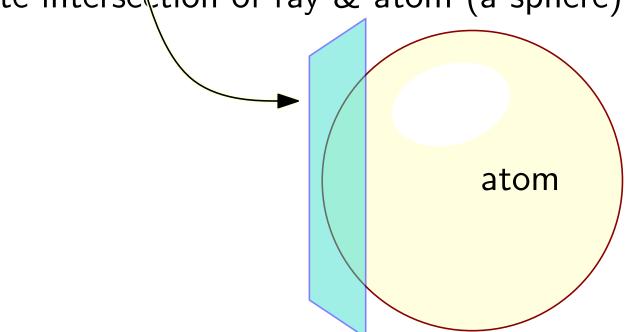
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camera

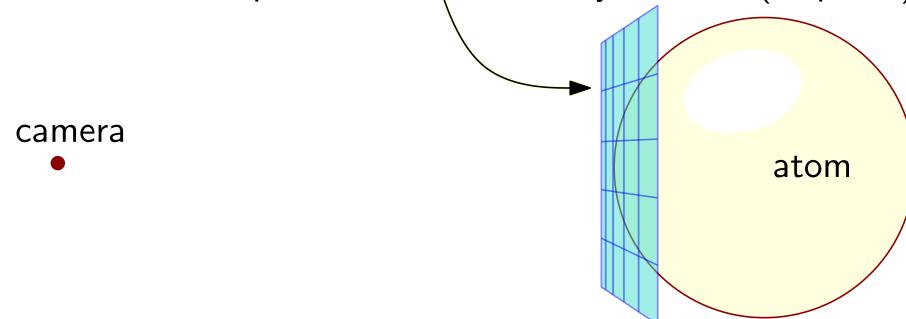
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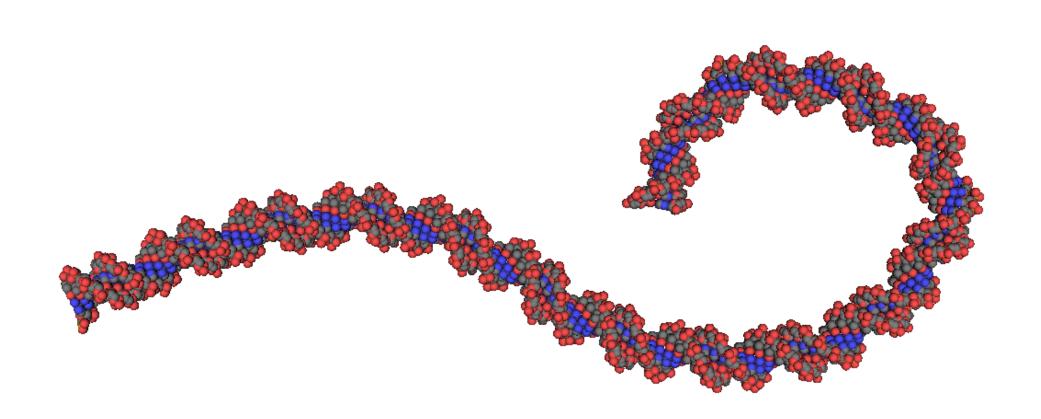
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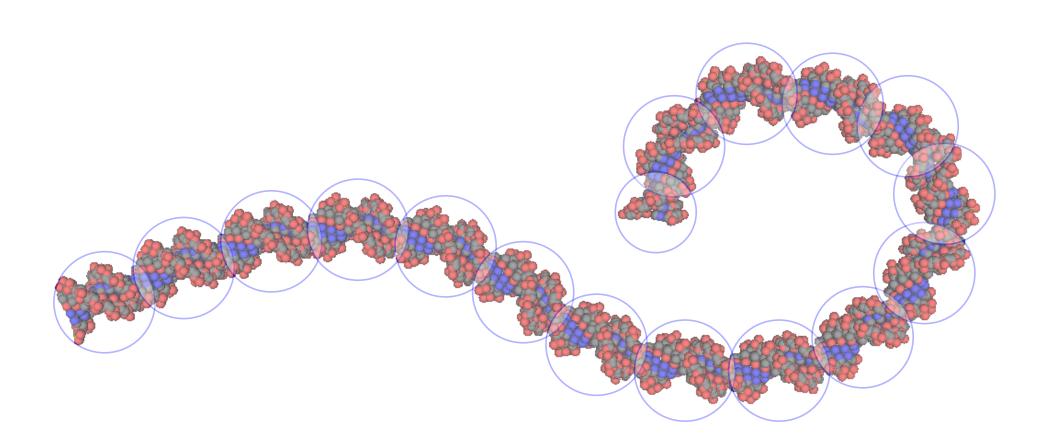
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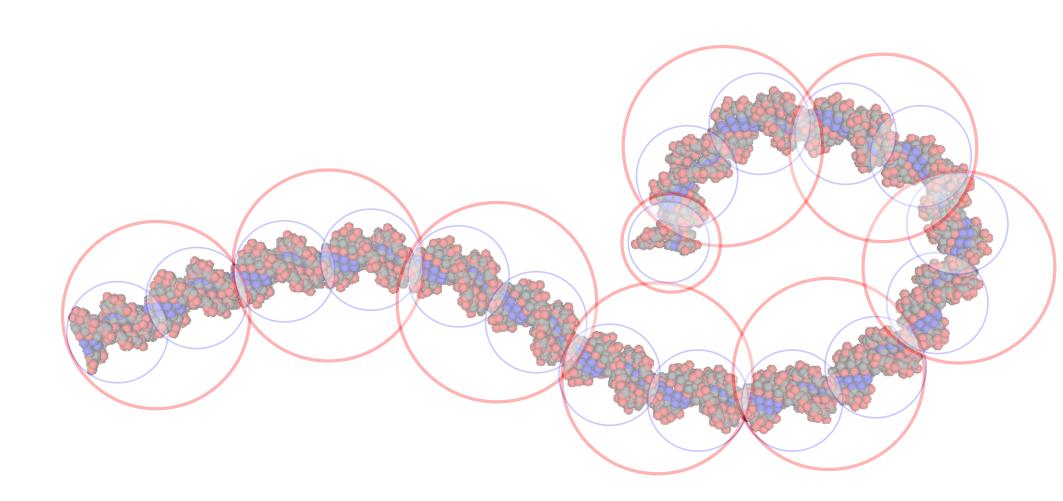
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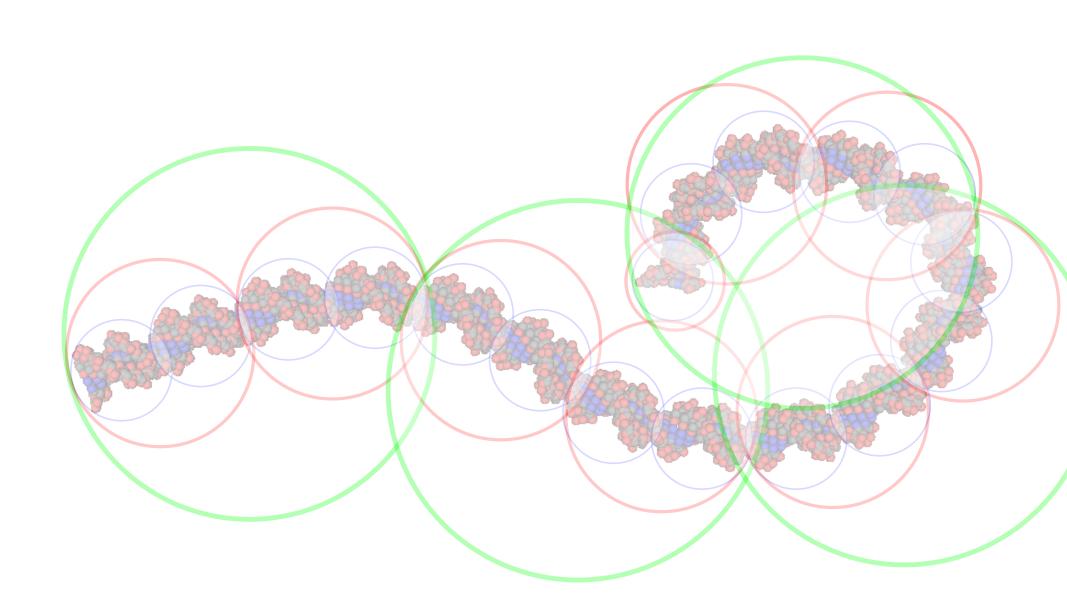
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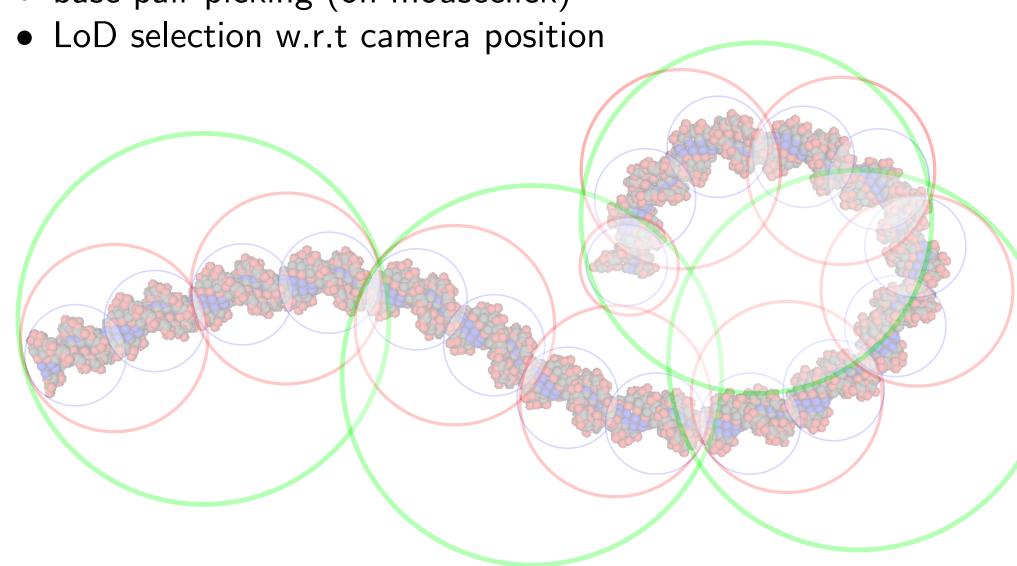




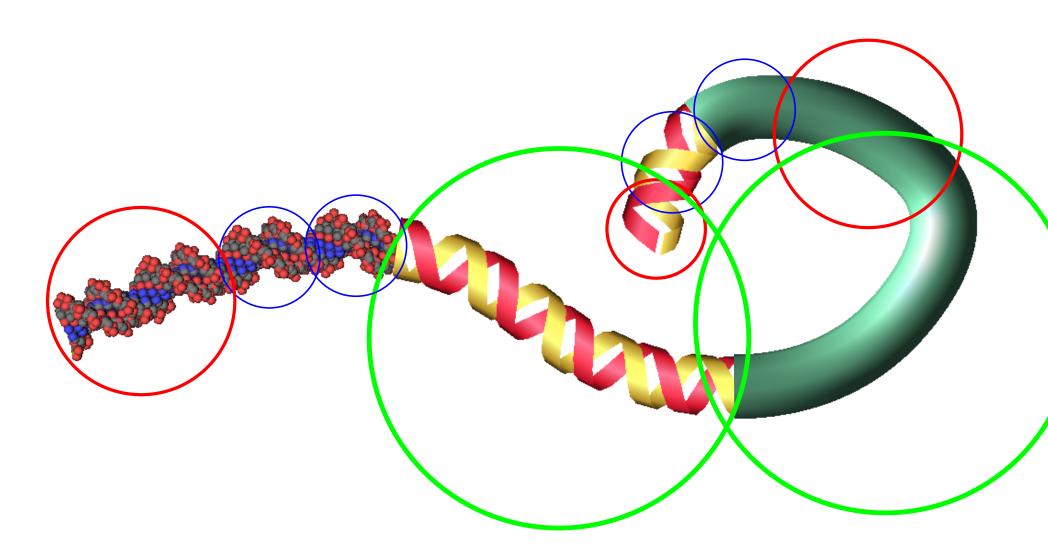


#### Hierarchy used for

base-pair picking (on mouseclick)



← Camera is left of screen





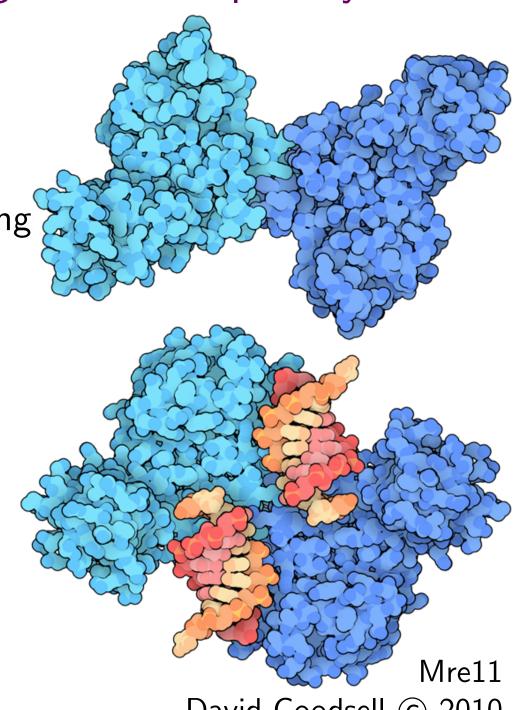
# Why modeling biological scenes spatially?

#### Medical illustration

Popularizing knowledge

Help scientists' understanding

Dynamic simulation



David Goodsell © 2010

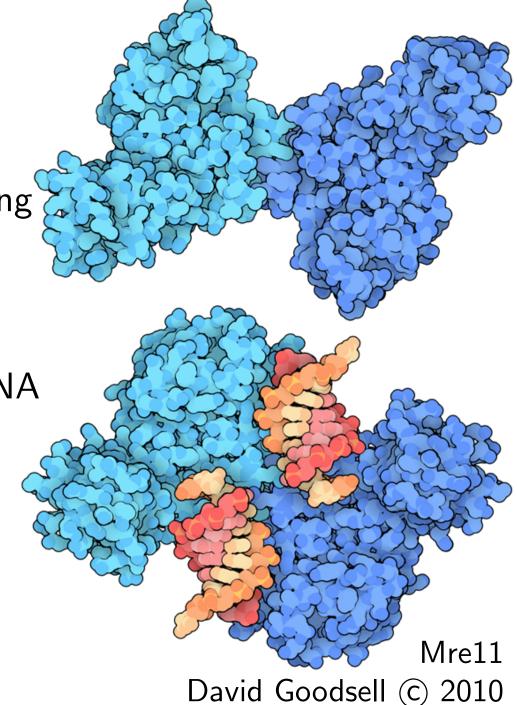
# Why modeling biological scenes spatially?

#### Medical illustration

- Popularizing knowledge
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Scientific reasons specific to DNA

Later in this talk...



Growing importance of modeling and simulation for experiments

⇒ need for specialized spatial modeling tools for biologists

⇒ DNA is an important target

"Modeling DNA in space is such a tedious job!"

— microbiologists and illustrators

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Use advanced 3D modeling software

Maya
3D Studio
Blender

Or command-line tool and web services with form-based input

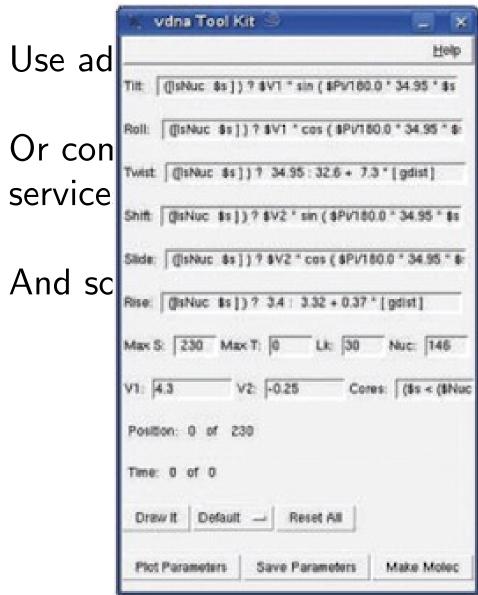
3DNA • 3D-DART • DNA Maker

And some with "UI"

VDNA (VMD plugin)

"Modeling DNA in space is such a tedious job!"

microbiologists and illustrators



Blender 4 Maker plugin)