Biomolecular Visualization Framework

Citation: Dries et al (2017) *Biochemistry and Molecular Biology Education* 45:69-75

Atomic Geometry (AG) - three-atom and four-atom (dihedral) angles, metal size and metal-ligand geometries, steric clashes.

AG1. Students can describe the ideal geometry for a given atom within a molecule and deviations from the ideal geometry due to neighboring interactions.

AG1.01 Students can identify atomic geometry/hybridization for a given atom. (Novice)

AG1.02 Students can measure bond angles for a given atom. (Novice)

AG1.03 Students can identify deviations from the ideal bond angles. (Amateur)

AG1.04 Students can explain deviations from the ideal bond angles due to local effects. (Amateur, Expert)

AG1.05 Students can predict the effect of deviations from ideal bond angles on the structure and function of a macromolecule. (Expert)

AG1.06 Students can identify the structural features of a peptide bond. (Novice, Amateur)

AG2. Students can compare and contrast different structural conformations with regard to energy, addition of substituents, and impact on structure/function of a macromolecule.

AG2.01 Students can describe different conformations that a cyclic structure can adopt using visualization tools. (Amateur)

AG2.02 Students can describe different conformations of atoms about a bond using visualization tools. (Novice)

AG2.03 Students can distinguish energetically favorable and unfavorable conformations that a structure can adopt. (Amateur)

AG2.04 Students can predict the effect of a given conformation on the structure and function of a macromolecule. (Expert)

AG3. Students can describe the effect of torsion angles on macromolecular structure.

AG3.01 Students can identify a torsion angle in a three-dimensional representation of a macromolecule. (Novice)

AG3.02 Students can identify the planes between which a torsion angle exists within a three-dimensional representation of a macromolecule. (Novice)

AG3.03 Students can identify phi, psi, and omega dihedral angles in a three-dimensional representation of a macromolecule. (Amateur)

Alternate Renderings (AR) - Rendering of a macromolecular structure such as a protein or nucleic acid structure in various ways from the simplest possible way (connections between alpha carbons) to illustration of secondary structure (ribbons) to surface rendering and space filling.

AR1. Students can create meaningful molecular images to convey features such as secondary structure, cpk coloring, active sites and molecular interactions.

AR1.01 Students will be able to manipulate rendered structures in 3D space. (Novice)

AR1.02 Students will be able to align rendered structures in 3D space. (Amateur)

AR1.03 Students can annotate the differences between multiple aligned structures. (Expert)

AR1.04 Students can infer information from rendering a structure in different ways. (Novice, Amateur, Expert)

AR1.05 Students can create renderings that distinguish secondary structural features. (Novice)

AR1.06 Students can create an information rich rendering of a structure that depicts structural features found in the literature. (Amateur)

AR1.07 Students can create an information rich rendering of a structure containing heteroatoms and noncanonical amino acids or nucleotides. (Expert)

AR1.08 Students can use molecular visualization to tell a story about a macromolecular structure. (Expert)

AR1.09 Given the rendering of a macromolecule, students can find hydrogen bonds, ionic bonds and van der Waals contacts in the structure. (Expert)

AR1.10 Students can convert textbook images of small molecules into 3D representations in a molecular visualization program. (Amateur)

AR2. Students can produce the best rendering of a macromolecule to use in a given situation.

AR2.01 Students recognize that a cartoon rendering is a summary of the detail in a line rendering. (Novice, Amateur)

AR2.02 Students will describe the atoms that are represented in different renderings. (Novice)

AR2.03 Students will identify the best rendering for a specific purpose. (Novice, Amateur)

AR2.04 Students identify the limitations in various renderings of molecular structures.

(Amateur)

AR2.05 Students understand the level of detail of different molecular representations. (Novice, Amateur, Expert)

AR2.06 Students transition comfortably between equivalent 2D and 3D renderings of biomolecules. (Novice, Amateur, Expert)

AR2.07 Students can interpret the meaning of color in context. (Novice)

Construction and Annotation (CA) - Ability to build macromolecular models, either physical or computerized, and, where possible, add commentary, either written or verbal, to tell a molecular story.

CA1. Students can compose information-rich renderings of macromolecule-ligand interactions.

CA1.01 Students will construct a model of a protein with a ligand. (Novice)

CA1.02 Students will construct a model of a protein with a ligand and identify the types of molecular interactions. (Amateur)

CA1.03 Students will construct a model of a protein with a ligand and assess the importance of molecular interactions. (Expert)

CA1.04 Students will identify major and minor groove of DNA and describe whether protein interactions within the grooves are more likely to be sequence specific or not. (Novice, Amateur, Expert)

CA1.05 Students will identify protein and nucleic acid components of the ribosome. (Novice, Amateur, Expert)

CA2. Students can predict the cellular location/function of a protein based on position of hydrophobic and polar residues.

CA2.01 Students can design a rendering that conveys the cellular location or function of a macromolecule based on position of hydrophobic and polar functional groups. (Amateur)

CA2.02 Students will explore protein images with colored hydrophobic/polar residues to determine whether they fold with a hydrophobic core. (Novice)

CA2.03 Students will create images to display hydrophobic/polar residues and propose a role for the protein and/or how it interactions with its environment - and that the predictions would be plausible based on the protein. (Amateur)

CA2.04 Students will make accurate predictions of the location/function of the protein that incorporates additional protein features, such as transmembrane helices, apparent docking surfaces, etc. (Expert)

Hetero Group Recognition (HG) - Metals and metal clusters, posttranslational additions such as glycosylation, phosphorylation, lipid attachment, etc.

HG1. Students can identify heterogeneous groups within a rendered structure.

HG1.01 Students can use the annotation associated with a pdb file to identify and locate heterogeneous groups in a given biomolecule. (Amateur)

HG1.02 Students can visually identify non-protein chemical components in a given rendered structure. (Amateur)

HG1.03 Students can distinguish between nucleic acid and ligands (e.g. metal ions) in a given nucleic acid superstructure. (Amateur)

HG1.04 Students can explain how a heterogeneous group in a given rendered structure associates with the biomolecule (i.e., covalent interaction with residue X). (Amateur)

HG1.05 Students can explain and demonstrate how heterogeneous groups are identified in unannotated structures. (Expert)

HG2. Students can describe the impact of a heterogeneous group on the structure/function of a macromolecule.

HG2.01 Students can look at a given rendered structure and describe how the presence of a specific heterogeneous group alters the structure of that biomolecule. (Amateur)

HG2.02 Students can explain how the removal of a particular heterogeneous group would alter the structure of a given biomolecule. (Expert)

HG2.03 Students can explain how a specified heterogeneous group contributes to the function of a given protein. (Amateur)

HG2.04 Students can predict how heterogeneous groups contribute to the function of a protein for which the structure has been newly solved. (Expert)

Macromolecular Assemblies (MA) - Polypeptides, oligosaccharides, and nucleic acid and lipid superstructures.

MA1. Students can describe various macromolecular assemblies.

MA1.01 Students can identify individual structures in a macromolecular assembly. (Novice, Amateur, Expert)

MA1.02 Students can describe functions of individual structures within a macromolecular assembly. (Novice, Amateur, Expert)

MA1.03 Students recognize the various lipid ultrastructures (micelles, bicelles, vesicles, and lipid bilayers) in a 3D structure. (Novice)

MA2. Students can compose information-rich renderings of macromolecular assemblies.

MA2.01 Students can render a macromolecular assembly to highlight individual structures. (Amateur)

MA2.02 Students can render a macromolecular assembly to illustrate structural features. (Amateur, Expert)

Molecular Dynamics (MD) - Animated motion simulating conformational changes involved in ligand binding or catalysis, or other molecular motion/dynamics.

MD1. Students can describe the impact of the dynamic motion of a biomolecule on its function.

MD1.01 Students will recognize that biological molecules have different conformations. (Novice, Amateur)

MD1.02 Students will correlate molecular movement with function. (Novice, Amateur, Expert)

MD2. Students can predict limits to macromolecular movement.

MD2.01 Students will locate potential regions of flexibility and inflexibility in the structure of a biomolecule. (Novice, Amateur)

MD2.02 Students will recognize acceptable/unacceptable movement within a macromolecule by determining whether the movement is within allowable bond angles. (Expert)

MD2.03 Students will recognize acceptable/unacceptable movement within a macromolecule by determining whether the movement results in steric hindrance. (Amateur)

MD2.04 Students will recognize acceptable/unacceptable movement within a macromolecule by considering the atomic packing constraints. (Expert)

Molecular Interactions (MI) - Covalent and noncovalent bonding governing ligand binding and subunit-subunit interactions.

MI1. Students can predict the existence of an interaction using structural information (e.g. bond lengths).

MI1.01 Students can distinguish between covalent and noncovalent interactions. (Novice)

MI1.02 Students can identify the different non-covalent interactions given a 3D structure. (Amateur)

MI1.03 Students can predict whether a functional group (region) would be a hydrogen bond donor or acceptor. (Amateur)

MI1.04 Students can render the 3D structure of a biomolecule so as to explain the electronic origin of the different non-covalent interactions. (Amateur)

MI1.05 As it relates to a particular rendered structure, students can rank the relative strengths of covalent and noncovalent interactions. (Amateur)

MI2.Students can evaluate the effect of the local environment on various molecular interactions.

MI2.01 Students identify regions of a biomolecule that are exposed to or shielded from solvent. (Novice)

MI2.02 Students can identify other molecules in the local environment (e.g. solvent, salt ions, metals, detergents, other small molecules) that impact a molecular interaction of interest. (Novice)

MI2.03 Students can predict the impact of other molecules in the local environment (e.g. solvent, salt ions, metals, detergents, other small molecules) on a molecular interaction of interest. (Amateur)

MI2.04 Students predict the pKa of an ionizable group based on the influence of its local three-dimensional environment. (Amateur)

MI2.05 Students can propose a change to the local environment that would yield a desired change in a molecular interaction. (Expert)

MI2.06 Using molecular visualization tools, students can determine which intermolecular force is most critical to stabilizing a given interaction. (Expert)

Monomer Recognition (MR) - Recognition of both native and modified amino acids, nucleotides, sugars, and other biomonomer units. Understanding of their physical and chemical properties, particularly regarding functional groups.

MR1. Students can identify the monomer units of biological polymers.

MR1.01 Given a rendered structure of a biological polymer students will be able to identify the ends of a biological polymer. (Novice, Amateur, Expert)

MR1.02 Given a rendered structure, students will be able to divide the polymer into its monomer units. (Novice)

MR1.03 Given a rendered structure, students will be able to identify the monomer units. (Novice)

MR2. Students can describe the contributions different monomers make in determining the 3-D shape of the polymer.

MR2.01 Students can describe the physical properties of a monomer in a rendered structure of a polymer. (Amateur)

MR2.02 Students will describe the significance of the location of monomer units within the 3D structure of a polymer (protein, carbohydrate or nucleic acid). (Novice, Amateur, Expert)

MR2.03 Students can identify a monomer in a visualized structure that will interact with the surrounding environment (solvent and other monomers). (Amateur)

MR2.04 Using a visualized structure, students will identify stereochemical differences in carbohydrate structures. (Amateur)

MR2.05 Using a visualized structure student will be able to modify a monomer to design it to have particular physical properties. (Expert)

Symmetry/Asymmetry Recognition (SA) - Recognition of symmetry elements within both single chain and oligomeric macromolecules.

SA1. Students can identify symmetric or asymmetric features in rendered molecules.

SA1.01 Students can identify symmetric features in a rendered molecule (shown in fixed orientation). (Novice)

SA1.02 Students can rotate a given, rendered molecule and identify axes of symmetry. (Amateur)

SA1.03 Students will identify symmetric and asymmetric features in rendered molecules after coloring a given rendered molecule to reveal structural features (charge, hydrophobicity, etc.) (Amateur)

SA2. Students can hypothesize the functional significance of symmetry or asymmetry in rendered molecules.

SA2.01 Students will explain functional significance of symmetry (or asymmetry) in a given rendered molecule. (Novice, Amateur, Expert)

SA2.02 Students will predict functional significance of symmetry (or asymmetry) in a given rendered molecule. (Amateur, Expert)

Structure-Function Relationship (SF) - Active/binding sites, microenvironments, nucleophiles, redox centers, etc.

SF1. Students can evaluate biomolecular interaction sites using molecular visualization tools.

SF1.01 Students can distinguish protein, cofactors and small molecule ligands or substrates. (Novice)

SF1.02 Students will recognize that the size and shape of the ligand must match the size and shape of the binding site. (Novice, Amateur)

SF1.03 Students will recognize that the polarity of a surface complements that of the ligand or substrate. (Novice, Amateur)

SF1.04 Students will recognize that the hydrophobicity of a surface complements that of the ligand or substrate. (Novice)

SF1.05 Students will recognize that the electrostatic potential of a surface can guide or direct the binding of a ligand or substrate. (Amateur)

SF1.06 Students will use docking software to predict how the surface properties of a macromolecule guides and allows the binding of a ligand or substrate. (Amateur)

SF2. Students can predict the function of biomolecules using molecular visualization tools.

SF2.01 Students can recognize structurally related molecules. (Novice)

SF2.02 Students can align structurally related molecules. (Novice, Amateur)

SF2.03 Students will use molecular visualization software to identify functionally relevant features of a macromolecule. (Amateur)

SF2.04 Using molecular visualization software, students will propose changes that would test potential interactions within a structure. (Amateur)

SF2.05 Students can produce a model of a biomolecule based on a known structure of a related biomolecule. (Amateur, Expert)

Structural Model Skepticism (SK) - Recognition of the limitations of models to describe the structure of macromolecules.

SK1. Students can critique the limitations of a structural model of a macromolecule.

SK1.01 Students can explain that the pdb file is a model based on data and that, as a model, it has limitations. (Novice, Amateur)

SK1.02 Students associate resolution with reliability of atom positions. (Amateur)

SK1.03 Students can identify monomeric units (for example, amino acid sidechains) whose orientation in a biopolymer is uncertain. (Expert)

SK1.04 Students can evaluate the flexibility/disorder of various regions of a macromolecular structure. (Novice, Amateur, Expert)

SK1.05 Students can reconcile inconsistent numbering of monomers among species and structure files. (Novice)

SK1.06 Students can utilize a Ramachandran plot to interpret the validity of a structure. (Amateur)

SK1.07 Students can describe the limitations of a macromolecule-ligand docking simulation. (Expert)

SK2. Students can evaluate the quality of 3D models including features that are open to alternate interpretations based on molecular visualization and PDB flat files.

SK2.01 Students will evaluate a crystal structure for crystal packing effects. (Novice, Amateur, Expert)

SK2.02 Students can resolve differences between the asymmetric unit and the functional biological assembly. (Expert)

SK2.03 Students can identify molecules present in a crystal structure that may not be associated with function. (Novice, Amateur, Expert)

SK3. Students can discuss the value of altering a structure to elucidate function.

SK3.01 Students will identify non-native structural features. (Amateur)

SK3.02 Students will propose structural modifications to facilitate structure determination. (Amateur, Expert)

SK3.03 Students will propose a purpose for the introduction of non-native structural features. (Amateur, Expert)

Topology and Connectivity (TC) - Following the chain direction through the molecule, translating between 2D topology mapping and 3D rendering.

TC1. Students can describe the linkages between building blocks within a macromolecule.

TC1.01 Students can trace the backbone of a macromolecule in three dimensions. (Novice, Amateur)

TC1.02 Students use appropriate terms to describe the linkages/bonds/interactions that join monomeric units together in a macromolecule or macromolecular assembly. (Novice, Amateur)

TC1.03 Given a virtual model of monomeric units, students will predict the types of linkages/bonds/interactions that are possible or favorable. (Amateur)

TC2. Students can describe the overall shape and common motifs within a 3D macromolecular structure.

TC2.01 Using molecular visualization software, students can describe the three-dimensional structure of a macromolecule, including overall shape and common structural motifs. (Novice, Amateur, Expert)

TC2.02 Students can identify common domains/motifs within a macromolecule. (Amateur, Expert)

TC2.03 Students can identify connectivity features between domains or subunits in a macromolecular structure. (Amateur)

TC2.04 Students can identify interactions between domains or subunits in a macromolecular structure. (Amateur, Expert)

TC2.05 Students can describe how domains/motifs in a macromolecule work together to achieve a concerted function in the cell. (Amateur, Expert)

TC2.06 Students can parse a tertiary structure into a series of secondary structures and the ways in which they are connected from a three-dimensional structure. (Novice, Amateur, Expert)

TC3. Students can explain how any given biomolecular interaction site can be made by a variety of topologies.

TC3.01 Students recognize that the groups that comprise a functional site only require proper arrangement in three-dimensional space rather than a particular order or position in the linear sequence. (Amateur)

TC3.02 Students recognize similarities and differences in two similar - but not identical - three dimensional structures. (Amateur)

TC3.03 Students describe dissimilar portions of homologous proteins as arising from genetic insertions/deletions/rearrangements. (Amateur)