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2017 Summer School

Topic: How to Add a New Collective Variable (CV) Presenter: Michael A. Webb, University of Chicago



How to Add a new CV...

Collective variables (CVs) are system descriptors with reduced complexity compared to the full phase space. They are functions of many variables that are useful as biasing coordinates and macro-state analysis.

Many CVs already included in SSAGES

Angles

- Particle Separation
- Box Volume
- Torsions •
- Gyration Tensor •
- Particle Coordinate Rouse Modes
- Secondary Structure

SSAGES makes it very easy to add new CVs to accomplish your research goals

- *modular (minimal tinkering with code)*
- straightforward (organized structure)
- efficient (many existing tools)

What you need:

- *literacy and generic programming*
- basics of C++ syntax
- some familiarity with MPI

...but current research often dictates specific use cases/analysis \rightarrow more complex CVs not presently featured

Next 20-25 minutes:





Basic Overview



A new CV can be added by creating a new class that derives from the CollectiveVariable base class in SSAGES

This only requires the addition/modification of 3 files!

From within the SSAGES directory:	webbm@midway-lo uild MakeLists.txt	ogin2 SSAG doc Examples	ES]\$ ls hooks include	LICENSE.txt README.md	schema src	test Tools
./src/CVs/CollectiveVariables.cpp Only need to add 2 lines here to handle "building" of your CV						
 ./src/CVs/CoolThingCV.h (new) The bulk of your effort and coding goes here to edit/add member functions (straightforward to just copy format of existing files) 						
CoolThingC		ize(),	Evaluate	(), Buil	d(),	
constructor	checks nece variable	ssary co s val	omputes your ue (and gradi	CV builds your ient!) from	r CV object JSON	
./schema/CVs/coolthing.cv.json (new) Sets expectations for JSON fields that must be defined for the CV class						



Basic Overview



A new CV can be added by creating a new class that derives from the CollectiveVariable base class in SSAGES

Step 1. Formulate the CV Step 2. Begin writing CoolThingCV.h Step 3. Craft your JSON schema

Step 4. *Finish writing* CoolThingCV.h **Step 5**. *Make it buildable*

./src/CVs/CollectiveVariables.cpp

Only need to add 2 lines here to handle "building" of your CV

./src/CVs/CoolThingCV.h (new)

The bulk of your effort and coding goes here to edit/add member functions (straightforward to just copy format of existing files)

CoolThingCV(),Initialize(),Evaluate(),Build(),constructorchecks necessary
variablescomputes your CVbuilds your CV object
from JSON

./schema/CVs/coolthing.cv.json (new)

Sets expectations for JSON fields that must be defined for the CV class



Example: Polymer Rouse modes

The Rouse modes of a polymer are CVs that involve the coordinates of all "beads" in the polymer; they ...

- represent the normal-mode coordinates for a Gaussian chain
- describe dynamics/relaxation over different lengthscales
 - p=0 describes the chain center-of-mass
 - p>0 describes sub-chains of (N-I)/p beads
- characterize chain conformations at those lengthscales

$$\mathbf{X}_{p} = \sqrt{\frac{c_{p}}{N}} \sum_{i=1}^{N} \mathbf{R}_{i} \cos\left[\frac{p\pi}{N}\left(i - \frac{1}{2}\right)\right] \begin{array}{l} p = 0, \dots, N-1 \\ c_{p} = \begin{cases} 1, & \text{if } p = 0 \\ 2, & \text{otherwise} \end{cases}$$



- \mathbf{R}_i Cartesian vector coordinate of the *i*th bead in the polymer chain
- N Number of beads comprising the polymer chain
- P Rouse mode index
- X_p Vector coordinate of the *p*th Rouse mode



Step 1. Formulate the CV

What are the probable use cases?

Atomistic or coarse-grained polymer/macromolecule simulations Different modes and discretization levels

How will it be calculated? (must be a scalar)

We will compute the CV as the Euclidean norm of the Rouse mode coordinate: $CV = \sqrt{X_p \cdot X_p}$

Bead coordinates will be the center-of-mass of a group of particles: $\mathbf{R}_{i} = \frac{1}{M_{i}} \sum_{j \in \mathbb{G}_{i}} m_{j} \mathbf{r}_{j} \qquad \mathbb{G}_{i} = \{ \mathrm{id}_{1}, \mathrm{id}_{2}, \cdots, \mathrm{id}_{N_{i}} \}$

How will the gradient (for particle positions) be calculated?

By chain rule, the gradient with respect to the position of the jth particle:

$$\nabla_{\mathbf{r}_{j}} \mathsf{CV} = \frac{\mathrm{X}_{p}}{\mathrm{CV}} \sqrt{\frac{c_{p}}{N}} \sum_{i=1}^{N} \cos\left[\frac{p\pi}{N}\left(i-\frac{1}{2}\right)\right] \frac{m_{j}}{M_{i}} \underline{\delta_{j}(\mathbb{G}_{i})}$$

What information will be needed?

- mode index
 number of "beads"
- Particle positions/masses → bead position/mass
- atom indices comprising the particle groups

Note: You can assume that all typical simulation info (particle positions, velocities, masses, etc.) is exposed within SSAGES through "Snapshot" (more on this later)





I if *j* is in the group 0 otherwise



Base Class Snippet:



#praqma once ./src/CVs/MockCV.h #include "CollectiveVariable.h" #include <array> #include <cmath> namespace SSAGES //! Mock collective variable for testing purposes. class MockCV : public CollectiveVariable private: brivate variable //! User defined gradient vector. Vector3 usergrad_; & function space public: 1/1 public variable & /*1 * \param value Value the Mock CV will ret function space * \param grad Gradient vector the Mock CV * \param upper Value for the upper bound param lower Value for the lower bound of the CV. nstruct a mock CV MockCV(double value, const Vector3& grad, double upper, double lower) usergrad (grad) I. the constructor-called val = value; bounds_ = {{upper, lower}}; when the CV is setup //! Initialize necessary variables. /*! * \param snapshot Current simulation snapshot. */ void Initialize(const Snapshot& snapshot) override // Initialize gradient 2. Initialize() – called at auto n = snapshot.GetPosition grad .resize(n, usergrad); beginning of simulation //! Evaluate the CV. /*1 * \param snapshot Current simulation snapshot. */ void Evaluate(const Snapshot& snapshot) override 3. Evaluate() - called at every simulation timestep };

To write CoolThingCV.h, we need to craft *four* main member functions; we will start with the first *three*

In Evaluate(), we need to compute
val_ and grad_; everything else is
 mostly bookkeeping

My suggested workflow:

- a. Shamelessly copy the code for an existing CV with similar features
- Make all your private variable declarations (that you can initially think of)
- c. Write the constructor
- d. Write Initialize()
- e. Write Evaluate()
- f. Patch up needed variables/functions

g. Write Build()



For RouseModeCV.h, we'll start with looking at ParticleSeparationCV.h

```
#pragma once
                                                                ParticleSeparationCV.h
#include "CollectiveVariable.h"
#include "Validator/ObjectRequirement.h"
#include "Drivers/DriverException.h"
                                               We will basically keep all
#include "Snapshot.h"
                                                this stuff to begin with
#include "schema.h"
#include <numeric>
namespace SSAGES
   //! Collective variable on the distance between two particles' centers of mass.
This structure is good, we just
       Collective variable on two particle positions. This CV will r
                                                                      need to change the variable
       distance between two specific atom groups of the simulation.
                                                                            names/comments
       \ingroup CVs
     */
   class ParticleSeparationCV : public CollectiveVariable, public Buildable<ParticleSeparationCV>
    private:
                                                           This CV uses a group, we can make this
       Label group1_; //!< Atom ID's of group 1.
       Label group2 ; //!< Atom ID's of group 2.
                                                           a vector instead for our specific case. A
       //! Each dimension determines if it is applied by the few more variables will be needed...
       Bool3 dim_;
    public:
        //! Constructor
                                                                            Two constructors are
       ParticleSeparationCV(const Label& group1, const Label& group2) :
       group1 (group1), group2 (group2), dim {true, true, true}
                                                                            shown here: we'll stick
        1
                                                                                   with one
        //! Constructor
       ParticleSeparationCV(const Label& group1, const Label& group2, bool fixx, bool fixy, bool fixz) :
       group1_(group1), group2_(group2), dim_{fixx, fixy, fixz}
        1
```





passed to the constructor here

RouseModeCV(const std::vector<Label>& groups, int p) :

groups_(groups), p_(p), N_(groups_.size())

{ massg .resize(groups .size(),0.0); }

c. Write the constructor

namespace SSAGES

\ingroup CVs

Bool3 dim ;

/*1

*/

private:

public:

 $\{\}$

{}

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```
//! Initialize necessary variables.
void Initialize(const Snapshot& snapshot) override
                                                              This looks good
   using std::to string;
                                                                                                      d. Write Initialize()
   auto n1 = group1_.size(), n2 = group2_.size();
                                                               We should add
   // Make sure atom ID's are on at least one processor
                                                               checks on the
   std::vector<int> found1(n1, 0), found2(n2, 0);
   for(size_t i = 0; i < n1; ++i)</pre>
                                                                mode index
                                                                                                       Initialization appears to mostly be
       if(snapshot.GetLocalIndex(group1_[i]) != -1)
          found1[i] = 1;
                                                                                                        checking for consistency between
                                                       This checks groups I and 2;
                                                        we should change to check
   for(size_t i = 0; i < n2; ++i)</pre>
                                                                                                           variables from simulation and
                                                            the vector of groups
       if(snapshot.GetLocalIndex(group2_[i]) != -1)
                                                                                                              user-supplied parameters
           found2[i] = 1;
   MPI_Allreduce(MPI_IN_PLACE, found1.data(), n1, MPI_INT, MPI_SUM, snapshot.GetCommunic
                                                                                   \delta r():
   MPI Allreduce(MPI IN PLACE, found2.data(), n2, MPI INT, MPI SUM, snapshot.GetCommunicator());
   unsigned ntot1 = std::accumulate(found1.begin(), found1.end(), 0, std::plus<int> //! Initialize necessa
                                                                                                       ariables.
                                                                                                                                                 RouseModeCV.h
   unsigned ntot2 = std::accumulate(found2.begin(), found2.end(), 0, std::plus<int>
   if(ntot1 != n1)
                                                                               * \param snapshot Curr
                                                                                                      simulation snapshot.
       throw BuildException({
           "ParticleSeparationCV: Expected to find " +
                                                                              void Initialize(const Snapshot& snapshot) override
          to_string(n1) +
          " atoms in particle 1, but only found " +
                                                                                 using std::to string;
          to string(ntot1) + ".
       });
                                                                                 // Check for valid p
                                                                                 if (p > groups .size())
   if(ntot2 != n2)
                                                                                     throw std::invalid argument(
       throw BuildException({
                                                                                         "RouseModeCV: Expected to find p to be less than " +
           "ParticleSeparationCV: Expected to find " +
                                                                                         to string(groups .size()) +" but found p = " +
          to string(n2) +
           " atoms in particle 2, but only found " +
                                                                                         to string(p )
          to string(ntot2) + ".
                                                                                     );
       });
                                                                                 // Check for valid groups
                              ParticleSeparationCV.h
                                                                                 for (size_t j = 0; j < groups_.size(); ++j) {</pre>
                                                                                     auto nj = groups [j].size();
                                                                                     // Make sure atom IDs in the group are somewhere
                                                                                     std::vector<int> found(nj,0);
                                                                                     for (size_t i = 0; i <nj; ++i) {</pre>
                                                                                         if(snapshot.GetLocalIndex(groups_[j][i]) != -1)
                                                                                             found[i] = 1;
                  We should set up the
                                                                                     MPI Allreduce(MPI IN PLACE, found.data(), nj, MPI INT, MPI SUM, snapshot.GetCommunicator());
                                                                                     unsigned njtot = std::accumulate(found.begin(), found.end(), 0, std::plus<int>());
                  same, tailored for the
                                                                                     if(njtot != nj)
                                                                                         throw std::invalid_argument(
                        RouseModeCV
                                                                                             "RouseModeCV: Expected to find " +
                                                                                             to string(nj) +
                                                                                             " atoms in group " + to_string(j) +", but only found " +
                                                                                             to string(njtot) + "."
                                                                                         );
                                                                                                                                          We'll add a placeholder for
                                                                                 // Set the masses of each particle group in massg
                                                                                                                                      initializing the masses of the groups
                                                                                 this->setMasses( groups_, snapshot);
```



```
void Evaluate(const Snapshot& snapshot) override
                      e. Write Evaluate()
                                                                                               // Get data from snapshot.
                                                                                               auto
                                                                                                           ntot = snapshot.GetNumAtoms(); // total number of atoms
                                                                                               const auto& masses = snapshot.GetMasses(); // mass of each atom
       Available information in Evaluate() is
                                                                                               // Initialize working variables
                                                                                               double ppi n = p * M PI / N; // constant
   determined during construction/initialization
                                                                                               xp_.fill(0.0);
                                                                                                                 // vectorial Rouse mode
                                                                                               r .resize(N );
                                                                                                                 // position vector for beads in Rouse chain (unwrapped)
                or provided through snapshot
                                                                                               grad .resize(ntot, Vector3{0,0,0}); // gradient set to 0.0 for all atoms
                                                                                               std::fill(grad .begin(), grad .end(), Vector3{0,0,0});
void Evaluate(const Snapshot& snapshot) override
                                                                                               // Iterate over all N_ atom groups and compute the center of mass for each
                                                                                                                    rcom; // vector of COM positions
                                                                                               std::vector<Vector3>
   // Get local atom indices.
                                                                                               for (size_t i = 0; i < N_; ++i) {</pre>
   std::vector<int> idx1, idx2;
                                             √indices for a
                                                                                                  Label idi; // list of indices
   snapshot.GetLocalIndices(group1_, &idx1);
                                                                                                   snapshot.GetLocalIndices(groups_[i], &idi);
   snapshot.GetLocalIndices(group2 , &idx2);
                                                                                                  rcom.push_back(snapshot.CenterOfMass(idi,massg_[i])); // center of mass for group
                                             group of particles
   // Get data from snapshot.
   auto n = snapshot.GetNumAtoms();
                                                                                               // Now compute differences vectors between the neighboring beads
                                           ✓ masses for particles
   const auto& masses = snapshot.GetMasses();
                                                                                               // accumulate displacements to reconstruct unwrapped polymer chain
                                                                                               // for simplicity, we consider the first bead to be the reference position
    // Initialize gradient.
                                                                                               // in all snapshots
    std::fill(grad_.begin(), grad_.end(), Vector3{0,0,0});
                                                                                               r[0] = rcom[0];
   grad_.resize(n, Vector3{0,0,0});
                                                                                               for (size_t i = 1; i< N_; ++i) {</pre>
   boxgrad = Matrix3::Zero();
                                                                                                   Vector3 dri = snapshot.ApplyMinimumImage(rcom[i] - rcom[i-1]);
                                                                                                  r[i] = r[i-1] + dri; // ri = r\{i-1\} + (ri - r\{i-1\})
    // Get centers of mass.
   auto mtot1 = snapshot.TotalMass(idx1); 

   auto mtot2 = snapshot.TotalMass(idx2);
                                                                                               // Determine the value of the Rouse coordinate
   Vector3 com1 = snapshot.CenterOfMass(idx1, mtot1);
                                                     ✓ center-of-mass
                                                                                               // Xp(t) = 1/sqrt(N) * sum {i=1}^{N} ri, p = 0
   Vector3 com2 = snapshot.CenterOfMass(idx2, mtot2);
                                                                                               // Xp(t) = sqrt(2/N) * sum_{i=1}^{N} ri * cos[p*pi/N*(i-0.5)], p = 1,...,N-1
                                                                                               // Note: this solution is valid for homogeneous friction
                                                                                               xp .fill(0.0);
    // Account for pbc.
                                                                                                tor (size_t i = 0; i<N_; ++i) {</pre>
   Vector3 rij = snapshot.ApplyMinimumImage(com1 - com2).cwiseProduct(dim_.
                                                                             uble>())
                                                                                                  xp_ += r_[i]*cos ( ppi_n * (i+0.5) );
                                                     ✓MIC
       compute gradient.
        ij.norm(); / vector norm
                                                                                               xp_ /= sqrt(N_);
   val
                                                                                               if ( p_ != 0 ) xp_ *= sqrt(2.0) ;
    for(auto& id : idx1)
                                                                                               // Compute Rouse vector norm as the CV
                                                                                                    = sqrt(Xp*Xp), Xp = (Xp1, Xp2, Xp3)
       grad [id] = rij/val *masses[id]/mtot1;
                                                                                              val
                                                                                                     xp .norm();
       boxgrad += grad [id]*rij.transpose();
                                                                                               // Now perform gradient operation
                                                                                               // dCV/dxjd = (Xpd/CV)*(c/N)**0.5*sum i=1^N cos[p*pi(i-0.5)/N] mj/Mi *delta j({i})
    for(auto& id : idx2)
                                                                                               // delta_j({i}) = 1, if j in {i}, 0 otherwise
       (grad_[id) = -rij/val_*masses[id]/mtot2;
                                                                                               Vector3 gradpcon = xp_ / sqrt(N_) / val_;
                                       ParticleSeparationCV.h
                                                                                               if ( p_ != 0) gradpcon *= sqrt(2.0);
                                                                                                                                       // (Xpd/CV)*(c/N)**0.5
                                                                                               for (size_t i = 0; i < N_; ++i) {</pre>
                                                                                                  Label idi; // list of indices
                                                                                                  snapshot.GetLocalIndices(groups_[i], &idi);
 Note: Most of Evaluate() changes, BUT you can
                                                                                                  // go over each atom in the group and add to its gradient
                                                                                                  // Note: performance tradeoff here. All gradient elements have a common factor of
 learn a lot about the SSAGES snapshot functionality by
                                                                                                  // Xpd/CV*sqrt(c/N) = prefactor, with c = 2 if p != 0
                                                                                                  // this could be factored out, but if ntot >> number of atoms in groups
 looking at the various .h files. Otherwise, take a look
                                                                                                  // then it won't be worth it to post multiply all gradient terms...
                                                                                                  // Could also go over loop again after to do the multiplication, but
                                                                                                  // that is troublesome if atom ids appear in multiple groups for some reason
 at ./src/Snapshot.h or the API reference to see
                                                                                                  double cosval = cos(ppi_n*(i+0.5)) / massg_[i]; // cos[p*pi(i-0.5)/N] / Mi
                                                                                                  for (autos id : idi) {
 all the member variable/functions.
                                                                                   12
                                                                                                      grad [id])+= gradpcon* cosval * masses[id];
                                                                                                                                               RouseModeCV.h
```





Step 3. Craft the JSON Schema



A file specifying the JSON schema must be created in ./schema/CVs/

This file acts as pre-filter that sets the conditions for variables in your programming environment



Step 4. Finish up CoolThingCV.h



Knowing the set up of the JSON, we need to finish up CoolThingCV.h



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Knowing the set up of the JSON, we need to finish up CoolThingCV.h



Step 5. Make it buildable

Finally, we must ensure that the CV can be built in CollectiveVariables.cpp!

```
#include "CollectiveVariable.h"
                                                            CollectiveVariable.cpp
#include "AngleCV.h"
#include "BoxVolumeCV.h"
#include "CoordinationNumberCV.h"
#include "GyrationTensorCV.h"
#include "ParticleCoordinateCV.h"
#include "ParticlePositionCV.h"
#include "ParticleSeparationCV.h"
#include "RouseModeCV.h"
#include "TorsionalCV.h"
#include "json/json.h"
#include <stdexcept>
namespace SSAGES
   CollectiveVariable* CollectiveVariable::BuildCV(const Json::Value &json, const std::string& path)
        // Get move type.
        auto type = json.get("type", "none").asString();
        if(type == "Angle")
            return AngleCV::Build(json, path);
        else if(type == "BoxVolume")
            return BoxVolumeCV::Build(json, path);
        else if (type == "CoordinationNumber")
            return CoordinationNumberCV::Build(json, path);
        else if(type == "GyrationTensor")
                                                              These conditional statements
            return GyrationTensorCV::Build(json, path);
        else if(type == "ParticleCoordinate")
                                                               handle the building of each
            return ParticleCoordinateCV::Build(json, path);
        else if(type == "ParticlePosition")
                                                                     CV; just add one!
            return ParticlePositionCV::Build(json, path);
        else if(type == "ParticleSeparation")
            return ParticleSeparationCV::Build(json, path);
        else if(type == "Torsional")
            return TorsionalCV::Build(json, path);
       else
            throw std::invalid argument(path + ": Unknown CV type specified.");
```

Summary

A new CV can be added by creating a new class that derives from the CollectiveVariable base class in SSAGES



Step 6. Add a unit test
-good practice & self-contained
check that all is well
-See ./test/unit_tests
for examples

Expanding on Phase I

Step I. Formulate the CV --pen and paper portion --how will it be used?/what is needed? Step 2. Begin writing CoolThingCV.h --must add a file for this! --bulk of the effort goes here --easiest to start with an existing CV Step 3. Craft your JSON schema --must add coolthing.cv.json -easy based on previous steps Step 4. Finish writing CoolThingCV.h --easy now based on Step 3 Step 5. Make it buildable -- just edit CollectiveVariable.cpp --very trivial modifications

