

How Rosetta is a cheeseburger:  
a simile, unless that's like a metaphor

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Organization exists, but I prefer questions

This may be a firehose, but at least you'll get wet

New developers to the front!

# Tutorial

- I assume:
  - You know some C++
  - You know what classes are, and inheritance
  - You've glanced at the codebase at least once
- We'll cover:
  - Conventions
  - Structure/organization
  - Major classes
- Use FloppyTail as an example

# Mini has layers

Apps (executables)

Devel (not-yet-mature code)

Protocols (large and varied)

Core:  
Minimization, Packing  
Scoring, Pose  
Kinematic  
Chemical

Basic, Numeric, Utility

External (zlib, ObjexxFCL, Boost)

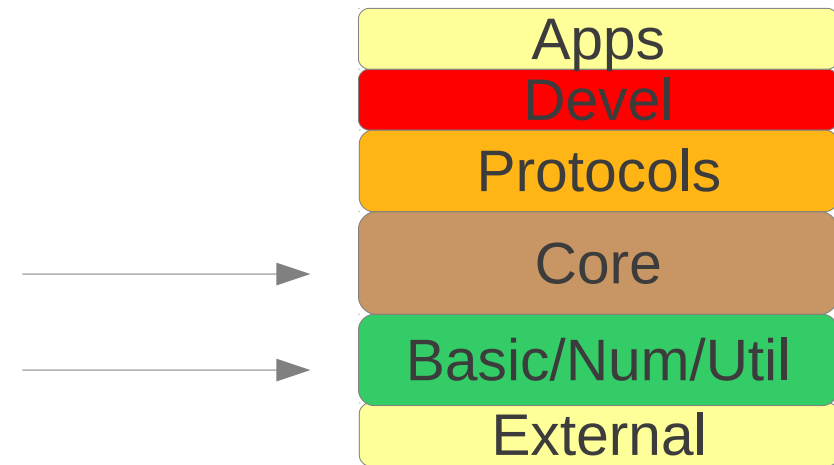
- Layers = libraries
- Organization
- Enforcement:
  - Directory structure
  - Namespacing
  - SCons building

5 patties

20 slices of cheese

# Basic conventions

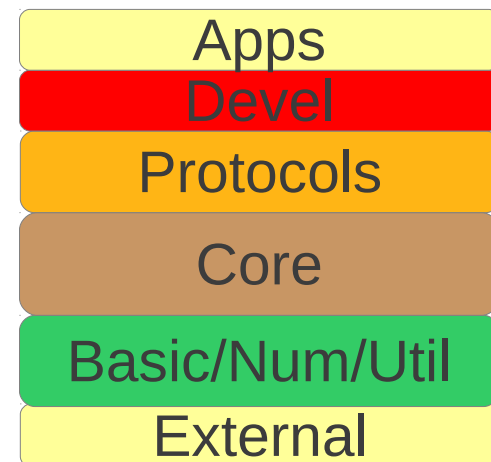
- Owning pointers
  - OP, COP
  - Inherit from `ReferenceCount`
- `vector1`
  - Index from 1, not 0
  - Bounds check `<=`
- `Core::Size (uint)`
- `Core::Real (double)`



- Tracer
  - Replaces `std::cout`
  - Labels output
  - Provides mute control

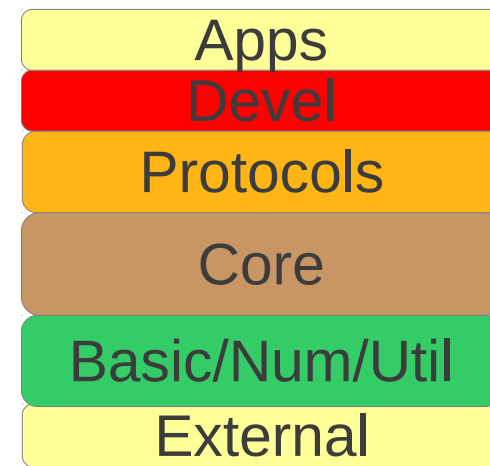


# Core::chemical classes



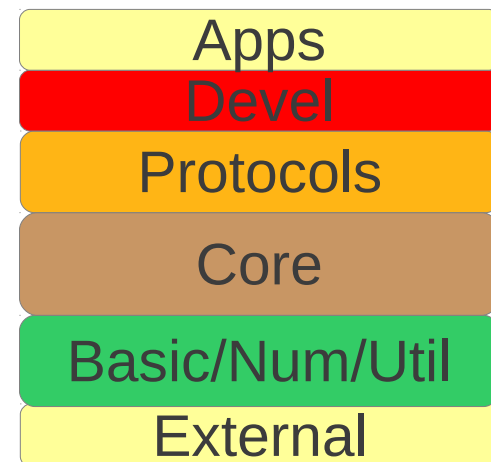
- **Abstract** representations
- `AtomType`
- `ResidueType`
  - Defines what atoms are in a residue (or ligand)
  - How they connect internally
- Variant system
  - C-terminal OXT atom
- `ResidueTypeSet`
- `ChemicalManager`
  - Singleton
  - Single read of database

# Core::kinematics classes



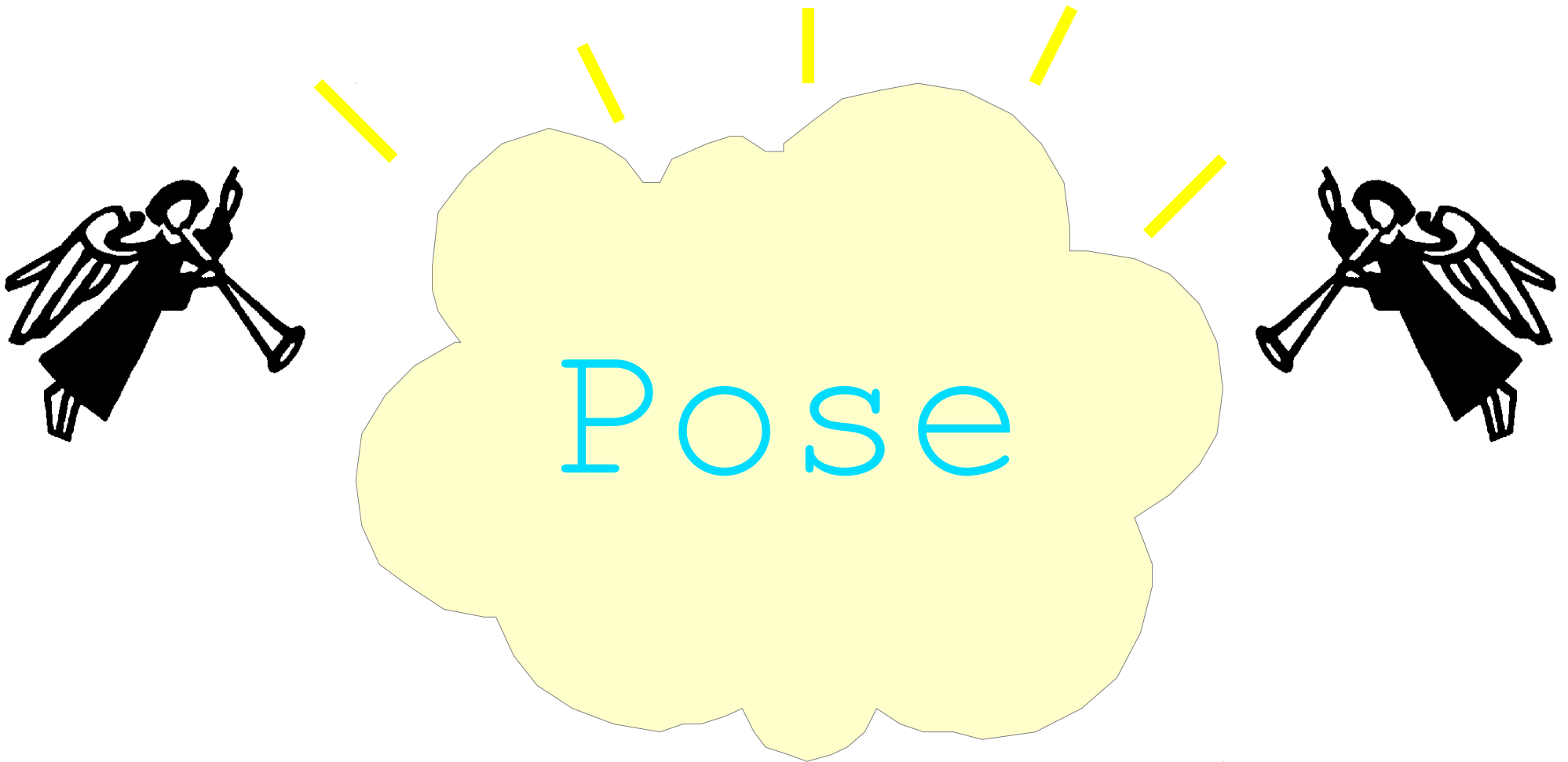
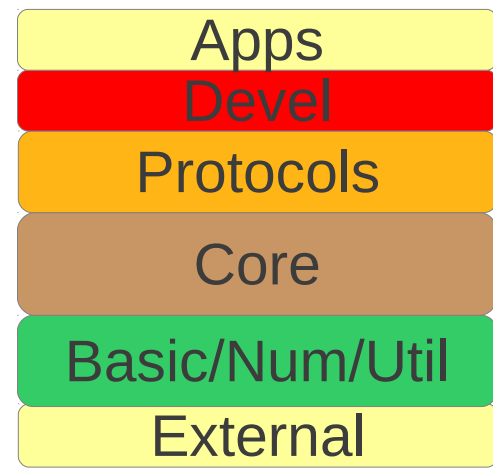
- AtomTree
  - Defines atomic connectivity
  - Internal  $\rightarrow (x, y, z)$
- FoldTree
  - Defines residue connectivity
  - Human interface
- MoveMap
  - Contains lists of mobile, immobile degrees of freedom

# Core::conformation classes

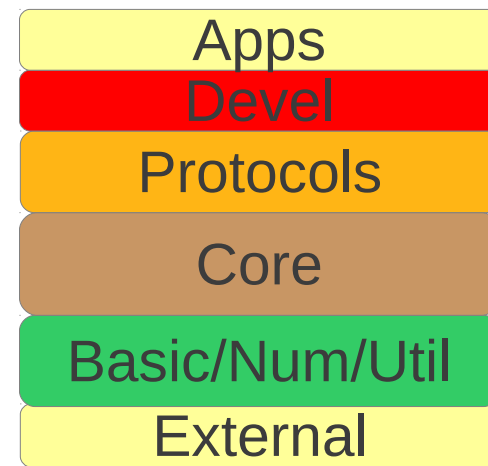


- Abstract chemical + kinematic layers
  - **Concrete**, distinct
- Atom
  - Gives an (x, y, z) to an AtomType
- Residue
  - Puts Atom objects on ResidueType skeleton
- Conformation
  - Contains Residue objects
  - Linked by kinematic layer to describe internal-coordinate folding



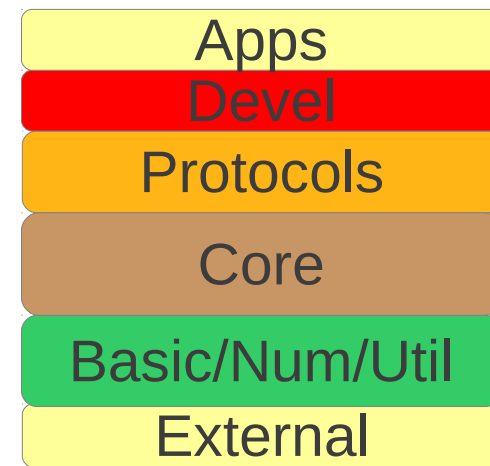


# Core::scoring classes



- `Energies`
  - Caches scores, lives in `Pose`
- `ScoreFunction`
  - Scores
  - OPs to `EnergyMethods`
- `EnergyMethod`
  - Scoring terms
  - Many & varied
- `ScoringManager`
  - Singleton!
  - Single read of database

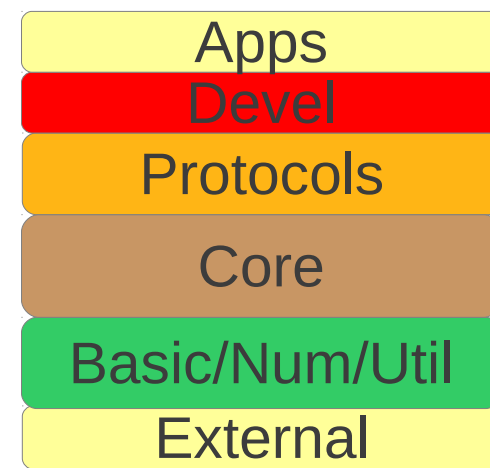
# Core::pack & ::optimization



- Guts of packing and minimization
- Very little direct use – almost all through protocols layer
- `PackerTask`
  - Set up what's allowed in packing
  - Disposable
- `TaskFactory`
  - Set up new `PackerTasks` as needed
  - uses `TaskOperations`

# Protocols layer

- `MonteCarlo`
  - Tracks trajectory
- Job distribution
  - `1UBQ_0001.pdb ...`
  - Communication layer for MPI
  - New system in Rosetta 3.1 from 3.0
- `Init`
  - Load time factory reg.

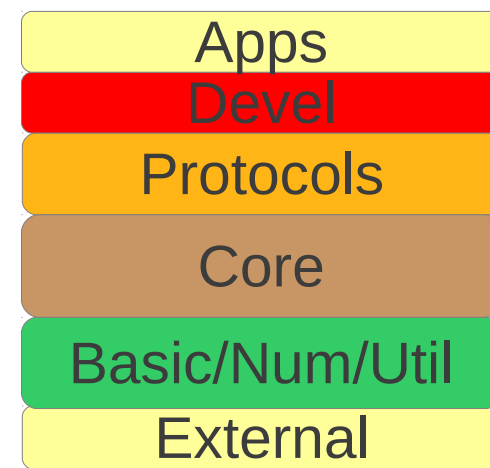


- Gobs of protocols
  - Abinitio
  - Loops
  - Relax
  - Fixbb
- `Mover...`

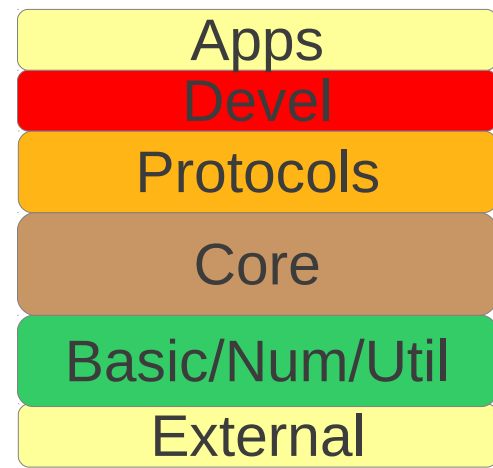
(protocols graph)

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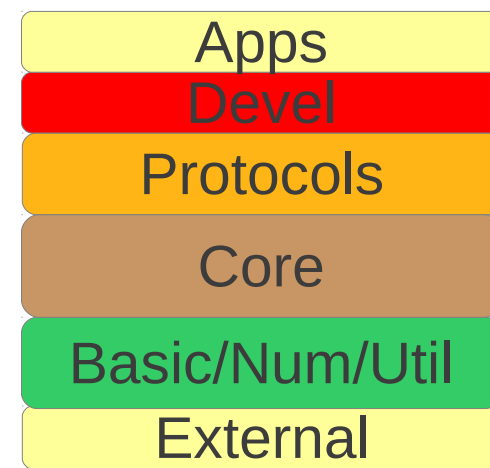


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# Movers

- Mover...
  - Beloved workhorse
  - Centralizes `Pose` alteration
  - Movers can call other movers
    - A protocol is born
  - `virtual void apply( Pose & )`

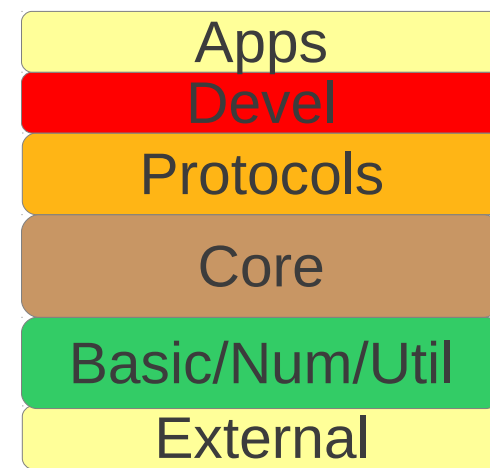


- Simple modifiers
- Empty boxes
- Not-really-a-Mover
- Whole protocols



# Simple Movers

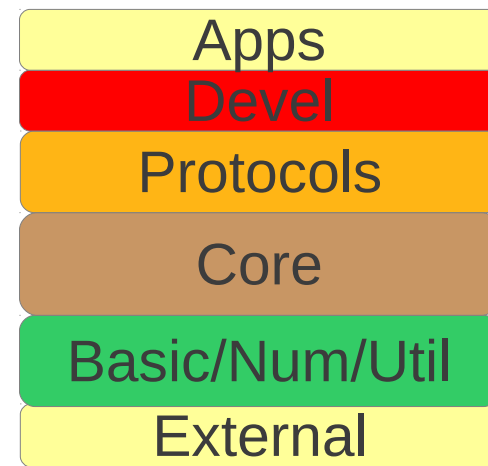
- Traditional R++ functions
- Packing
  - PackRotamersMover
  - RotamerTrialsMover



- Backbone movement
  - SmallMover
  - ShearMover
  - Fragment movers
- Minimization
  - MinMover

# Other Movers

- Whole protocols
  - Job distributor runs a `MoverOP`
  - Allows your protocol to call others
  - Pushes complexity out of Apps layer, into Protocols (reuse)



# Upper layers

- Devel
  - Not present in public releases
  - Code under development, not for general use

- Apps
  - Not a library: just executables
  - Pilot not released (under development)
  - Public released

