# Mining Mountains of Data: Organizing All Atom Molecular Dynamics Protein Simulation Data into SQL and OLAP Cubes

Andrew M. Simms

Daggett Lab

### Overview

- Background
  - Daggett Lab
  - On-line Analysis Processing (OLAP)
- OLAP Details
- An OLAP Cube Design for Simulations
- Implementation Results
- Conclusions

Daggett Lab

### **BACKGROUND**

# Daggett Lab

- Two areas of focus
  - Disease related proteins
  - Dynameomics
- Primarily computational
- Both focus areas study protein motion

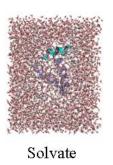
www.dynameomics.org

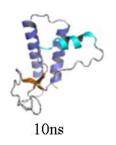


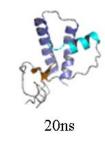
# Molecular Dynamics (MD)

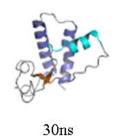
Atomic resolution structure and dynamics

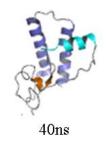














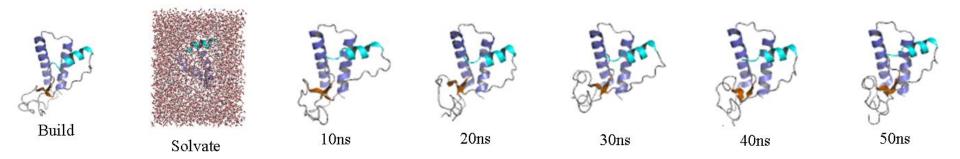






sim_id	struct_id	struct_inst	atom_number	step	x_coord	y_coord	z_coord	bin
678	122	1	1	0	-5.846	8.722	11.445	408
678	122	1	2	0	-5.989	8.026	12.191	480
678	122	1	3	0	-4.842	8.797	11.24	408
678	122	1	4	0	-6.157	9.627	11.775	480
678	122	1	5	0	-6.634	8.372	10.247	408

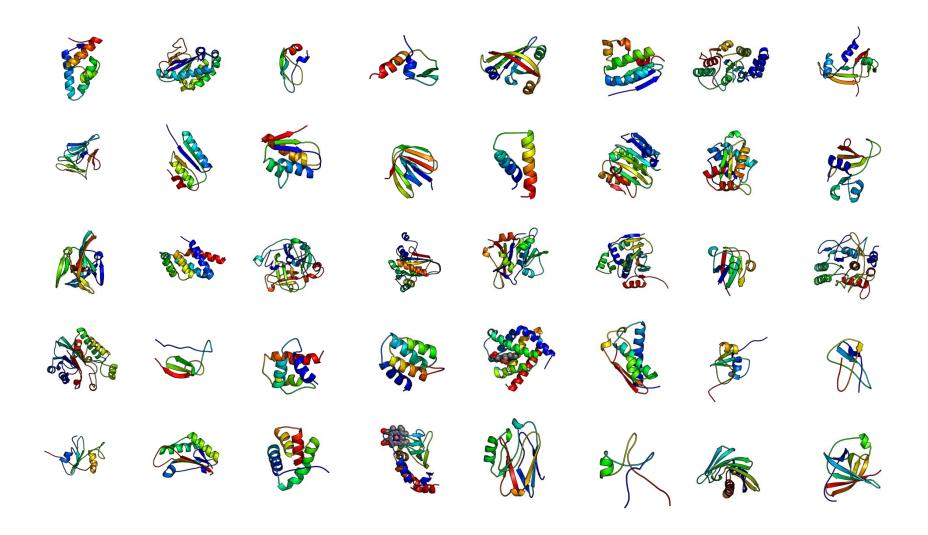
## One Simulation



### A "typical" simulation contains

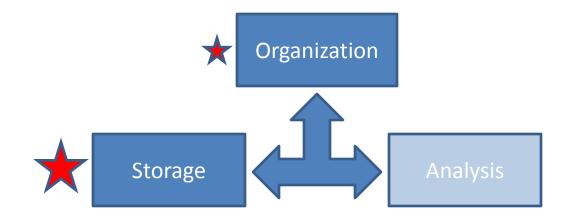
Protein Coordinates		Coordinate Table	Analysis Tables
29.3 x 10 <sup>6</sup>	$31.0 \times 10^3$	4.4GB	0.6GB

# 2,070 Targets Simulated



# Informatics Challenge (in 2007)

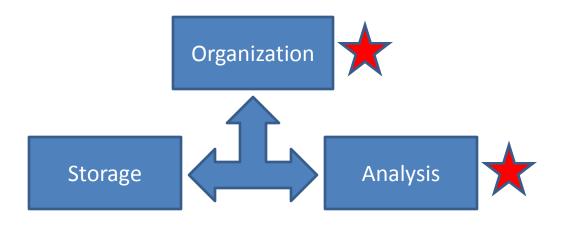
Storage and basic organization



Simulations	Targets	Time	Structures	SQL
2,300+	300+	35 μs	50,600,000	~24 TB

# Informatics Challenge Now

 The lab has run over 10,915 simulations, each containing millions to billions of protein atom coordinates and even more analyses



Simulations	Proteins	Time	Structures	Space
7,344+	1248+	186 μs	251 x 10 <sup>6</sup>	71+ TB

**BACKGROUND** 

# ONLINE ANALYSIS PROCESSING (OLAP)

## Online Analytical Processing (OLAP)

- Term coined by Ted C. F. Codd, the inventor of the relational data model
- Described as a set of principals that posit the type of database needed for transactional tasks is fundamentally different than the type of database needed for analysis

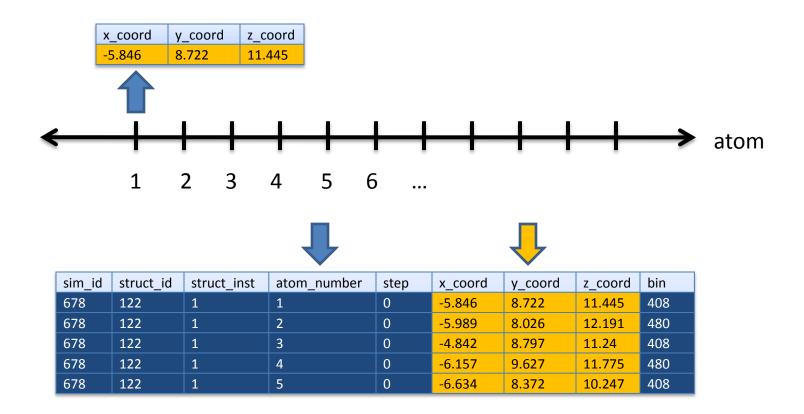
## **OLAP Concepts**

- Data are organized around FACTS and DIMENSIONS
- FACTS are continuous measurements on a item of interest
- DIMENSIONS are discrete quantities that classify measurements into useful groupings

sim_id	struct_id	struct_inst	atom_number	step	x_coord	y_coord	z_coord	bin
678	122	1	1	0	-5.846	8.722	11.445	408
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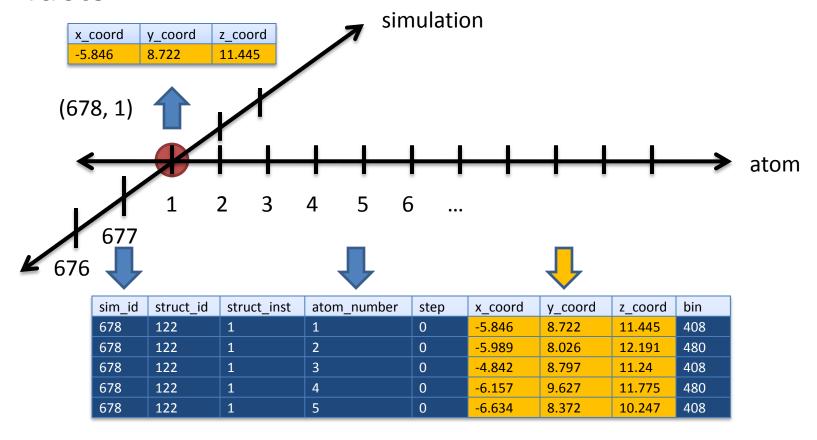
### **Dimensions**

 An individual dimension is similar to a number line, but you are not limited to integers



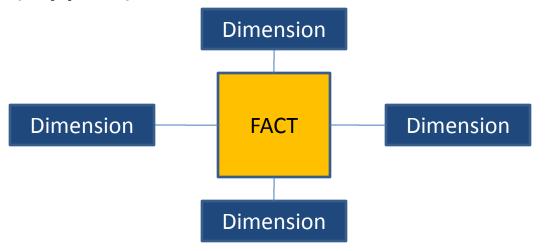
# Dimensions, Continued

A set of dimensions provide coordinates to facts



### **OLAP Cubes**

 A collection of facts and related dimensions form a (hyper) cube



 The cube concept can be implemented using relational tables in a star schema or using a multi-dimensional database...

### Multidimensional OLAP

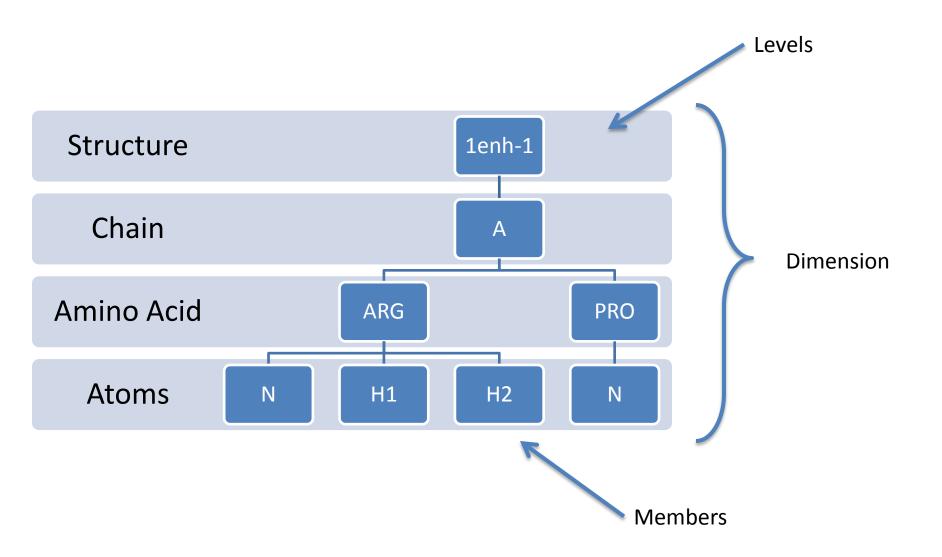
- MOLAP is an implementation of a OLAP database optimized for multidimensional storage
- SQL Server Analysis Services (SSAS) is a set of tools including a MOLAP storage engine and the Multi-Dimensional Expressions (MDX) language

### **OLAP IN DETAIL**

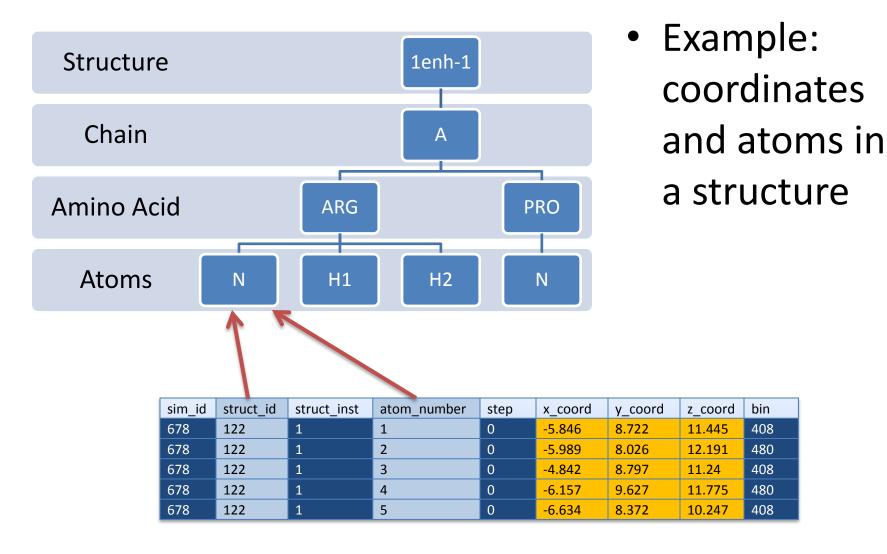
### **Dimensions**

- Recall dimensions uniquely identify facts
- Dimensions are composed of discrete values called members
- Fact data can be "addressed" by specifying a member from each associated dimension
- Members can be organized in a hierarchy

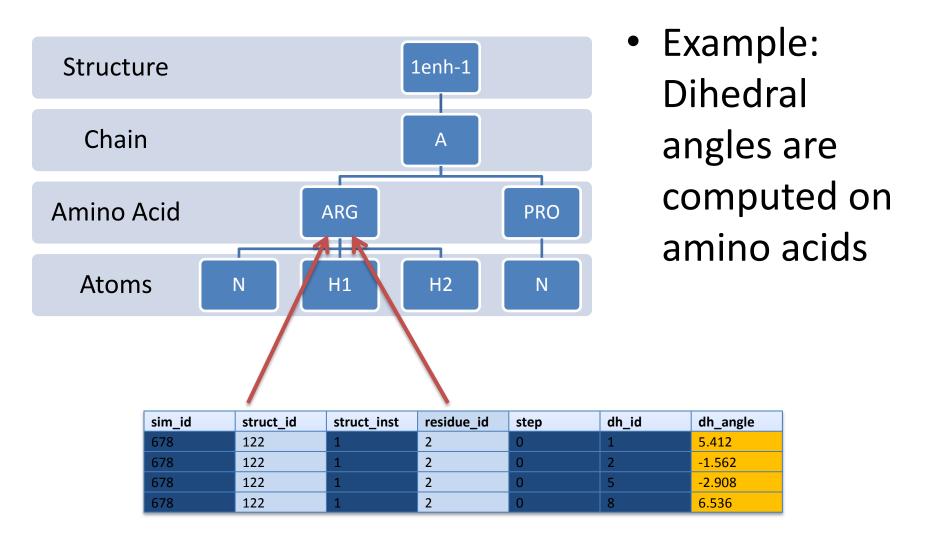
### Hierarchies



### Facts are Associated with Members



# Facts can be associated members at any level



## **Tuples and Sets**

- A tuple is the collection of dimension members that define a fact
- Similar to a multidimensional array in C#
  - Float[,,,,] myarray = new Int32[10000, 2400, 50, 900, 300000,255];
  - myarray[678,122,1,2,0,1] = 5.412
- Unlike a C# array, OLAP dimensions are self describing and can listed in any order
- A set is a collection of tuples

sim_id	struct_id	struct_inst	residue_id	step	dh_id	dh_angle
678	122	1	2	0	1	5.412
678	122	1	2	0	2	-1.562
678	122	1	2	0	5	-2.908
678	122	1	2	0	8	6.536

# **OLAP** and Aggregation

- Individual facts are specified by a "tuple"
- Leaving out a dimension means "\*" or all, resulting in a set
- Choosing a member above the base is short hand for a set of all descendants
- OLAP will apply the defined aggregation, typically SUM

sim_id	struct_id	struct_inst	residue_id	step	dh_id	dh_angle
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678	122	1	2	0	2	-1.562
678	122	1	2	0	5	-2.908
678	122	1	2	0	8	6.536

# **OLAP** is not for Managing Data

- OLAP cubes do not
  - care about integrity constraints
  - support easy or fast updates to data
  - worry about missing or sparse data
- One way to think of OLAP a materialized and optimized view of data stored somewhere other than the store of record (which is typically SQL)

# Microsoft SQL Server: OLAP and Relational

#### **Analysis Services (MOLAP)**

- Cube
- Proprietary Store\*
- Language is MDX
- Queries are top-down
- Results are multidimensional cubes
- Data are ORDERED

#### **SQL Server (Relational)**

- Database
- Relational Store
- Language is SQL
- Queries are bottom-up
- Results are two-dimensional tables
- Data are UNORDERED

<sup>\*</sup> No longer undocumented: I Gorbach, A. Berger, E. Melomed, Microsoft SQL Server 2008 Analysis Services UNLEASHED, 2009 Pearson Education, Inc.

# **SQL Server Analysis Services**

- Discrete dimensional values mean indexes can be implemented as bit vectors—fast but difficult to update and create
- Data are inherently ordered, making it easy to do things like compute medians
- Cubes effectively must be compiled from other sources

### Multidimensional Expressions (MDX)

- The query language for Analysis Services is MDX
- An MDX query defines a sub-cube, possibly multi-dimensional, derived by slicing and dicing (their words) data from the source cube

### A Quick Look at MDX

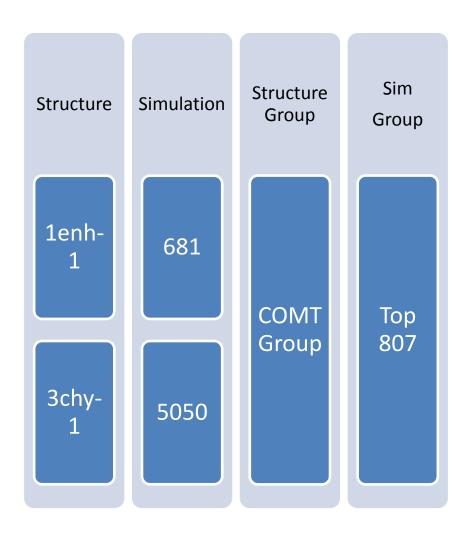
```
WITH
MEMBER [Measures].[atm type] as '[Structure].[Atom Type].membervalue'
MEMBER [Measures].[res_type] as '[Structure].residue.membervalue'
MEMBER [Measures].[res num] as '[Structure].[residue number].membervalue'
MEMBER [Measures].[atm_num] as '[Structure].[Structure Hierarchy].Properties("Atom Number")'
SELECT {
           [Measures].[atm num]
                       , [atm_type]
                       , [res type]
                       , [res_num]
                       , [x Coord]
                       , [y Coord]
                       , [z Coord] } on AXIS(0)
           , { [Structure].[Structure Hierarchy].[Atom].&[122]&[1]:
              [Structure].[Structure Hierarchy].[Atom].&[122]&[5] } on AXIS(1)
FROM [UnifiedDSV]
WHERE ([Simulation].[Simulation Hierarchy].[Step].&[678]&[1]&[0])
```

	atm_num	atm_type	res_type	res_num	x Coord	y Coord	z Coord
N	1	N	ARG	1	-5.846	8.722	11.445
H1	2	Н	ARG	1	-5.989	8.026	12.191
H2	3	Н	ARG	1	-4.842	8.797	11.24
H3	4	Н	ARG	1	-6.157	9.627	11.775
CA	5	С	ARG	1	-6.634	8.372	10.247

### A CUBE DESIGN FOR SIMULATIONS

# Design

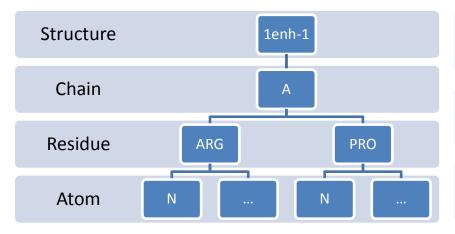
- Dynameomics has 4
   OLAP dimensions
  - Structure
  - Simulation
  - Simulation Group
  - Structure Group

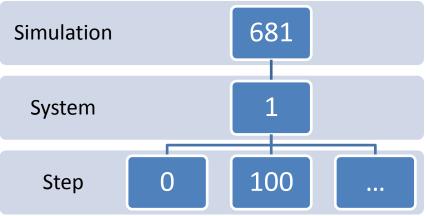


# **Primary Dimensions**

#### **Structure Dimension**

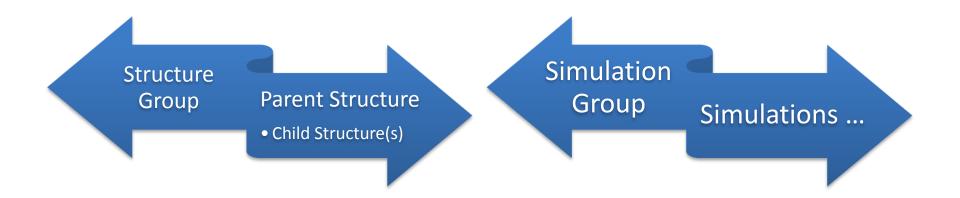
#### **Simulation Dimension**





# **Secondary Dimensions**

Structure Group is a Many-to-Many relationship between Structures Simulation Group is a Manyto-Many relationship with Simulations

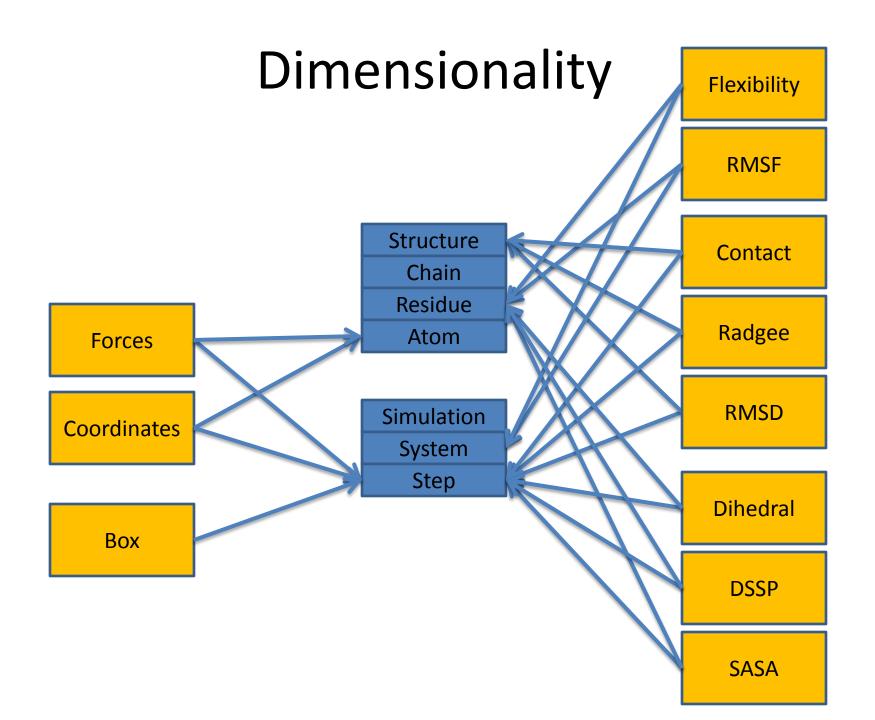


### Dimensions and SQL

- Dimensions are closely tied to SQL tables in the main warehouse
  - Simulation is keyed at the lowest level on sim\_id, struct\_inst, struct\_id and step
  - Structure is keyed at the lowest level on struct\_id and atom\_number
  - Structure Groups and Simulation Groups are related though intermediate tables to Structure and Simulation, respectively

# Facts (Measures)

- Atom Coordinates
- Box
- Forces
- Dihedral Angles
- DSSP
- Flexibility
- Solvent Accessible Surface Area (SASA)
- Cα RMSD
- Congenial
- Radius of Gyration (Radgee)
- Contacts



### **IMPLEMENTATION**

## **Starting Point**

A cube based on the top 6 Dynameomics targets:

Simulations	Structures	Time	SQL Space
63	1.5 x 10 <sup>6</sup>	1.15 μs	214GB

Contains coordinates, box size, and dihedral angles only

## **Initial Observations**

- Initial build/processing time ~2 hours
- Cubes are significantly smaller than their SQL counter parts:

Simulations	Structures	Time	SQL Space	OLAP Space
63	1.5 x 10 <sup>6</sup>	1.15 μs	214GB	41GB

# Test Query: Dihedral Angles

- Dihedral angles are used to study side-chain conformations
- One visualization technique is to make histograms, effectively binning observed angles into 1 degree buckets
- 855,484,304 rows of Dihedral data in my test set
- In SQL...

# **SQL Dihedral Query**

```
SELECT
           byres.residue
           , dh.angle name
           , byres.[bin]
           , SUM(byres.[count]) AS [count]
FROM (
           SELECT
                       i.residue
                       , d.dh id
                       , CAST (ROUND(d.dh_angle,0) AS INT) AS [bin]
                       , COUNT(*) AS [count]
           FROM
                       ( SELECT DISTINCT struct_id, residue_id, residue
                         FROM [Directory].dbo.Master ID ) AS i
                        JOIN [dynameomics-9].dbo.andrew TOP6 Dihed AS d WITH (NOLOCK)
                        ON (i.struct id = d.struct id
                                   AND i.residue id = d.residue id)
                       GROUP BY i.residue
                                   , d.dh id
                                   , CAST (ROUND(d.dh angle,0) AS INT)
                       UNION ALL
                       -- FOUR MORE SELECTS HERE
           ) AS byres
           JOIN dbo.Dihedral Angle AS dh
           ON (byres.dh_id = dh.dh_id)
GROUP BY byres.residue, dh.angle_name, byres.[bin]
ORDER BY
           byres.residue, dh.angle name, byres.[bin]
```

## SQL Results

- First version was too slow (I stopped it after 3 hours)
- Second version, 65 lines, took 32 minutes, 35,364 rows
- This query could be more thoroughly analyzed and perhaps made faster

residue	angle_name	bin	count
ALA	chi1	-180	53596
ALA	chi1	-179	107007
ALA	chi1	-178	105977
ALA	chi1	-177	104639
ALA	chi1	-176	103918

## Here's the MDX Version

## **MDX** Results

- ~6 lines
- Returned the same results as SQL, but conveniently pivoted for comparison (6,138 rows)
- Execution time: 4 seconds

		Alanine	Arginine	Asparagine	Aspartic acid	Cysteine	Glutamine	Glutamic acid
-180	Dihedral Count	53596	22116	76832	95041	674	8626	26797
-179	Dihedral Count	107007	44841	155320	190478	1477	18000	55579
-178	Dihedral Count	105977	46318	154486	192171	1457	18379	57658
-177	Dihedral Count	104639	47175	153191	193343	1484	19194	59307
-176	Dihedral Count	103918	47725	152868	192268	1415	19518	60685
-175	Dihedral Count	101764	47928	149364	190889	1396	19569	62164

#### **Contacts**

- Atom-Atom contacts are frequently analyzed in simulations
- Two heavy atoms (i.e. not Hydrogen) are said to be in contact if they are less than 4.6 Å apart unless both atoms are Carbon; then they must be 5.4 Å apart or less

#### **Contact Matrices are BIG**

- A brute-force comparison of all atoms in a simulation frame is the Cartesian product of all rows in that frame divided by two
- For 1enh, that amounts to 631,688 comparisons PER FRAME
- A SQL implementation involves a self-join on a Coordinate table

# SQL to just compute distances

```
SELECT
          c1.sim id
      , c1.step
      , c1.struct inst AS struct inst1
      , c1.struct id AS struct id1
      , c1.atom number AS atom number1
      , c2.struct inst AS struct inst2
      , c2.struct id AS struct id2
      , c2.atom number AS atom number2
      , SQRT ( SQUARE( c1.x_coord - c2.x_coord )
             + SQUARE(c1.y coord - c2.y coord)
             + SQUARE(c1.z coord - c2.z coord)) AS [dist]
FROM dbo.Coord_112 AS c1
      JOIN dbo. Coord 112 AS c2
      ON (c1.sim_id = c2.sim id
          AND c1.step = c2.step
          AND (
                -- different instances
                (c1.struct inst <> c1.struct inst)
                -- different atoms in same structure
                OR (c1.struct inst = c1.struct inst
                    AND c1.atom_number <> c2.atom_number
                    AND c1.atom number < c2.atom number )))
```

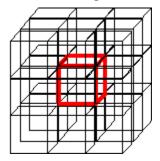
## Brute Force SQL Result

- Limiting to heavy atoms, and applying filtering based on distances for a *single* 1enh simulation:
- Result: 36,210,336 rows, 2 hours 26 minutes
- Clearly not scalable...

# Hash3D Optimization

- For contact distances, we can safely exclude atoms more than 5.4Å apart
- Simulation box can be divided into 5.4Å cubes, each atom can be placed in a cube
- "bin" a 1-dimensional integer hash can uniquely identify a cube
- "neighbors" are the 26 adjacent cubes





## Bins Stored with Coordinates

- Bins are computed and stored with each simulation at load time
- A C# Stored Procedure computes neighbors for each bins, and is stored in another table and indexed (under 1 second)
- Contact query with Hash3d: 36 minutes

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#### MDX?

- Cube design is in progress
  - Building a dimension and hierarchy using bin and neighbors
  - Determining syntax to utilize hierarchy and find results
- A manuscript describing hash3d, support functions, tables, and index design and in progress

## **CONCLUSIONS**

#### **OLAP**

#### Good

- Queries can be FAST
- Storage seems to be extremely efficient
- Certain classes of queries seem trivial to write (and much less complicated than SQL)

#### Bad

- MDX syntax can be complicated
- Shares keywords but no semantics with SQL
- Processing time and initial set up are non-trivial
- Documentation is often lacking sufficient detail

## Conclusions and Future Directions

- OLAP/MDX and SQL are complementary technologies, not replacements for each other
- More investigation is needed to tune OLAP design to maximize performance and usability
- Specific Next Steps
  - Finish hash3d OLAP design and compare to SQL
  - Additional performance and scale testing

## Acknowledgements

 Special thanks to Amanda Jonsson and Rudesh Toofanny for their insights and help

## Questions?

http://www.dynameomics.org