

## National Data Service Pilot

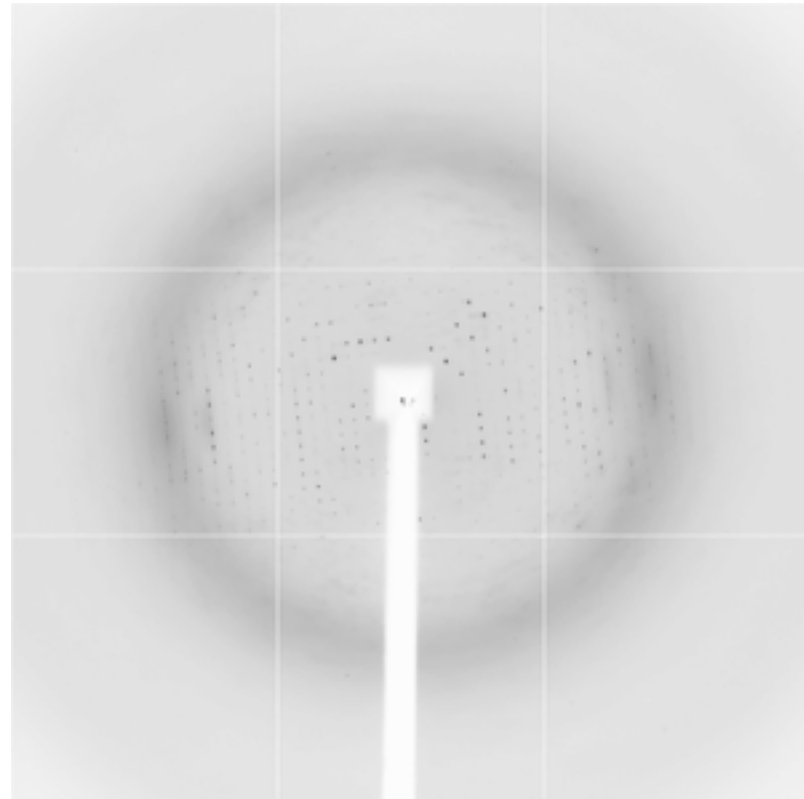
Establishing an effective system to  
facilitate access  
to biomedical datasets.

Peter Meyer

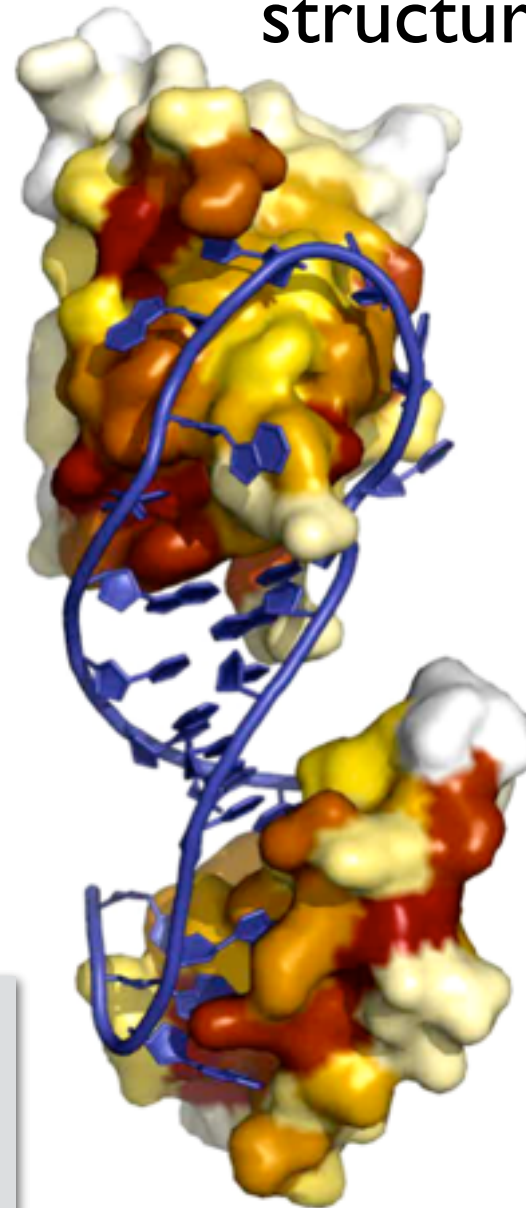
Piotr Sliz, Merce Crosas, Ian Foster

National Data Service  
UNC-Chapel Hill, April 5th, 2016

# Motivation



Lin28  
structure



Nam et al., Cell, 2011

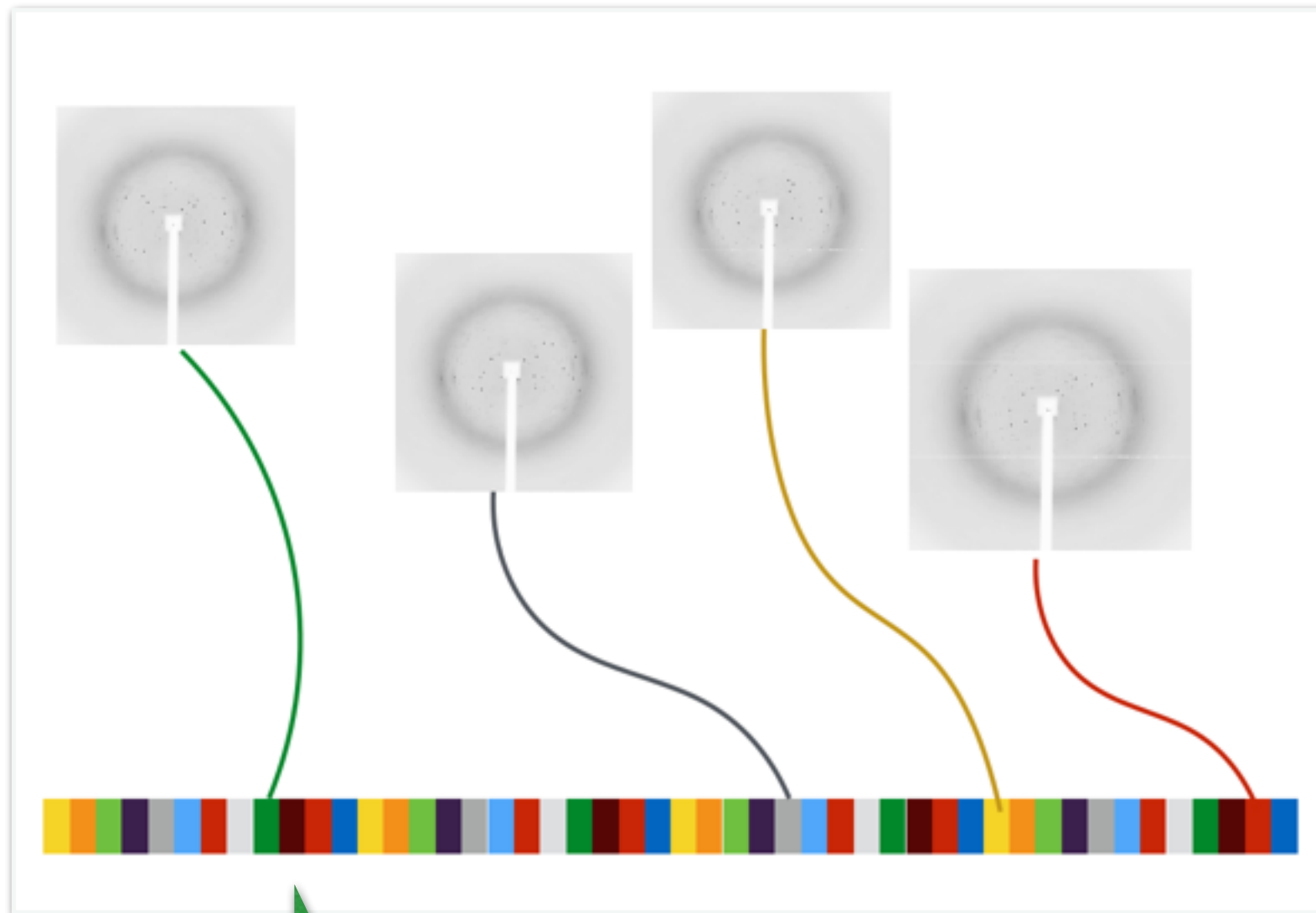


MD  
Models

- Different software packages (e.g. XDS vs HKL2000: 3D vs 2D profile fitting)
- Different assumptions (e.g. symmetry, mosaicity, radiation damage, number of frames)
- New software packages (e.g. DIALS)
- Improved criteria (e.g. resolution limits such as CC1/2, Karplus and Diederichs, 2012, or anisotropic correction)
- New corrections (e.g. data anisotropy)
- Additional features: (e.g. anisotropic diffuse scattering signals)



# Four Essential Components of a biomedical data grid



Data Publication

Data Access

Live Analysis

Sustainability

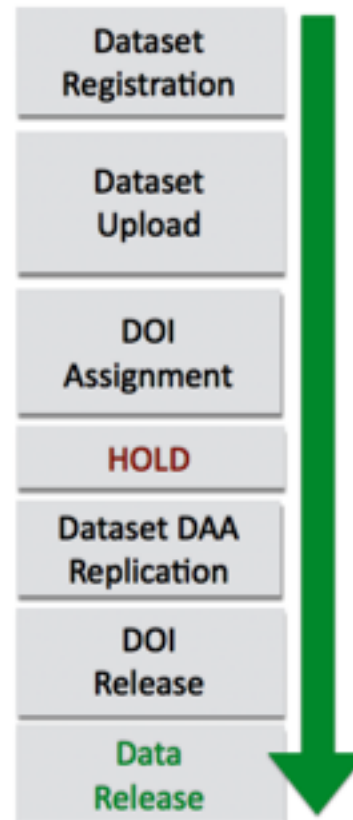


# Structural Biology Data Grid Website

[data.sbgrid.org](http://data.sbgrid.org)

## Lab Collections

The screenshot shows the SBGrid Data Bank website. At the top, there's a navigation bar with links for 'For Depositors', 'Data', 'About', and 'Get Help'. Below this, a message states: 'We support publication of X-ray diffraction datasets. All visitors can access the following Laboratory and Institutional Collections. All SBGrid affiliates are invited to deposit datasets.' There are two tabs: 'Lab/Institutional Collections' (selected) and 'All Datasets'. A status bar indicates 'Datasets: 117', 'Lab/Institutional Collections: 50', and 'Next Update: Friday 5pm'. The main content area lists several laboratories with their logos and names: Anderson Laboratory (Yale University School of Medicine), Baxter Laboratory (Yale University), Boggon Laboratory (Yale University School of Medicine), Bonvin Laboratory (Utrecht University), Brett Laboratory (Washington U. School of Medicine), and Buschiazzo Laboratory (Institut Pasteur de Montevideo). Each laboratory entry is accompanied by small thumbnail images of protein structures.



doi:10.1038/ncomms10882

The screenshot shows the article page for 'Data publication with the structural biology data grid supports live analysis' in Nature Communications. The article is open access. The authors listed are: Peter A. Meyer, Stephanie Socias, Jason Key, Elizabeth Ransey, Emily C. Tjon, Alejandro Buschiazzo, Ming Lei, Chris Botka, James Withrow, David Neau, Kanagalaghatta Rajashankar, Karen S. Anderson, Richard H. Baxter, Stephen C. Blacklow, Titus J. Boggon, Alexandre M. J. J. Bonvin, Dominika Borek, Tom J. Brett, Amedeo Caffisch, Chung-I Chang, Walter J. Chazin, Kevin D. Corbett, Michael S. Cosgrove, Sean Crosson, Sirano Dhe-Paganon, Enrico Di Cera, Catherine L. Drennan, Michael J. Eck, Brandt F. Eichman, Qing R. Fan, Adrian R. Ferré-D'Amaré, J. Christopher Fromme, K. Christopher Garcia, Rachelle Gaudet, Peng Gong, Stephen C. Harrison, Ekaterina E. Heldwein, Zongchao Jia, Robert J. Keenan, Andrew C. Kruse, Marc Kvansakul, Jason S. McLellan, Yorgo Modis, Yunsun Nam, Zbyszek Otwinowski, Emil F. Pai, Pedro José Barbosa Pereira, Carlo Petosa, C. S. Raman, Tom A. Rapoport, Antonina Roll-Mecak, Michael K. Rosen, Gabby Rudenko, Joseph Schlessinger, Thomas U. Schwartz, Yousif Shamoo, Holger Sondermann, Yizhi J. Tao, Niraj H. Tolia, Oleg V. Tsodikov, Kenneth D. Westover, Hao Wu, Ian Foster, James S. Fraser, Filipe R. N. C. Maia, Tamir Gonen, Tom Kirchhausen, Kay Diederichs, Mercè Crosas, Piotr Sliz. The article was published in Nature Communications, Volume 7, Article number: 10882, doi:10.1038/ncomms10882. It was received on 16 October 2015, accepted on 28 January 2016, and published on 07 March 2016. The page includes links for 'Full text', 'PDF', 'Citation', 'Reprints', 'Rights & permissions', and 'Article metrics'.

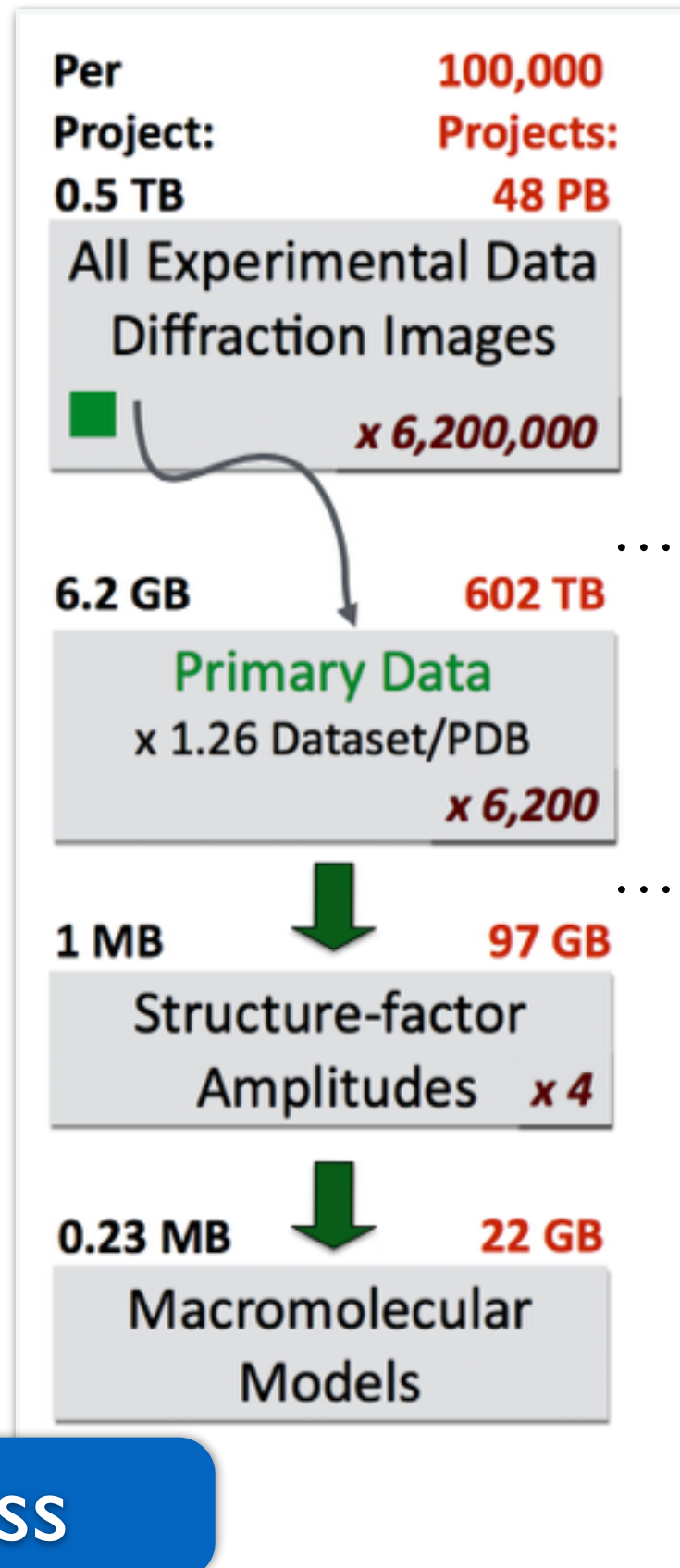
The 'Online attention' section displays an Altmetric score of 81. It includes a circular chart with the number 81 in the center. To the right, it lists the following metrics: 'Twisted by 36', 'Mentioned in 1 Google+ posts', 'Picked up by 7 news outlets', and 'Blogged by 1'. Below this, a text box explains: 'This Altmetric score means that the article is: in the 97 percentile (ranked 4,195th) of the 169,738 tracked articles of a similar age in all journals; in the 80 percentile (ranked 124th) of the 647 tracked articles of a similar age in Nature Communications'.

# Storage Requirements

(based on 100,000 PDB files and average dataset size in SBDG)

SBDG:  
110 datasets  
~0.5TB

PDB:  
100,000 models  
0.3 TB



Some of “All Experimental Data”  
preserved at national synchrotrons  
e.g. Tardis or Diamond



Primary Diffraction Datasets  
proposed to be stored on SB Data Grid



Molecular models and reduced datasets  
are stored in Protein Data Bank



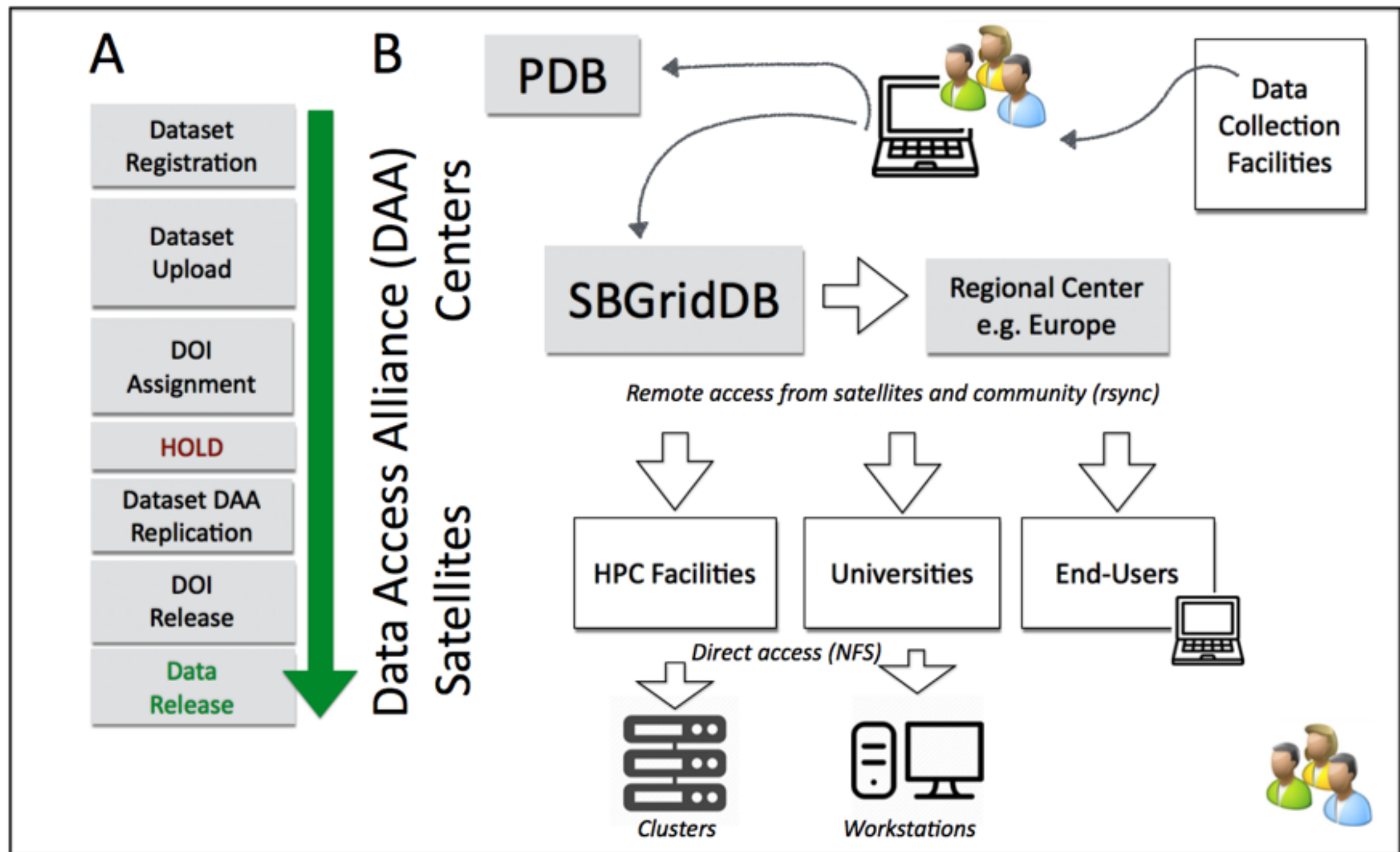
Data Access

@SBGrid



# Dataset Access Alliance:

## Local access through a growing list of Satellites



# Dataset Access Alliance: Local access through a growing list of Satellites



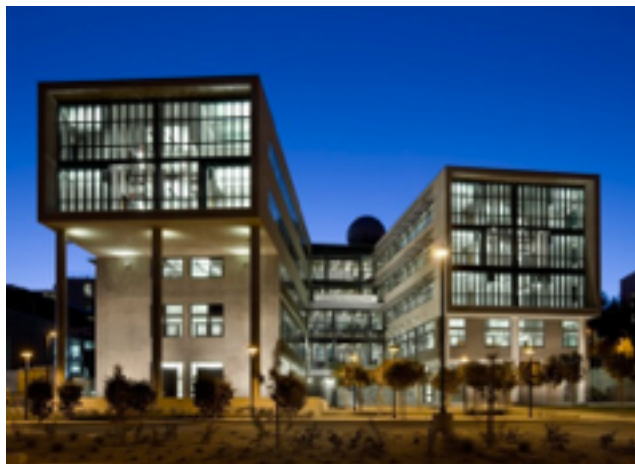
UPPSALA  
UNIVERSITET



Petrel Storage  
at Argonne Labs



Orchestra Cluster  
Harvard Medical School



San Diego  
Supercomputer  
Center

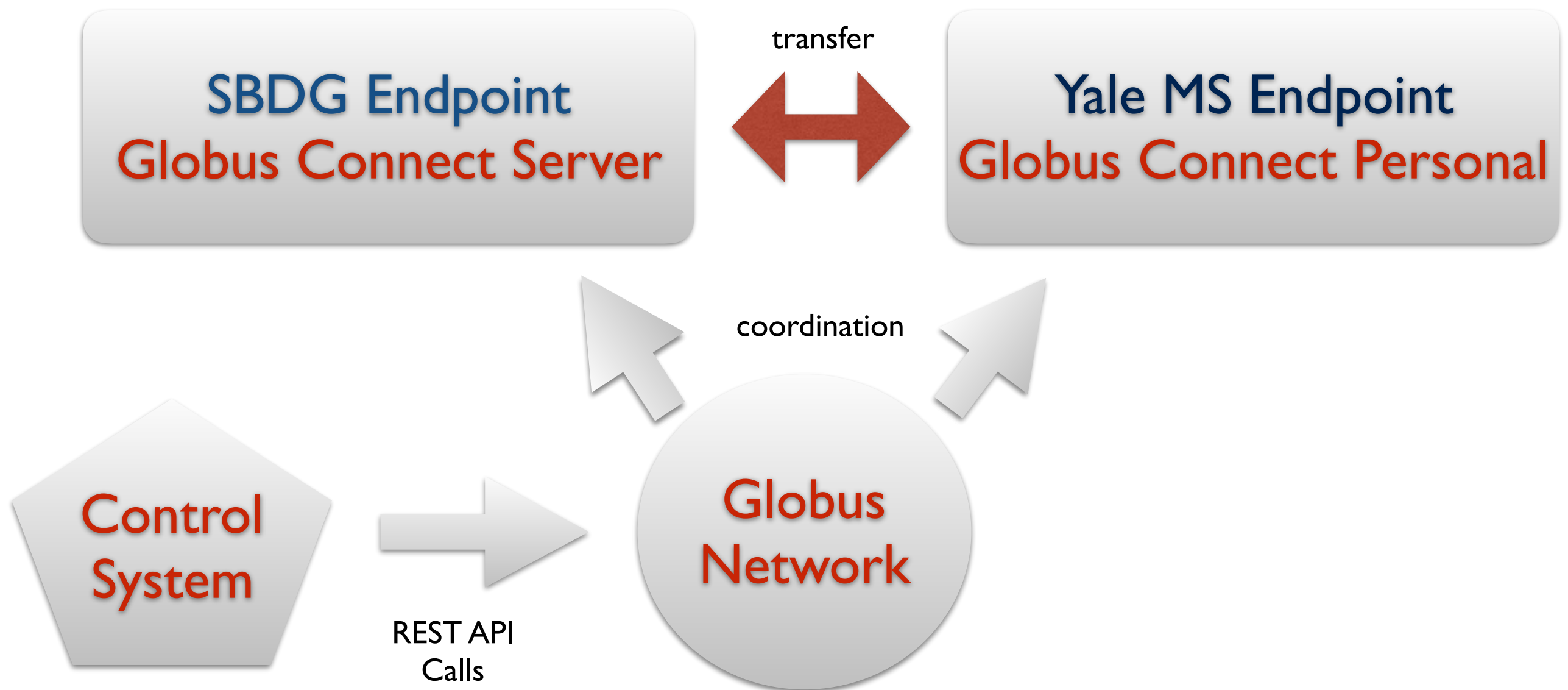


National Data Service Pilot



# Dataset Access Alliance:

## Local access through a growing list of Satellites



National Data Service Pilot



# Integration with Biomedical Software Support

The screenshot shows a software management window with a sidebar on the left and a main content area on the right. The sidebar has two sections: 'Packages' with 'Installed' and 'Pending' filters, and 'Collections' with a list of categories and their counts. The main content area has a table of packages and a details panel for the selected 'Cufflinks' package.

| Selected                            | Package   | Installed Version | Current Version |
|-------------------------------------|-----------|-------------------|-----------------|
| <input type="checkbox"/>            | a2ps      |                   | 4.14            |
| <input type="checkbox"/>            | Aline     |                   | 1.0.025         |
| <input type="checkbox"/>            | AMPS      |                   | 2.3a            |
| <input type="checkbox"/>            | ARIA      |                   | 2.3.1           |
| <input type="checkbox"/>            | AutoDock  |                   | 4.2.5.1         |
| <input type="checkbox"/>            | BLAST     |                   | 2.2.26          |
| <input type="checkbox"/>            | BLAST+    |                   | 2.2.31          |
| <input type="checkbox"/>            | Bowtie    |                   | 1.0.0           |
| <input type="checkbox"/>            | Bowtie 2  |                   | 2.2.1           |
| <input type="checkbox"/>            | breseq    |                   | 1.00rc8         |
| <input type="checkbox"/>            | BWA       |                   | 0.7.7-r441      |
| <input type="checkbox"/>            | CCP4      |                   | 6.5             |
| <input type="checkbox"/>            | Chimera   |                   | 1.10.2          |
| <input type="checkbox"/>            | CNS       |                   | 1.3r8           |
| <input type="checkbox"/>            | CTF       |                   | 20140609        |
| <input checked="" type="checkbox"/> | Cufflinks |                   | 2.1.1           |
| <input type="checkbox"/>            | cython    |                   | 0.21.1          |
| <input type="checkbox"/>            | DireX     |                   | 0.7.0           |
| <input type="checkbox"/>            | EMAN      |                   |                 |
| <input type="checkbox"/>            | EMAN2     |                   |                 |
| <input type="checkbox"/>            | EPMR      |                   |                 |
| <input type="checkbox"/>            | FASTA     |                   |                 |
| <input type="checkbox"/>            | FREALIGN  |                   |                 |
| <input type="checkbox"/>            | GROMACS   |                   |                 |
| <input type="checkbox"/>            | HADDOCK   |                   |                 |
| <input type="checkbox"/>            | IGV       |                   |                 |
| <input type="checkbox"/>            | MAFFT     |                   |                 |
| <input type="checkbox"/>            | MGLTools  |                   |                 |

**Cufflinks**

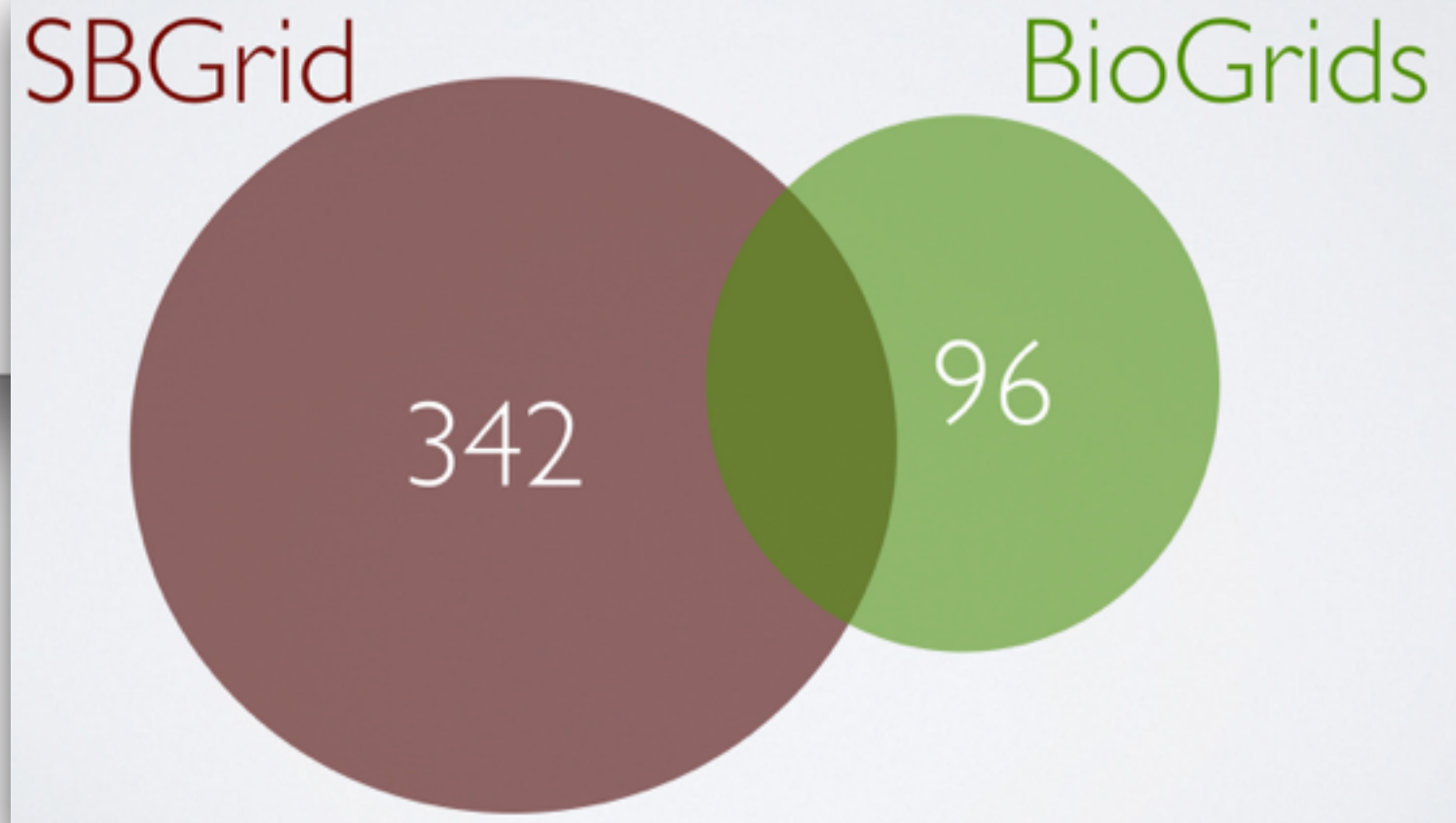
**Description**

a reference-guided assembler that assembles transcripts, estimates their abundances, and tests for differential expression and regulation in RNA-Seq samples.

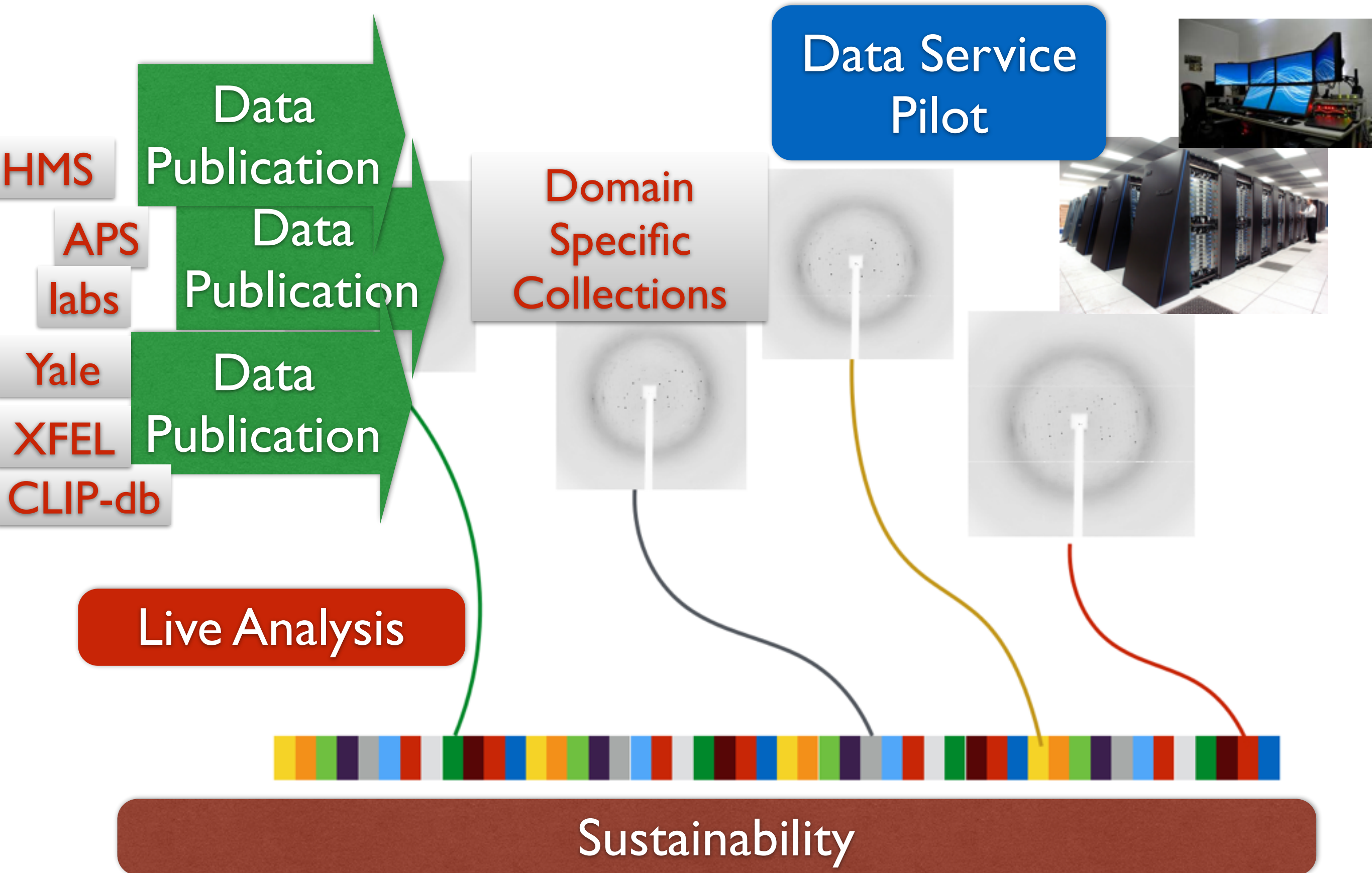
**Links**

- [Website](#)
- [Manual](#)
- [Forum help](#)

[sbgrid.org](http://sbgrid.org)  
[biogrids.org](http://biogrids.org)



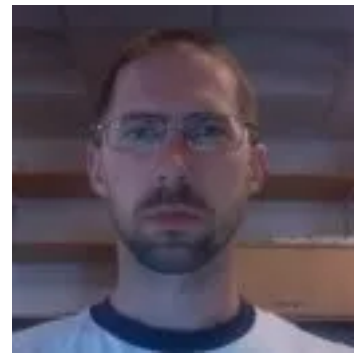
# Summary





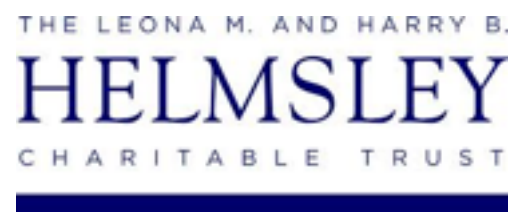


**Stephanie  
Socias**



**Pete  
Meyer**

# Thank you



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## Data publication with the structural biology data grid supports live analysis

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