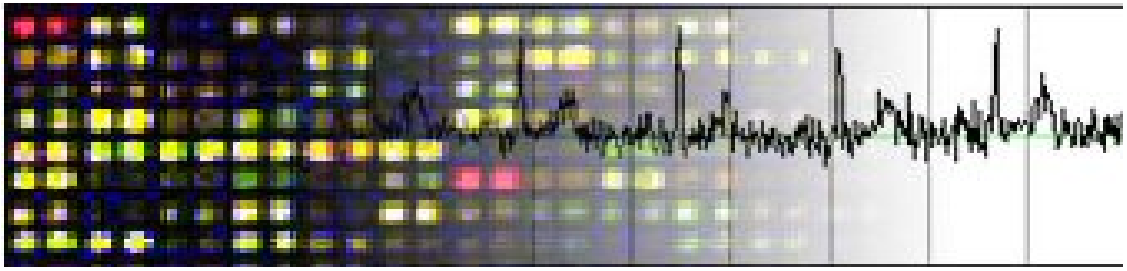


Biomedical Information Technology

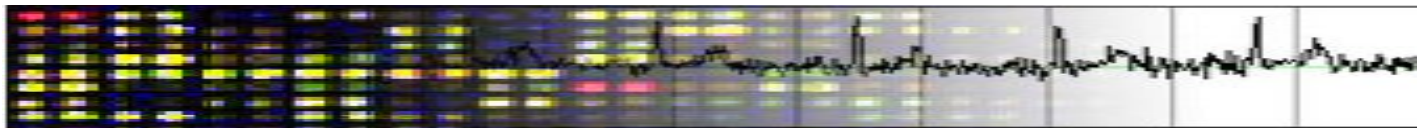
2.771J BEH.453J HST.958J Spring 2005

Lecture 21 April 2005

Biological Image Information II: Informatics Considerations

BIOLOGICAL IMAGE INFORMATION II

- A summary of required information for images
  - Sample characterization
  - Size and registration issues
  - Characterizing the optical path
  - Other experimental variables
  - Tracking multiple experiments (studies)
  - Methods of indexing images
- Similarities with other biological data objects
- Interoperability
- The OME: Open Microscopy Environment



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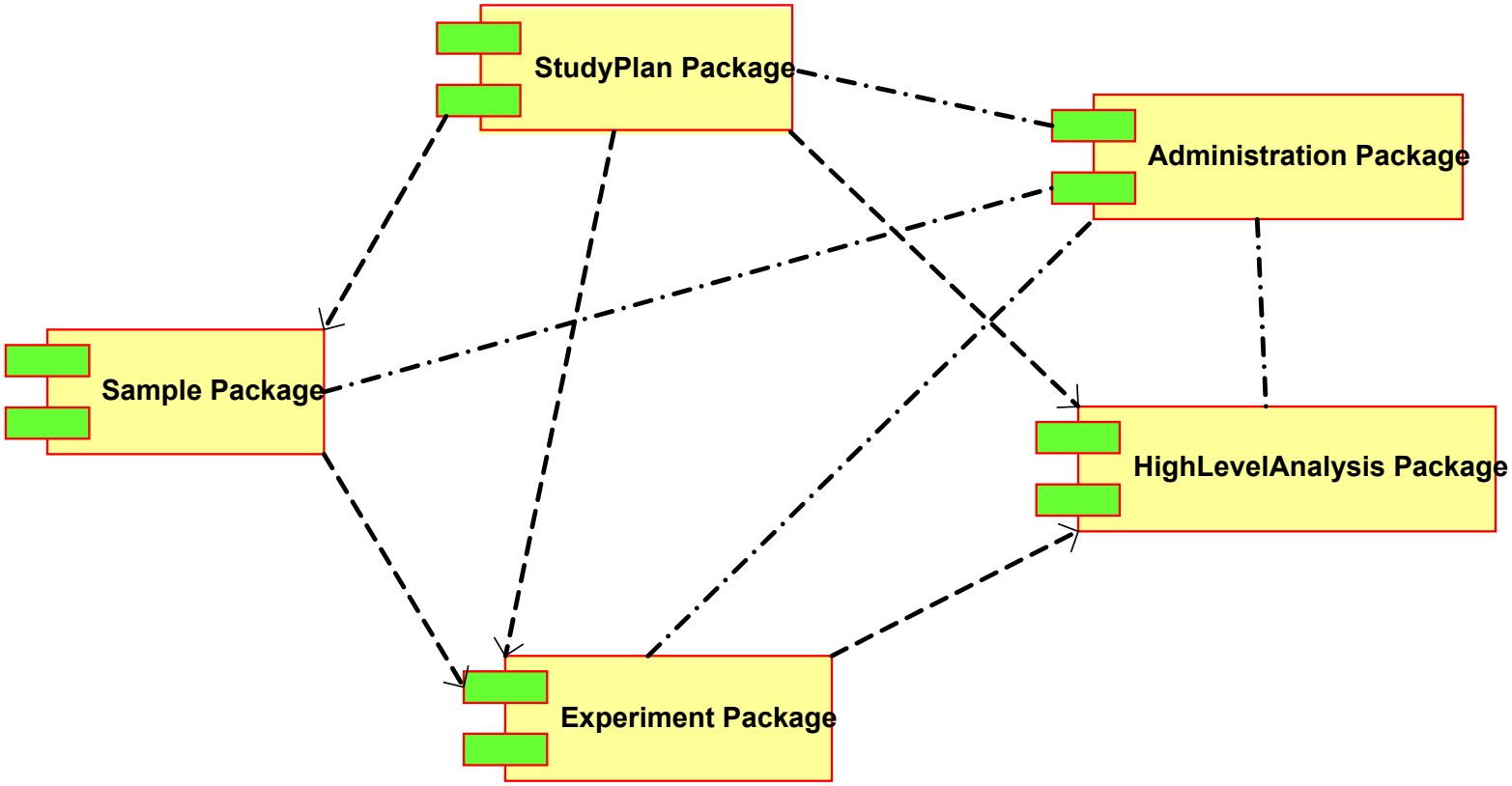
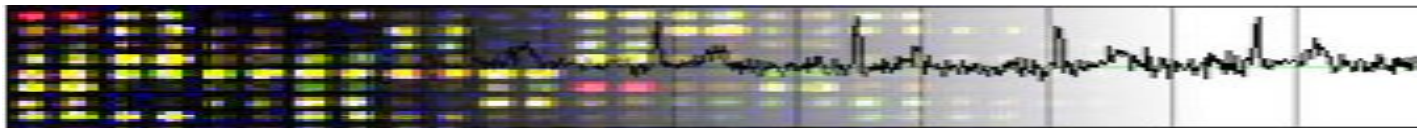
ExperiBase Design--*Summary and Review*



A->B: Dependency. The changes of A can cause changes in B.

-.-.-: Reference



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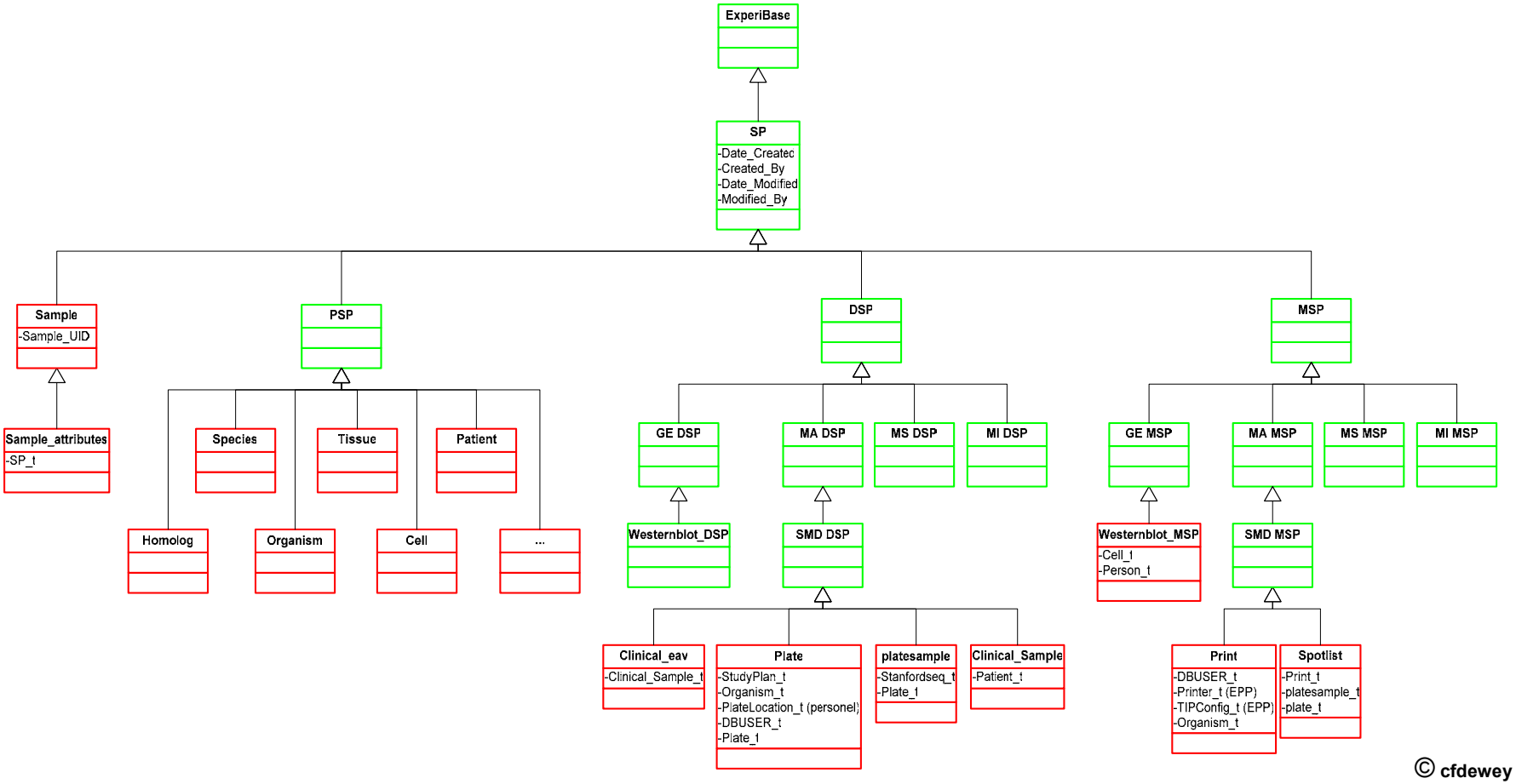
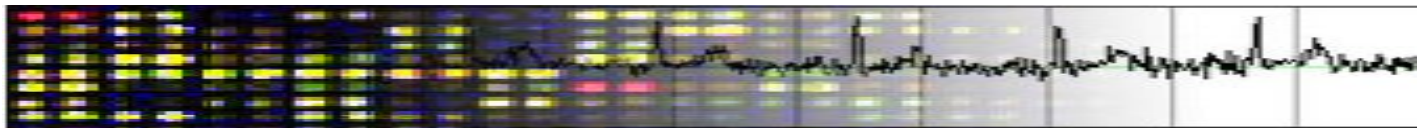
Detail of sample packages for Gell E. and MicroA.

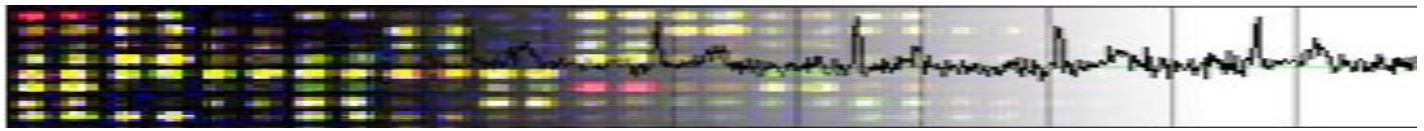
Red color represents that the entity is a table and data type.
Green color represents that the entity is a data type only.





Sample characterization for images

- Differences from gel electrophoresis and microarrays
  - Sample geometry is important (e.g. tracking)
  - Sample is alive and functioning
  - Time is important (changes in sample over time)
  - Need to characterize the visualization method
    - Dyes
  - Emphasis on processing original image and its derivatives
- Similarities
  - Species, organ, cell type. Need knockout data
  - Pretreatment (but probably different from GE, MA)
  - Administrative
- Missing
  - Administrative, extensive sample, study info.



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Experiment package: Confocal microscopy

- Overall geometry (fiduciary)
  - ~10 incl. angles, points
- Specimen and chamber
  - ~10 incl. thickness, flow, . .
- Excitation optics
  - ~10 incl. source, intensity, . .
- Detection path optics
  - ~10 incl. filter char., pinholes, .
- Detector characteristics
  - ~5 incl. temp., background, . .
- X,Y,Z motion control
  - ~9 incl. changes from fiduciary
- Total = ~54

Image removed for copyright reasons.

Fig.: www.microscopyu.com

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Expt. package: conventional wide-field microscopy

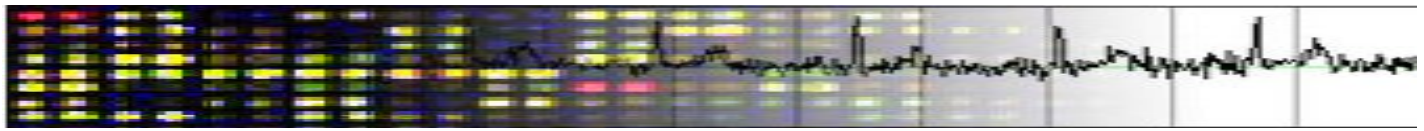
Approximately the same number of components as confocal micros.

~ 60

Image removed for copyright reasons.

Fig.: www.microscopyu.com

Consider reusing expt. packages as named protocols. Automatic association of elements with experiment

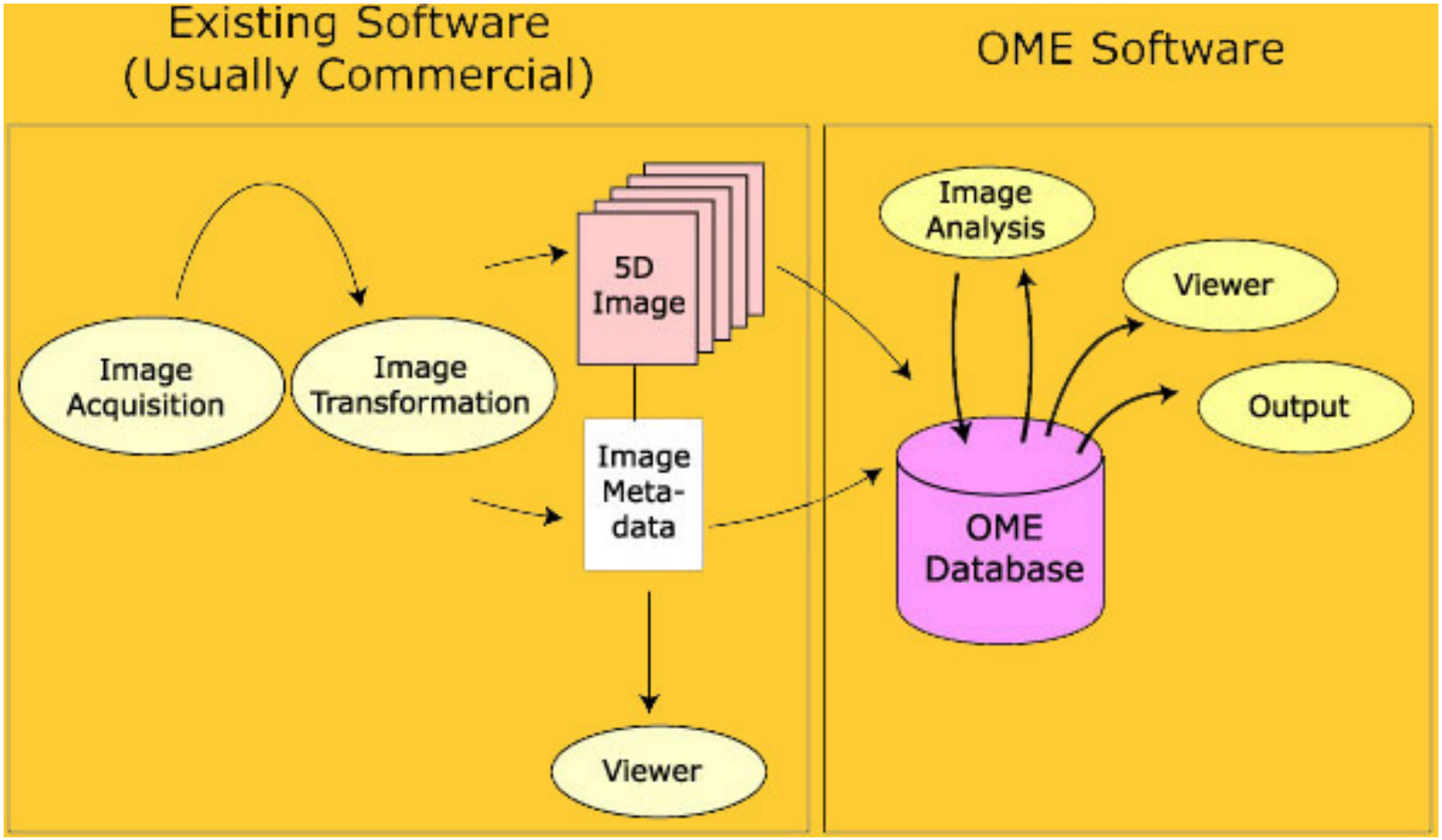


The Open Microscopy Environment (OME)

- Started in approximately 2000 at MIT:
  Sorger lab: Sorger, Swedlow, Goldberg
- Microscopy only, but claimed overlap to microarrays
- Heavy emphasis on strong typing of elements
- Major feature is support of analysis packages and resulting metadata
- Open source code (Gnu license)(Lesser Gnu license)
- Use of XML for transport of data
- Use of XML for creating internal tables in database

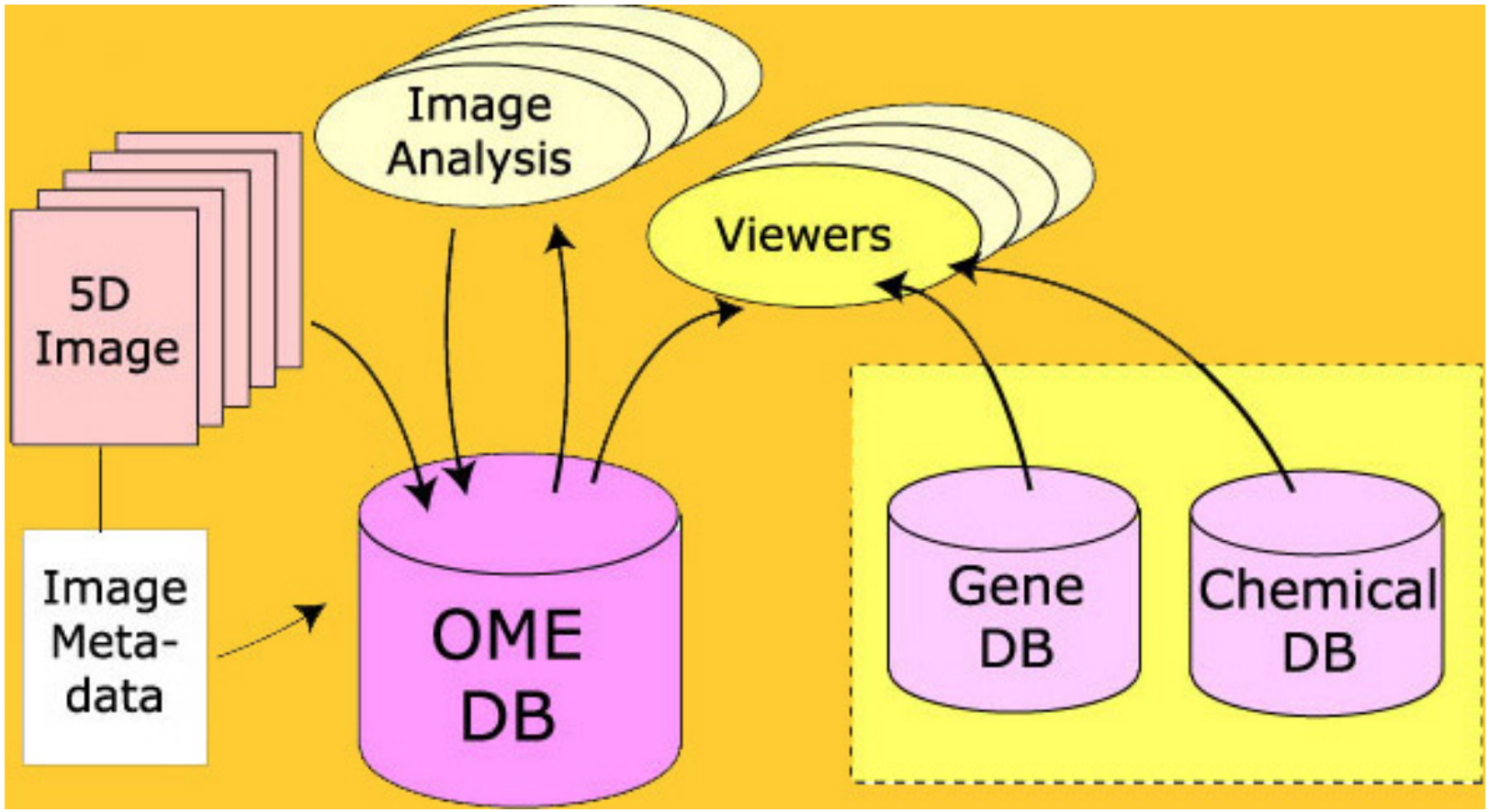
Ref: www.openmicroscopy.org

The paradigm for using a database



Ref: www.openmicroscopy.org

Using the database as a tool for analysis and the storage of metadata produced by the analysis.



Ref: www.openmicroscopy.org

Courtesy of Prof. Peter Sorger. Used with permission.

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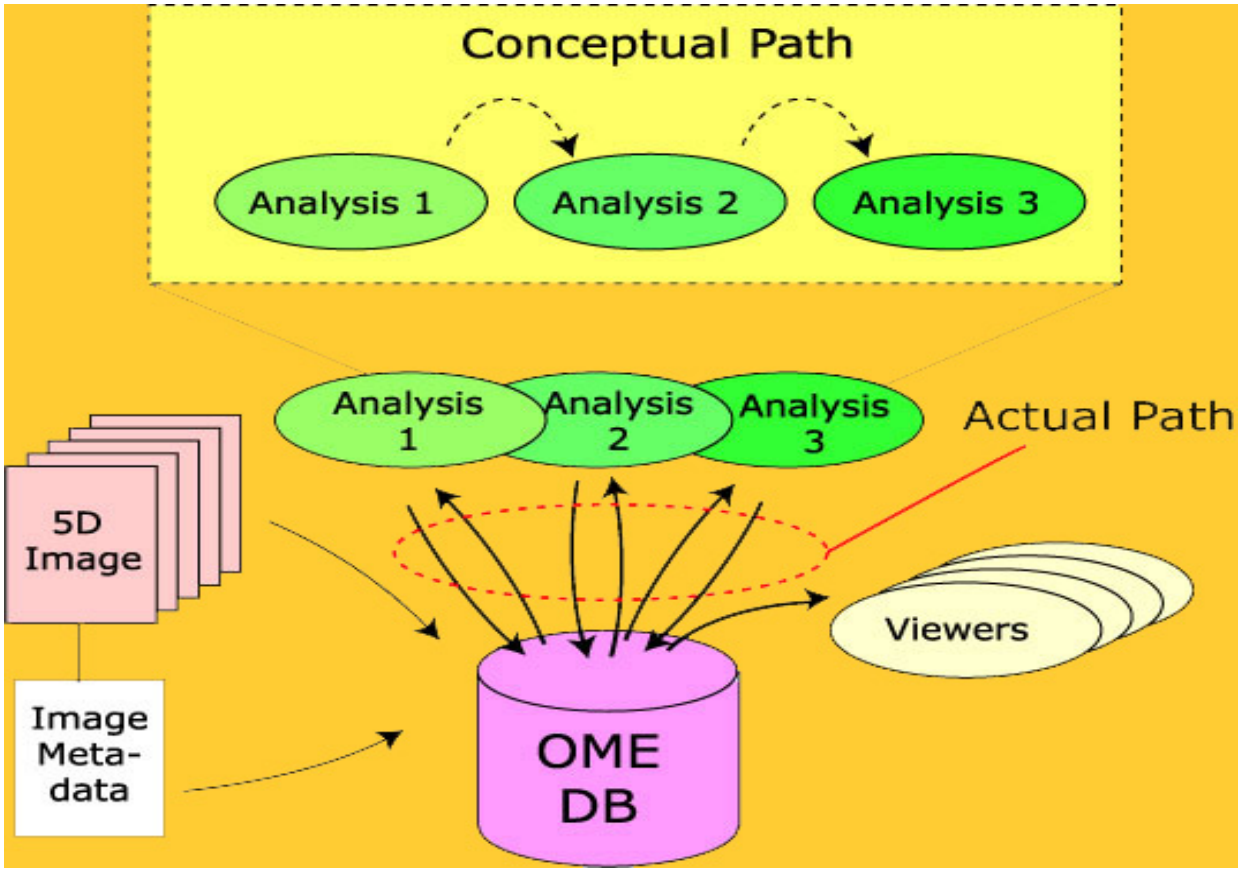
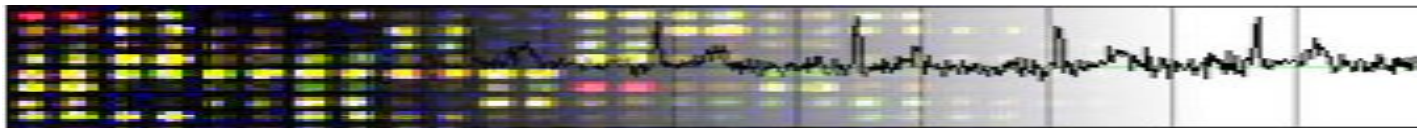
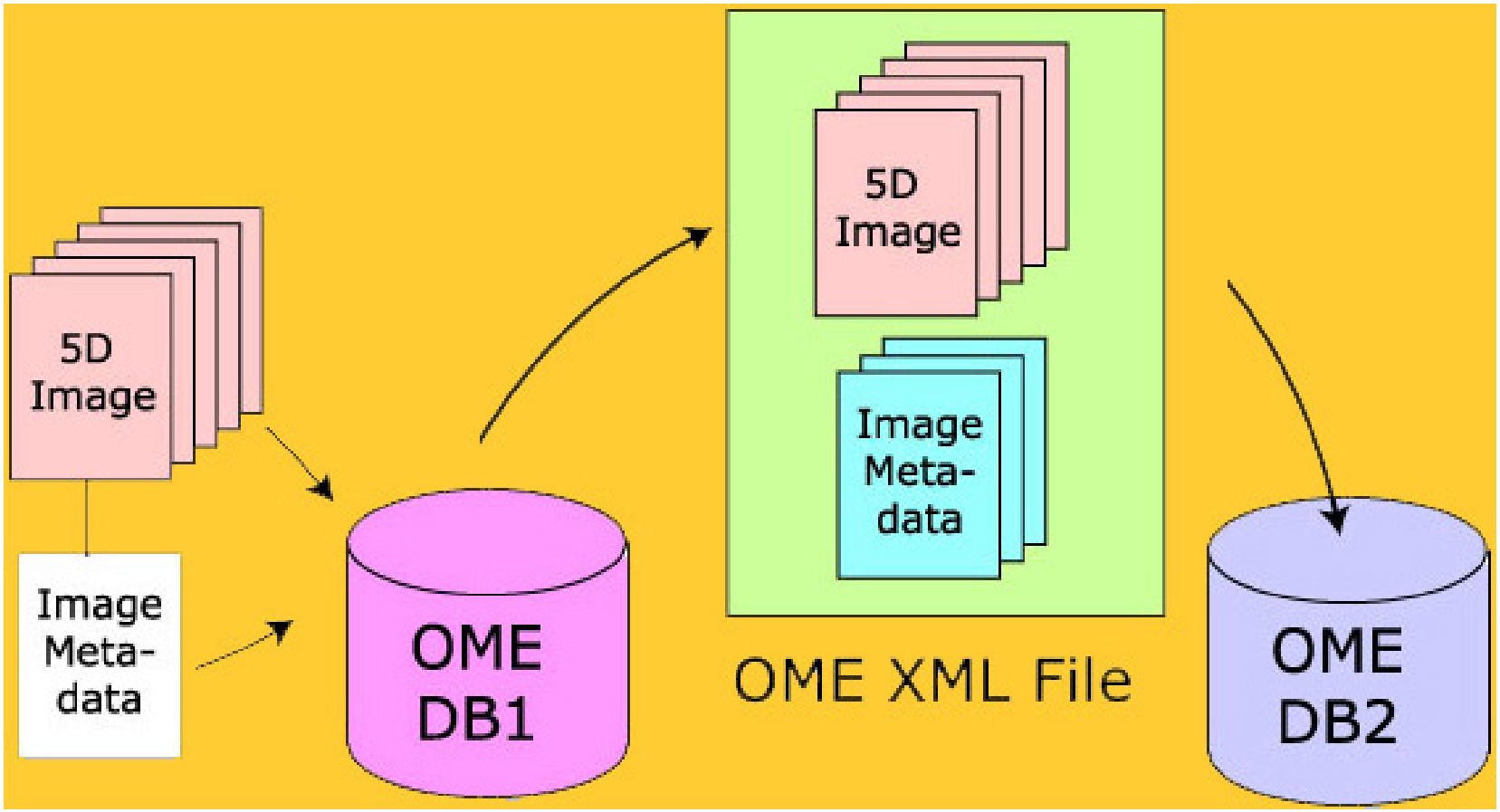
One way to implement the analysis. Performance issues are extremely serious.



Ref: www.openmicroscopy.org



XML as a transport protocol



Ref: www.openmicroscopy.org

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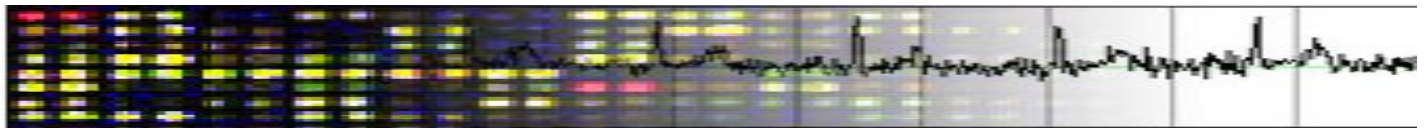
Details of the XML representation of metadata. Each value below will require ~10^2 attributes.

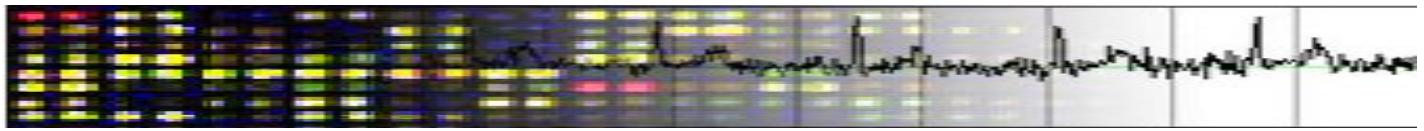
```
- xs:attribute name="Mode">
    - <xs:simpleType>
        - <xs:restriction base="xs:string">
            <xs:enumeration value="Wide-field" />
            <xs:enumeration value="Laser Scanning Microscopy" />
            <xs:enumeration value="Laser Scanning Confocal" />
            <xs:enumeration value="Spinning Disk Confocal" />
            <xs:enumeration value="Slit Scan Confocal" />
            <xs:enumeration value="Multi-Photon Microscopy" />
            <xs:enumeration value="Structured Illumination" />
            <xs:enumeration value="Single Molecule Imaging" />
            <xs:enumeration value="Total Internal Reflection" />
          </xs:restriction>
      </xs:simpleType>
  </xs:attribute>
```

Ref: www.openmicroscopy.org



Conclusions (I)

1. A single ExperiBase database schema covering gell electrophoresis, mircroarrays, microscopy images, mass spec data, and other experimental modalities looks quite feasible.
2. Packages for each experimental method can be constructed from the global schema, with useful commonality and overlap between methods.
3. A key ingredient is the liberal use of LSID identifiers to find common semantics and allow tight definitions of attributes.
4. A logical object-level schema design will promote a shorter learning time and the development of cooperative software.



Conclusions (II)

5. Particular attention should be given to the support of external analysis packages following the OME model.
6. XML can be used as a transport medium, with semantic information embedded in all appropriate files. Data can be parsed by external programs without explicit knowledge of ExperiBase itself.
7. Because individual images are most often parts of larger collections of image objects, study and series information must be embedded into every image information object.
8. Security is included through the Administration metadata package.