BioDataAnalysis GmbH

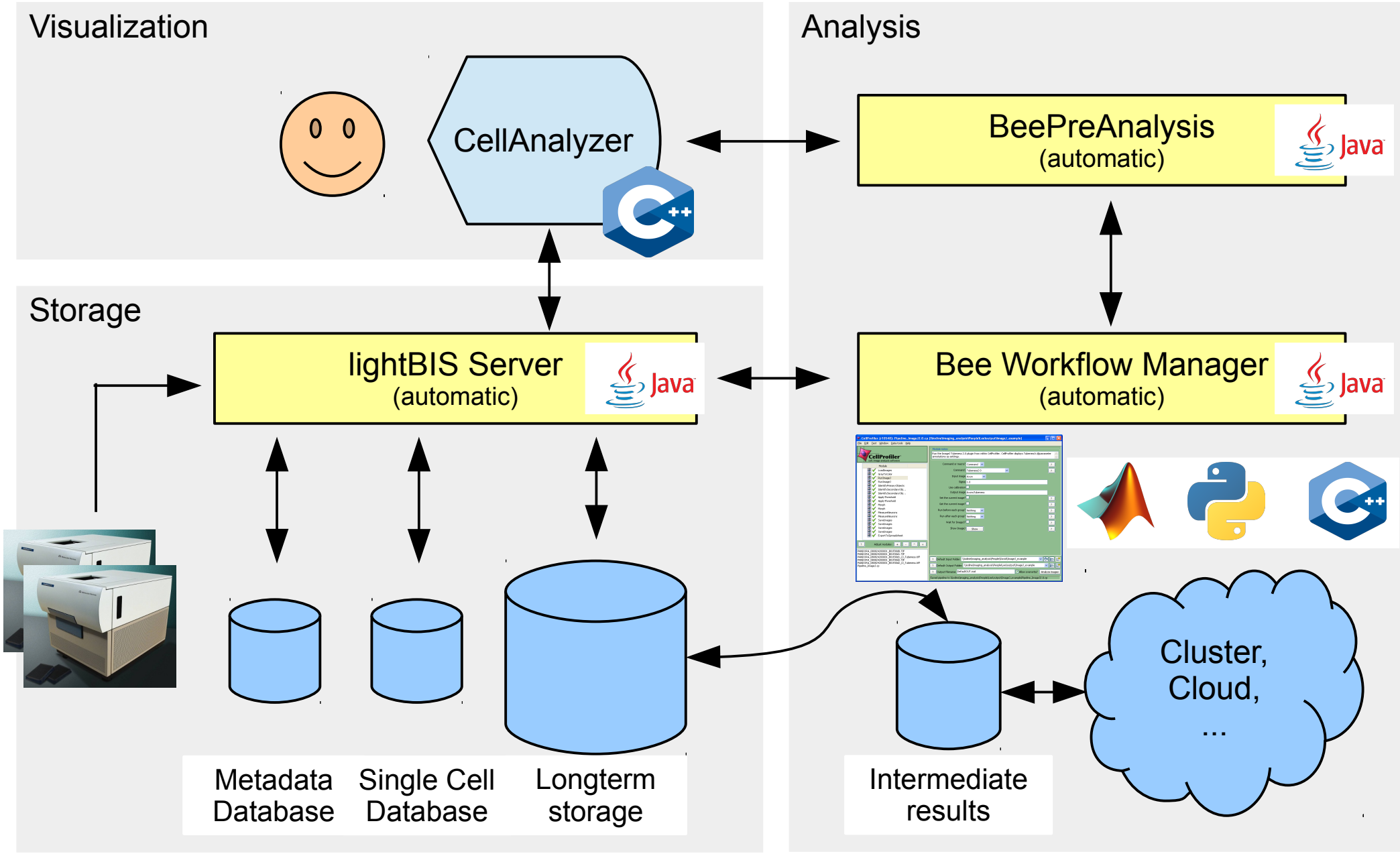
Next Generation Bio-Medical Image Analysis And Data Mining

Mario Emmenlauer, BioDataAnalysis GmbH, 10/2018

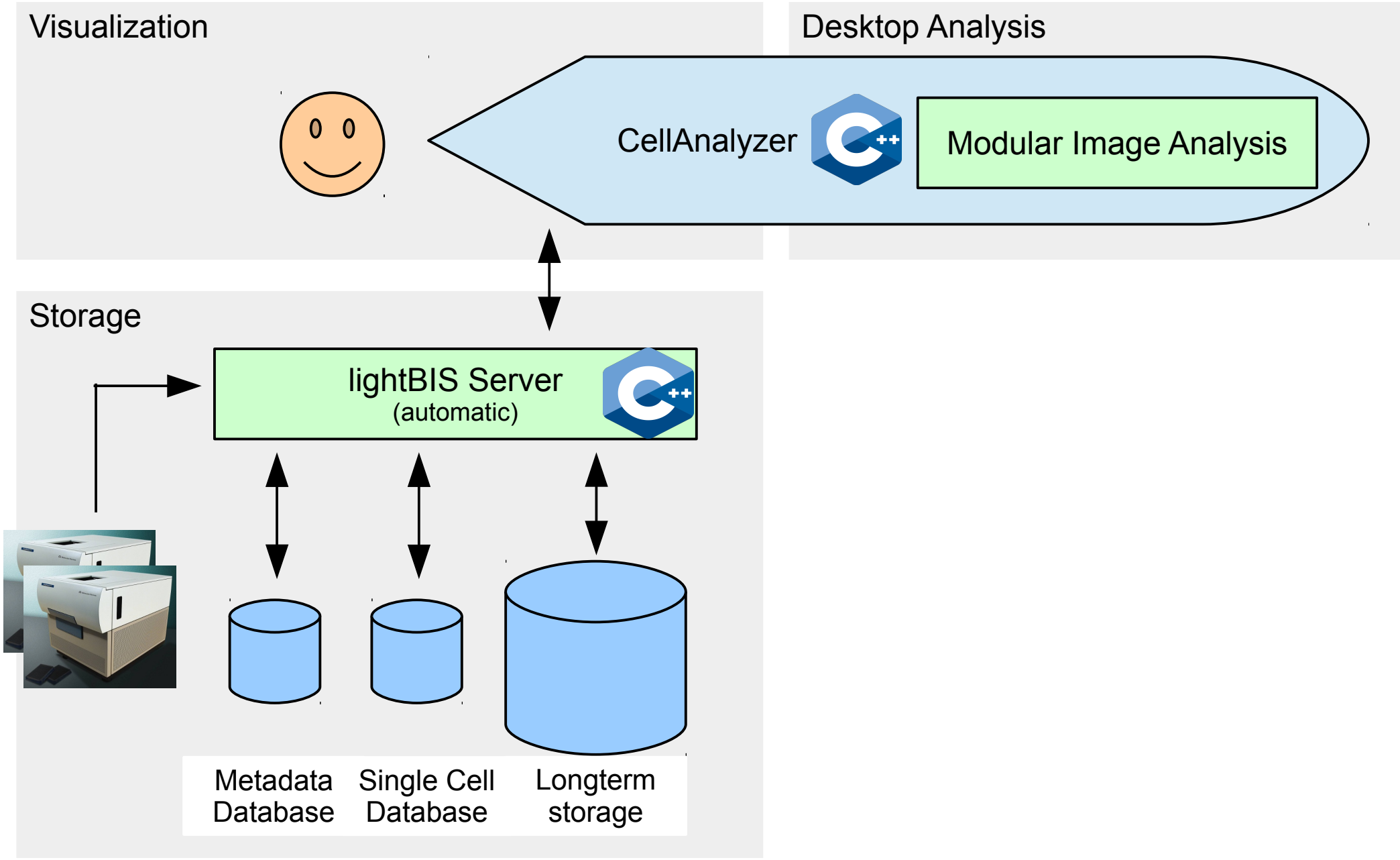
Software News and Current Status

- Software Stack Simplification
  - Better usability for “smaller” setups without cluster
- Shading Correction Increased Sensitivity
  - Using BaSiC shading correction to significantly increase sensitivity
- Segmentation Method Improvements
  - Implementation of standard and modern methods in C++
  - Student research project for assay optimization

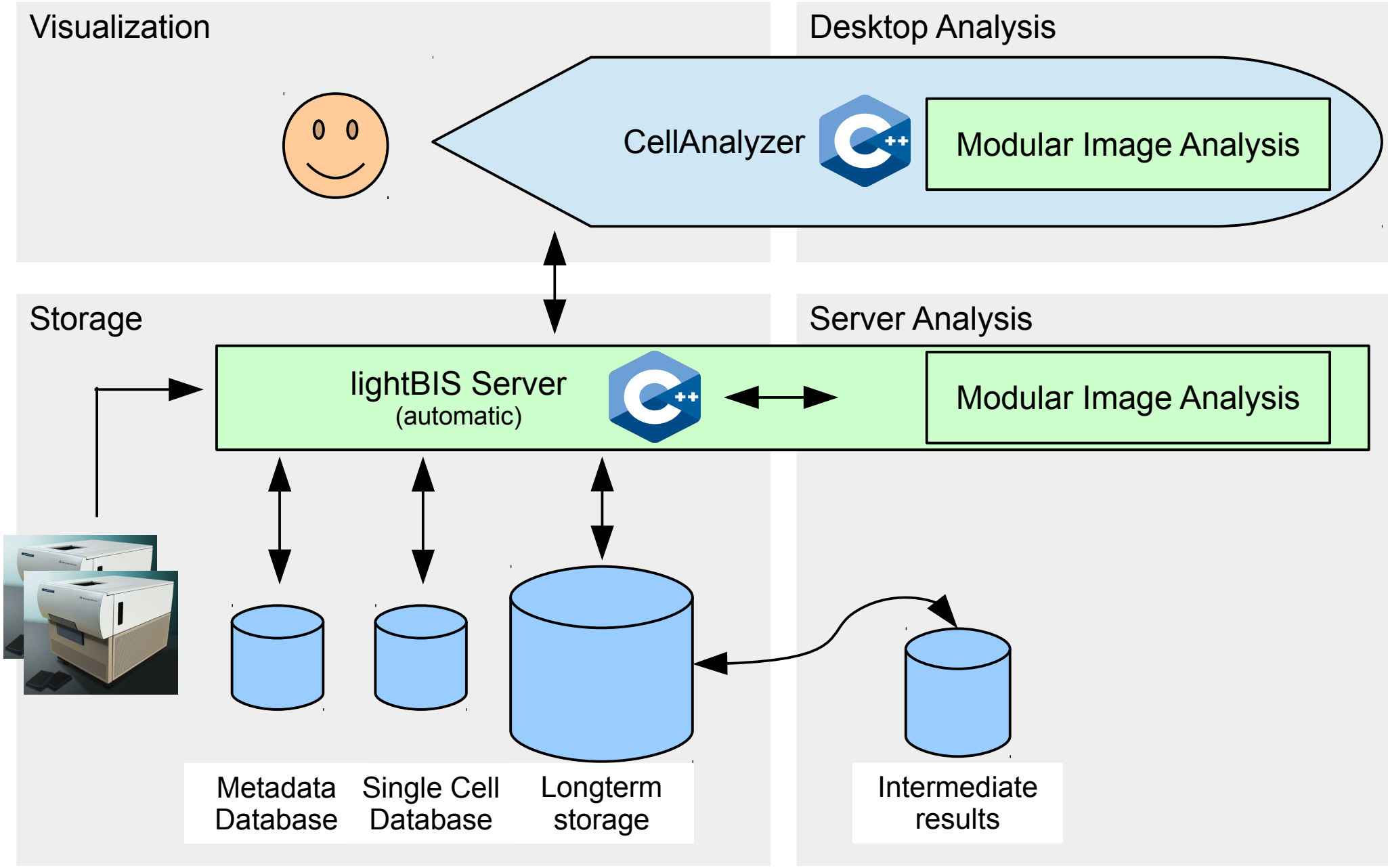
Software Stack at the Beginning of 2018



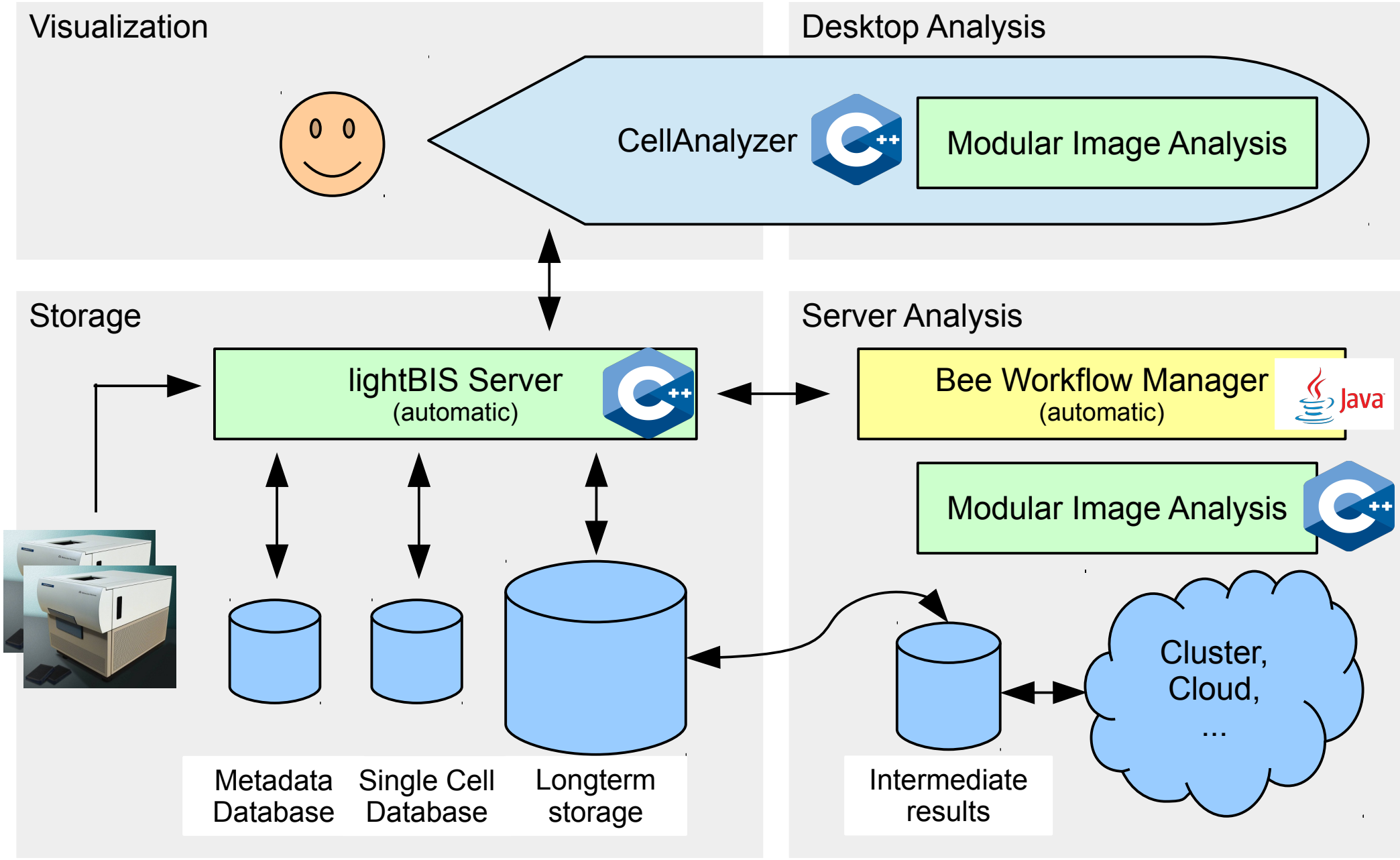
New, Simplified Software Stack for Desktop



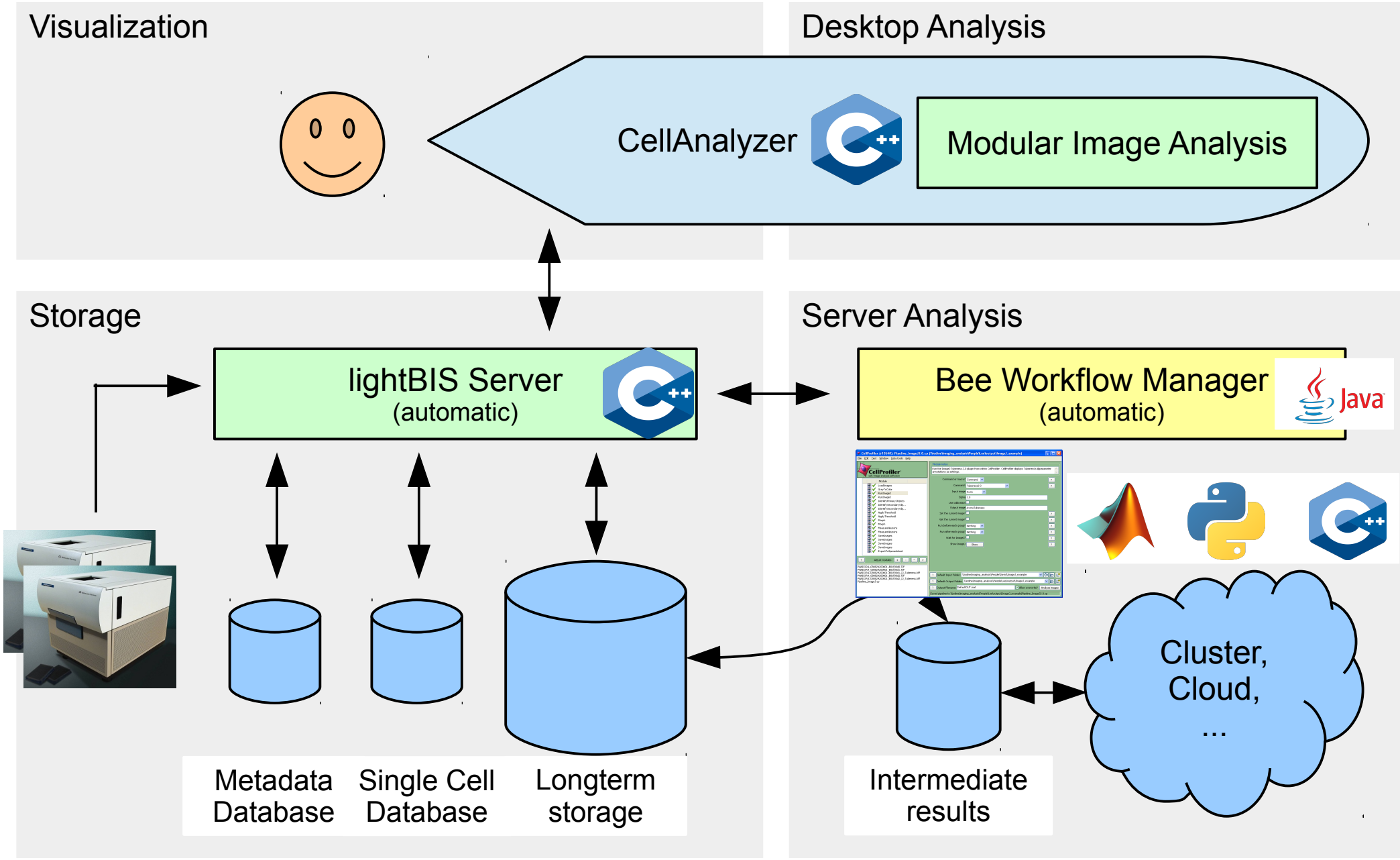
New, Simplified Software Stack for Server



New, Simplified Software Stack for Cluster

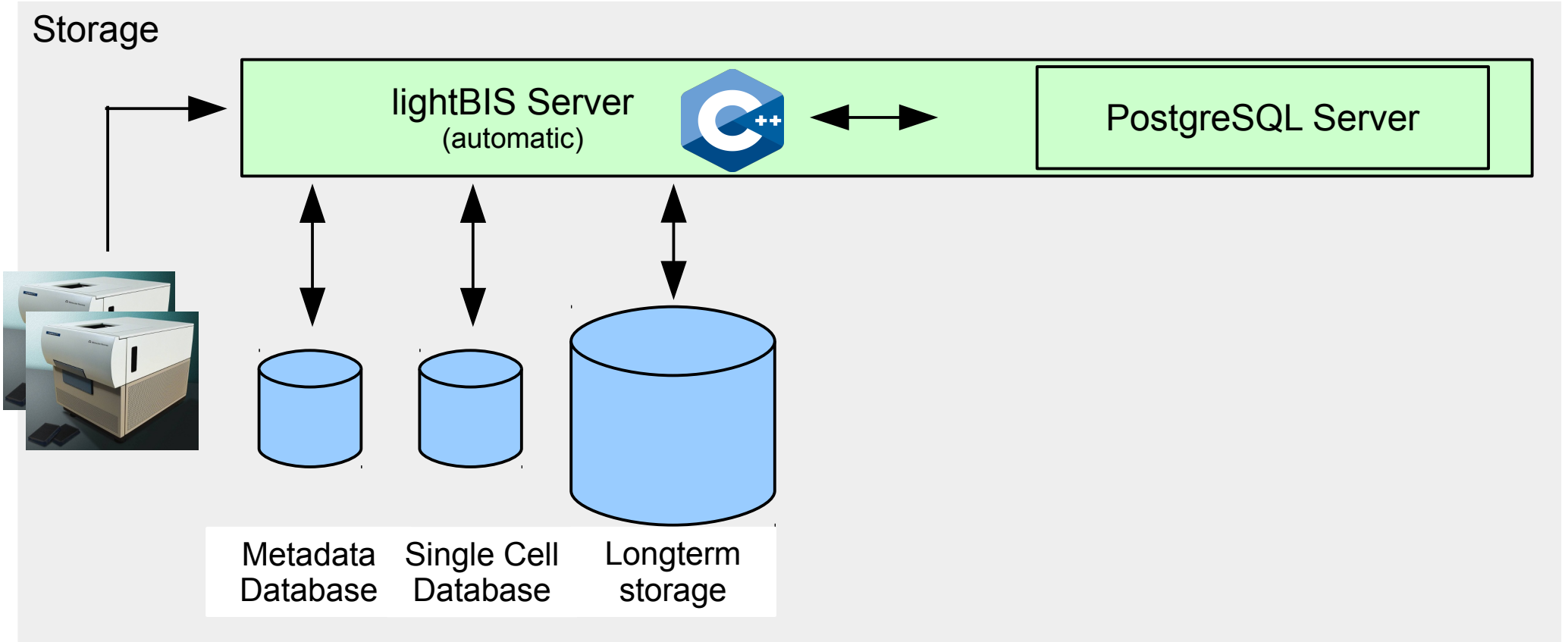


New, Simplified Software Stack for Cluster



Better Integration of PostgreSQL database

- PostgreSQL is now a direct sub-process of LightBIS Server
  - Better control of starting / stopping PostgreSQL
  - No administrators permissions required



Software News and Current Status

- Software Stack Simplification
  - Better usability for “smaller” setups without cluster
- Shading Correction Increased Sensitivity
  - Using BaSiC shading correction to significantly increase sensitivity
- Segmentation Method Improvements
  - Implementation of standard and modern methods in C++
  - Student research project for assay optimization

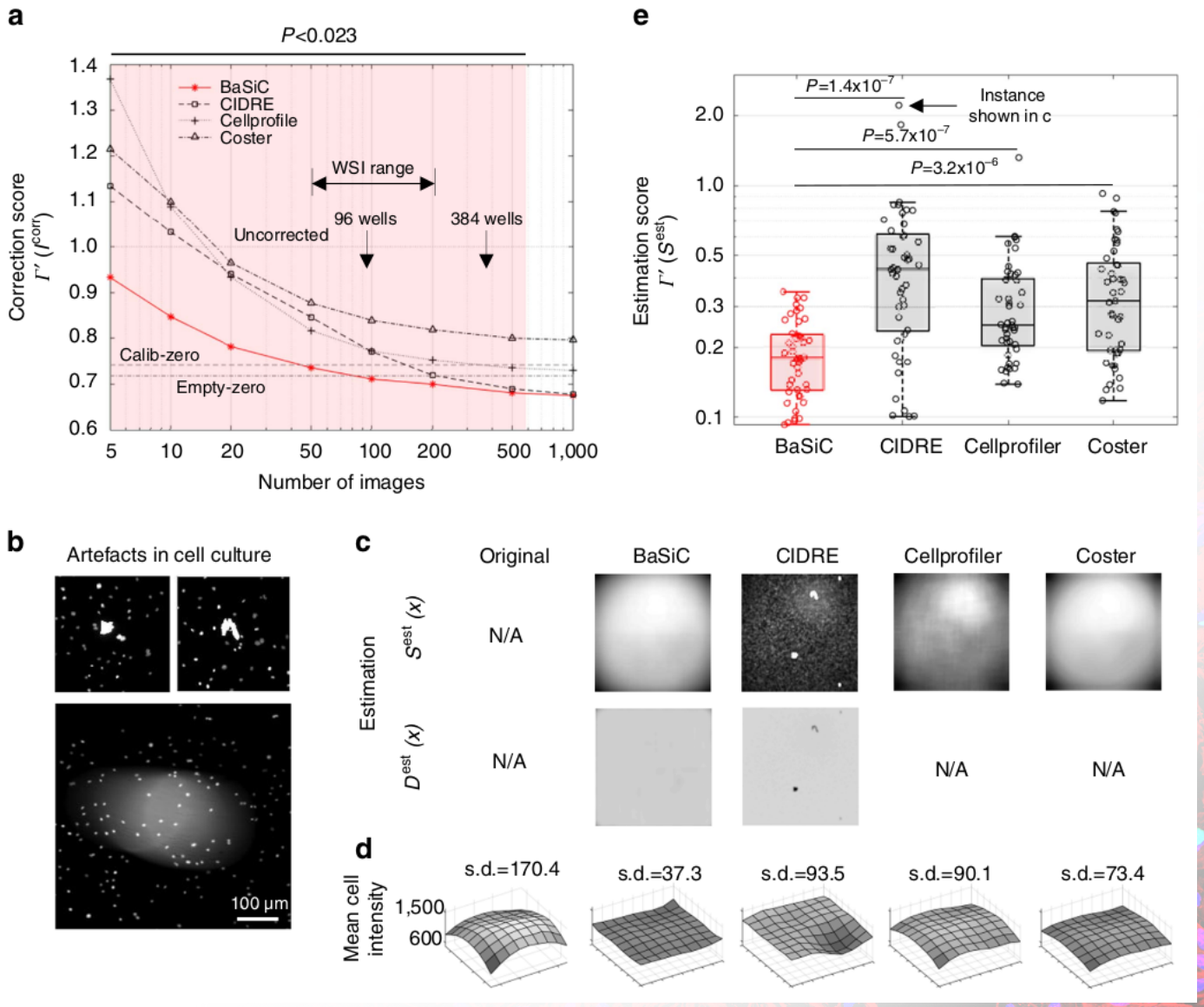
Increasing Sensitivity of the Shading Correction

- Cidre shading correction is very accurate, but has two limitations:
  - The number of images required for good convergence is relatively high
  - It has only limited support for time series

- BaSiC shading correction, Tingying Peng, Helmholtz Zentrum München
  - Achieves high accuracy with significantly fewer input images
  - Is more robust against artefacts
  - Can correct temporal drift in time-lapse microscopy

- Current status:
  - Performs well in our tests, converges to a good model with significantly less images
  - Implementation in C++ currently ongoing

BaSiC Shading Correction



Software News and Current Status

- Software Stack Simplification
  - Better usability for “smaller” setups without cluster
- Shading Correction Increased Sensitivity
  - Using BaSiC shading correction to significantly increase sensitivity
- Segmentation Method Improvements
  - Implementation of standard and modern methods in C++
  - Student research project for assay optimization

Segmentation Method Improvements

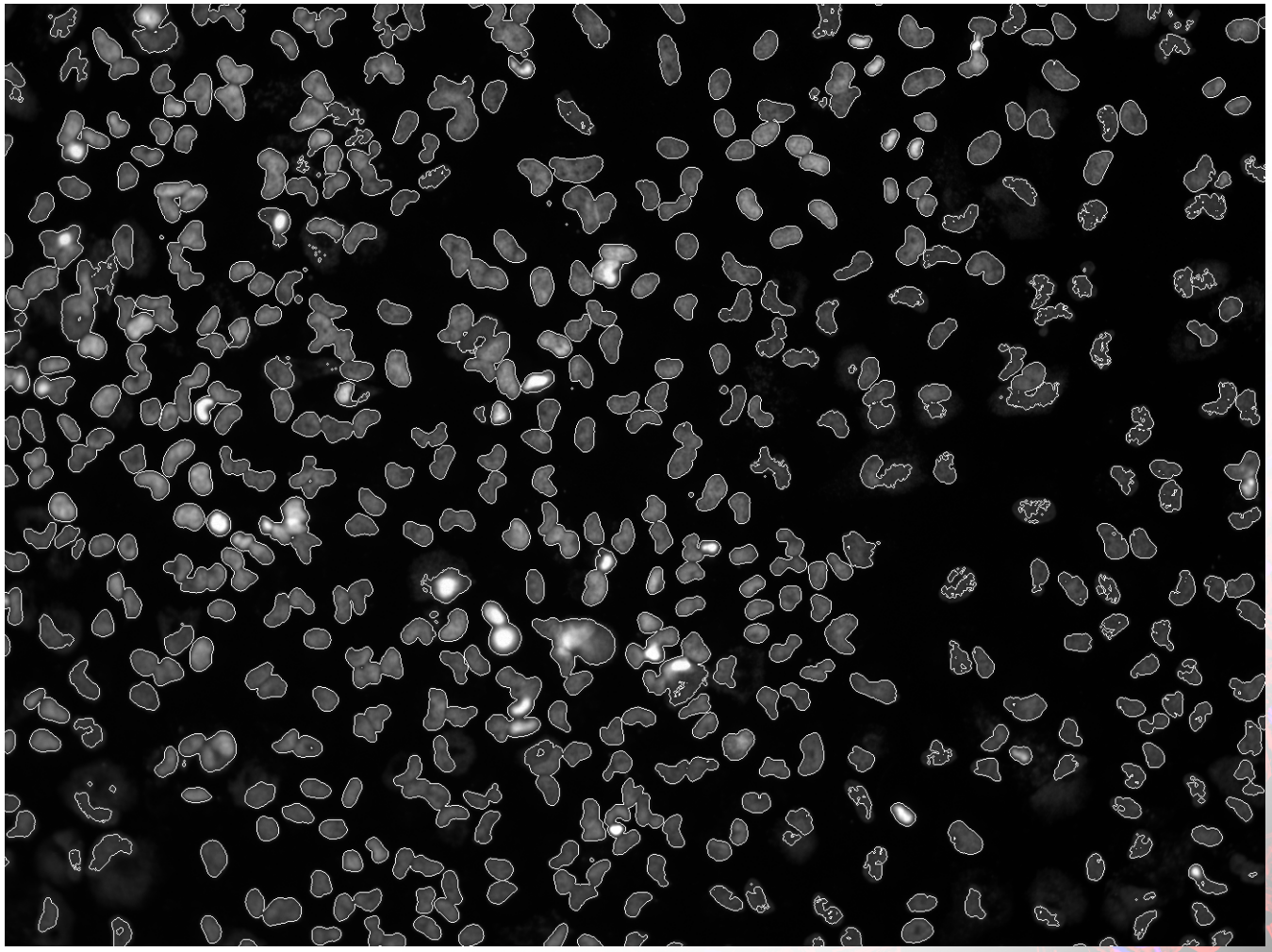
- Segmentation methods and their domains:
  - Fluorescence microscopy: **CellProfiler** is our reference and a “quasi-standard”.
  - CellProfiler uses intensity-based segmentation with limited support for shape.
  - For brightfield segmentation, **Ilastik** pixel classification is better by integrating “tissue thickness” and “texture”.
  - Darkfield and contrast microscopy are challenging to segment and at this time are not in our focus.

- Current status of our C++ image analysis:
  - We can cover all of the relevant CellProfiler segmentation methods: OTSU’s, Ridler-Calvard, Kapur, and Watershed.
  - We have two newer methods that support spacial information in addition to intensity: Superpixels and Graph-Cut.
  - Currently we do not cover: pixel classification for improved brightfield segmentation, darkfield segmentation, and contrast microscopy segmentation.

Segmentation Methods and their Domains

- No “silver bullet” segmentation can cover all bio-medical assays
  - Achieving good segmentation is very problem specific. Compare i.e. neurons vs fibroplasts vs actin vs …
- Comparing segmentation results is difficult
  - Visual inspection is very time consuming and subjective
- Objective segmentation method comparison
  - We use now the Kaggle challenge metric to weight dissimilarities in segmentation (https://www.kaggle.com/).
  - We will generate ground truth of “good” segmentation for different assays.

Example: OTSU's segmentation (no shading correction)



Objective segmentation method comparison

- Working student Adria Font Calvarons
  - TUM masters student with focus on bio-medical image analysis in C++.
  - Works 20hrs/week as a working student.
  - Works 10hrs/week on a semester practical for image segmentation.