

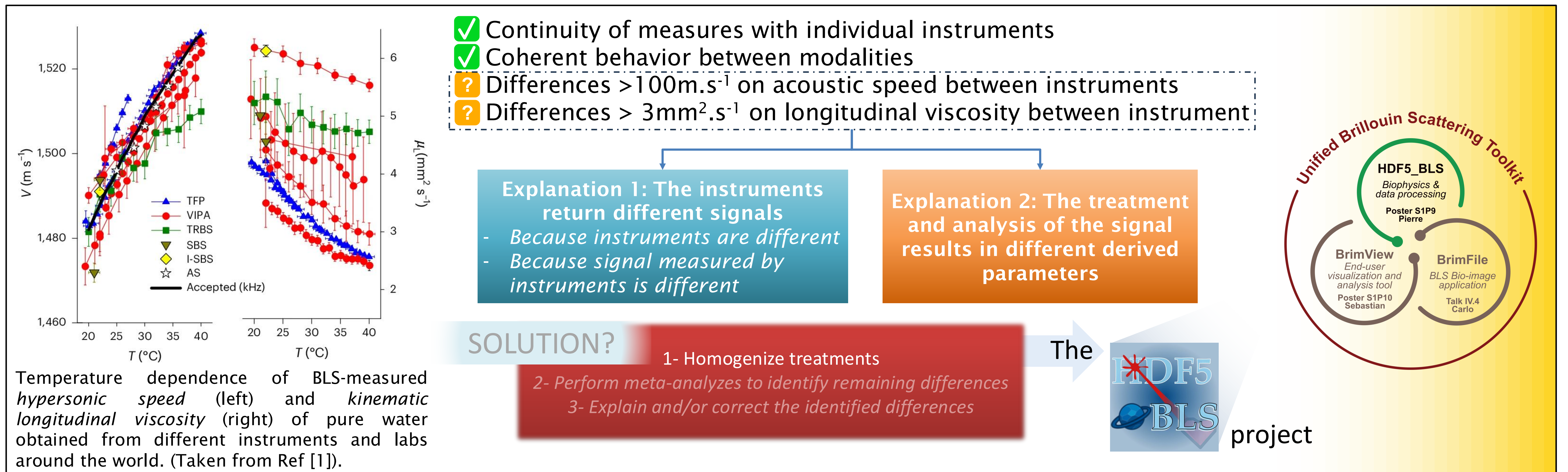
Universal data formats, analysis protocols, and visualization tools for Brillouin Light Scattering microscopy and spectroscopy

Pierre Bouvet¹, Carlo Bevilacqua², Sebastian Hambura², Sal La Cavera³, Robert Prevedel^{2,4}, Kareem Elsayad¹

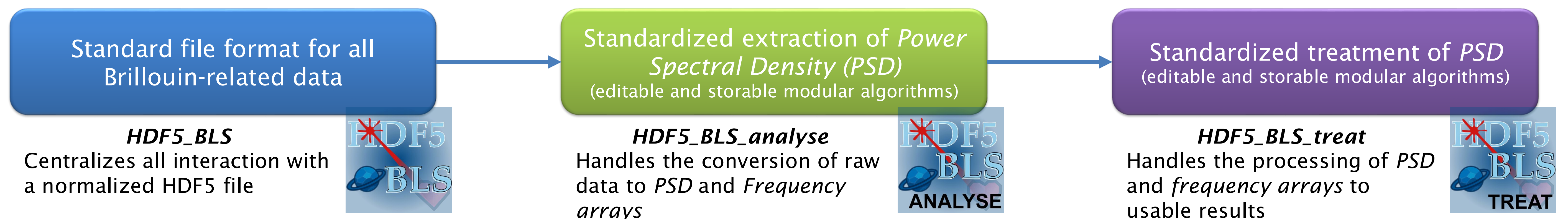
¹Division of Anatomy, Center for Anatomy and Cell Biology, Medical University of Vienna, Austria
²Cell Biology and Biophysics Unit, European Molecular Biology Laboratory, Heidelberg, Germany
³Optics & Photonics Group, Faculty of Engineering, University of Nottingham, Nottingham, UK.
⁴German Center for Lung Research (DZL), Heidelberg, Germany.

Pierre.Bouvet@meduniwien.ac.at
 Carlo.Bevilacqua@embl.de
 Sebasitan.Hambura@embl.de

Salvatore.Lacaveraiiii@nottingham.ac.uk
 Prevedel@embl.de
 Kareem.Elsayad@meduniwien.ac.at



Vision of the HDF5_BLS project: 3 independent and complementary Python libraries for the 3 steps in processing BLS data



The 3 pillars of HDF5_BLS

Universality
 All BLS experiments and projects can be stored with this solution:
 - Techniques (VIPA, TFP, SBS, Time Domain, ...)
 - Types of measurements (imaging, time evolutions, concentration/ perturbation dependent, ...)
 - Treatments/analysis: definition of standard algorithms, possibility to define custom ones, ability to save them both as standalone files and in the metadata of your measure files

Unification
 • BLS measurements coupled with equivalent metadata-files
 • BLS datasets treated and analyzed with standardized functions and protocols
 • Uncertainties/errors calculated and documented the same way
 • Treatment and analysis protocols accompany data, can be modified, shared and criticized (constructively 😊)

Simplicity
 • **File architecture:** analogous to the file system of an OS where datasets store data, groups act as directories, attributes store metadata
 • **Human readability:** No constraint on names of elements
 • All metadata is quickly editable in an independent spreadsheet
 • **The 3 minutes rule:** It should be possible to understand how to create your custom files in less than 3 minutes! How did we do? ->

Frequently Asked Questions (FAQ)

- **Why use the HDF5 file format?**
 It's a hierarchical format used in scientific community, cross-platform, safe and usable with a large range of software
- **What are the limitations?**
 None: all datasets and attributes can be stored without reformatting, and nomenclature is not imposed
- **How does for my treatments?**
 Nothing, you can choose to store results obtained with your own algorithms instead of the ones developed in the project
- **What are typical use cases?**
 Store both your data and the parameter you used for your experiment together. Store the results with your data (including results coming from different algorithms). Compare results of same experiments done by different people. Share data with collaborators and possibly editors. Standardize your processing steps. Prepare the ground for meta-analyses.
- **I have the best algorithm in the world; can I add it to the project?**
 Sure, just send an email to Pierre ☺
- **I am a spectrometer manufacturer, can I use this solution, can I expand on it?**
 Yes and yes, the project is under a GPL 3 license.
- **I have a custom solution; can we somehow make it compatible?**
 Yes, the HDF5_BLS project is the most basic and general solution for storing all BLS-related data. The only differences with the classic storage of data in a directory is the ability to associate metadata to individual experiments, and differentiate datasets by their type (PSD, Frequency, shift, ...)
- **What's the difference between the HDF5_BLS project and Brim [2]?**
 Brim is a format dedicated to storing a stack of hyperspectral Brillouin images, particularly for spatial mappings. HDF5_BLS aims at (1) storing any Brillouin-related data, with any relevant complimentary data (fluorescence images, temperature values associated with measuring points...) and (2) proposing solutions for unifying the processing of BLS data. Brim is based on a linear file structure, which is suitable for most imaging experiments studying at most single-parameter evolutions whereas HDF5_BLS uses a hierarchical structure, allowing storage of files with arbitrary complexity, from single spectra to multi-parameter studies combining different modalities. In short, Brim is made to easily integrate in the workflows of non-Brillouin experts relying on Brillouin imaging for their studies whereas HDF5_BLS targets the community of BLS researchers. Note that you can export Brim files from the HDF5_BLS library.

The (near) future : HDF5_BLS - The GUI

A Graphical User Interface (GUI) made with Qt to interface the project (HDF5 file and processing steps) in a script-free way. The project is under development but can already be run (from source) and tested -> Ask Pierre for demo!

+info and updates

Where do we go from here

- Scenario 1: This solution gains in popularity -> we build a new community-wide project to identify the causes of the differences between devices -> we find solutions to reduce or correct these differences -> we move towards establishing BLS as a new standard method for quantifying mechanical properties
- Scenario 2: This solution is not used -> Wow, this was a great poster!

[1] Bouvet, P. et al *Nature Photonics* 19, no. 7 (2025): 681-91.
 [2] Bevilacqua, C et al *Arxiv:2509:07566*

