CRITICAL UPDATE: Use new XMALab software for marker-based XROMM, and also for undistorting and calibrating biplanar X-ray setups.

XMALab replaces MATLAB XrayProject. See Bitbucket XMALab wiki for XMALab User Manual (not this wiki).

Note: there is a Table of Contents we recommend you use to navigate this xrommwiki. The links on this page are obsolete.

X-Ray Reconstruction of Moving Morphology (XROMM) is an X-ray imaging and computational process that produces precise and accurate 3D movies of skeletal movement.

*OBSOLETE* Recent Changes and DOWNLOADS

Brown XROMM Short Courses

At Brown University we have developed three main approaches to XROMM:

1) Marker-based XROMM workflow (Brainerd et al., 2010)

2) Scientific Rotoscoping workflow, i.e. manual markerless XROMM (Gatesy et al., 2010)

3) XROMM AutoScoper software, i.e. automated markerless XROMM (Miranda et al., 2011)

New: XROMM Undistorter, stand-alone undistortion program

We have also developed the X-ray Motion Analysis Portal (XMA Portal) for storing, viewing and managing X-ray movie data and associated metadata.

Resources for Keck Foundation XROMM Core Facility

This wiki contains instructions and software downloads, contributed by many users. See www.xromm.org and the publications below for general information about XROMM.


