

X-Ray Reconstruction of Moving Morphology (XROMM)

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

XMA Lab replaces MATLAB XrayProject. See Bitbucket XMA Lab wiki for XMA Lab 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.

*z_ *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.

Brainerd, E.L., D.B. Baier, S.M. Gatesy, T.L. Hedrick, K.A. Metzger, S.L. Gilbert, and J.J. Crisco. (2010) X-ray Reconstruction of Moving Morphology (XROMM): precision, accuracy and applications in comparative biomechanics research. *Journal of Experimental Zoology*, 313A: 262-279.

Gatesy S.M., Baier D.B., Jenkins F.A., Dial K.P. (2010) Scientific rotoscoping: a morphology-based method of 3-D motion analysis and visualization. *Journal of Experimental Zoology*, 313A:244-261.

Miranda, D.L., Schwartz, J.B., Loomis, A.C., Brainerd, E.L., Fleming, B.C., Crisco, J.J. (2011) Static and Dynamic Error of a Biplanar Videoradiography System Using Marker-Based and Markerless Tracking Techniques. *Journal of Biomechanical Engineering*, 133 (12): 1-8.

Knorlein, B.J., Baier, D.B., Gatesy, S.M., Laurence-Chasen, J.D. and Brainerd, E.L. 2016. Validation of XMA Lab software for marker-based XROMM. *Journal of Experimental Biology*, 219: 3701-3711. doi: 10.1242/jeb.145383.
