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URL: <http://biology.mcgill.ca/faculty/abouheif/> under Programs and Datasets

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Characterizing the phenotype is fundamental in several fields of biology, ranging from species identification to ontogeny description. Two methods are predominantly used by researchers for anatomical descriptions of body parts: standard linear measurements and geometric morphometrics (GM) (Zelditch et al. 2004). The revolution of GM in the last two decades has brought to quantitative morphometrics a more rigorous framework, but despite this major gain some obstacles remain true. Among those, the availability of biologically relevant homologous landmarks (Zelditch et al. 2004) and the researcher's bias in landmark assessment (personal observation) could be major, especially for structures presenting curved outlines. Elliptical harmonics are the two dimensional extension of Fourier techniques (Kuhl and Giardina 1982) and have been used extensively in medical research to analyze anatomical images. Despite this recognized efficacy, their use in biology still remains very limited. Recently, Shen et al. (2008) have proposed a proficient framework for the implementation of spherical harmonics (3D extension of Fourier techniques) but the acquisition of 3D data is resource demanding and many problems faced by biologists can be resolved by using a simpler 2D approach.

Here we present eFFECTIV, a software implementing an algorithm digitizing contours and calculating 2D Fourier descriptors for almost any shape. The software eFFECTIV is composed of two modules, EFT and DataInput, both supported by a front-end graphical user interface (GUI), written in Matlab (R2008b) and compiled to be used without a Matlab licence. The core of the software, the EFT module, works in three steps: first, the image contour is segmented using an active contour method, commonly referred to as a *snake* (Kass et al. 1987), which aligns itself onto image boundaries based on the image histogram. Subsequently, each contour pixel is given a pair of Cartesian coordinates. Secondly, two parametric functions are used to model the chain-encoded contour. The accuracy of the parametrization can be increased by adding terms (harmonics) into the Fourier equations. This parametrization outputs a set of Fourier coefficients that are descriptors of the original contour and can further be treated as biological variables. The module EFT also provides a function which estimates the required number of harmonics to explain a user-defined percentage of the variance. Thirdly, a reverse Fourier analysis can be performed to recreate the contour based on the Fourier coefficients estimated in step 2. This allows for a visual appreciation of the parametrization efficacy. The module DataInput complements the core module by performing a reverse Fourier transform for a given set of Fourier coefficients, thus providing a reconstructed image from these coefficients. This option is particularly useful in the creation of an phenotypic average (mean) of a population based on the pooled and averaged Fourier coefficients of each respective individual.

#### References:

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