SUMMARY
This paper proposes a methodological pipeline to acquire data required to build a musculoskeletal model of the long fingers, and to obtain from this model information on joint motion behaviour, tendon excursion and moment arms. This paper is a feasibility study.

The protocol has been applied on a non pathological hand issue from a fresh-frozen specimen. Several CT-scan image sets have been acquired to collect the hand posture in various discrete positions. Data processing has been performed in a customized software interface called « lhpFusionBox » to create a specimen-specific model and to reconstruct a motion based on the collected discrete positions with the help of virtual palpation. Tendon information have been added based on anatomical knowledge obtained from dissections. Helical axis orientation has been used to orientate the anatomical frames used from motion representation. Biomechanical information such as motion behaviour and tendon moment arms have been then computed.

This protocol provide « noise-absent » and accurate datasets which have been processed to better visualization of the biomechanical parameters. This allow obtaining reliable helical axis usable to orientate the anatomical frames.. The obtained model seems to be accurate to be used in more complex modelling activities.

INTRODUCTION
Functional understanding of the hand is at the center of interest for many years. Several models have been developed in the recent years and are available from the literature. Nevertheless, each model shows limits and developing a model incorporating anatomical data, biomechanics and kinematics information, remains a real challenge. The ultimate aim is to create a model which is as anatomically correct as possible.

This paper presents a method relying on medical imaging to build a complete 3D model of the long fingers. It includes : bone morphology, tendon path and wrapping and joint kinematics. The method is currently limited to in vitro conditions, future work should allow to apply this method in vivo.

METHODS
Specimen. One hand of a fresh-frozen specimen was obtained from the ULB Body Donation program. Sawing occurred in the upper area of the forearm bones.

The specimen was mounted on a Plexiglas jig. Forearm bones and metacarpal bones were rigidly attached to the jig using pins inserted transversally in the relevant diaphysis. The various wrist and finger flexor and extensor tendons were attached to fishing wires to allow tendon loading using weights (around 100 gr for each tendon).

Medical imaging and 3D reconstruction. The above jig was then processed through medical imaging (CT-scan). The jig allowed to set each finger in various discrete positions. One Ct-Scan dataset was obtained for each discrete position. Collected positions were : five during finger flexion, three in extension and three in abduction / adduction. The image data were then segmented (software: Amira®) to obtained bone 3D models that were exported (VRML format) for further use.

Digital segments. All reconstructed long finger bones (2nd, 3rd, 4th and 5th digital rays) were imported in a customized software (lhpFusionBox [3]) for visualisation and processing. The model includes the metacarpals bones and all phalanges (proximal, intermediate and distal) with their respective joints. Sesamoid bones were available at the level of the 2nd and 5th fingers for this particular specimen.

Virtual palpation. For each discrete position, anatomical landmarks (ALs) were added on each available bones using virtual palpation [1]. Virtual palpation allows to obtain the 3D coordinates of the palpated landmarks.

Motion concatenation. ALs coordinates were concatenated into one unique structure describing the different discrete positions of each individual bone segment.

Coordinate system and helical axis. From the above AL placement the mean helical axis was determined for each joint (metacarpo-phalangeal, proximal and distal interphalangeal joints). Then, for each joint proximal segment, one anatomical coordinate system was constructed using the above helical axis to orientate the Z-axis (flexion/extension axis) and to set the origin (at the helical axis pivot point).

Muscle information. Muscle lines-of-action and wrapping [5] were added to our model using information obtained during dissections. Validation of these muscle information by medical imaging is currently running to obtain a more realistic and reliable model.

RESULTS AND DISCUSSION
Results shows that using the helical axis as support for Z-axis orientation and origin setting is quite relevant since it optimizes the representation of the main degree-of-freedom motion (flexion-extension) in the main frame axis (Z-axis).

This protocol is robust and allows to acquire reliable data at both anatomical and kinematic levels. The absence of "noise" in the data set allows the movement to be fluid and therefore to perform various operations such as measuring...
tendon lever arms [2] of intrinsic and extrinsic muscles of the fingers which is currently our interest (Figure 1). Advanced results will be presented at the conference.

CONCLUSIONS
In order to develop long finger model that would be a detailed as possible, this method allows us to collect the required initial data which will form the basis of our future modelling work.

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REFERENCES

Figure 1. Model and results (for the second finger). A. The final model with mean helical axis (dark cyan) for the Proximal Interphalangeal (PIP) joint. Anatomical axes for the entire finger are also visible. Two muscle tendons are displayed: Extensor Digitorum (ED, in orange) and the Flexor Digitorum Profundis (FDP, in red). B. Tree of imported data and constructed models. C: PIP Motion representation (here OVP representation). D: ED (red curve) and FDP (green curve) moment arms determined using an indirect method (derivative of tendon excursion [see E] on instantaneous helical axis rotation [see F]). E: ED tendon excursion. F: instantaneous helical axis rotation.