BLIND INFERENCE OF TENDON NETWORKS THROUGH MINIMAL TESTING

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INTRODUCTION

Hand manipulation in humans requires intricate neuromuscular interactions, which are cardinally dependent on the actuation of the *extensor mechanism*, a network of tendons acting on the phalanges. Thus, malfunction of this tendon network can critically impair manipulation. We seek to (a) decipher the functional structure of the *extensor mechanism* (i.e., topological and parameter values, often approximated by Winslow's Rhombus (Valero-Cuevas et al, in Press)) by observing the functional behavior of the digits using sparse data obtained through a set of abduction, adduction, extension and flexion tasks, (b) infer such networks via minimal testing, and (c) recognize how such networks and their functionality varies amongst healthy and diseased subjects. Here, we accomplish the first step towards this goal by using the exploration-estimation algorithm (Bongard and Lipson 2004) to simulate the inference of a hidden planar tendon network on the basis of space tests that record input-output forces.

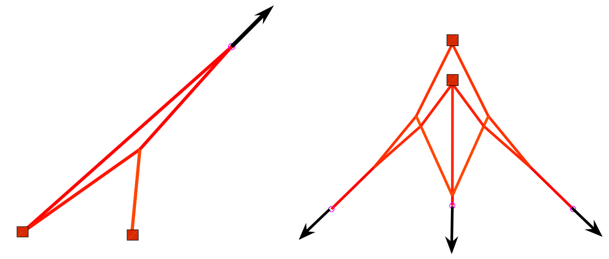
METHODS

The exploration-estimation algorithm **(**Valero-Cuevas et al, in Press**;** Bongard and Lipson 2004**)** extracts the functional topology of a hidden system, treated as a "target" or a "black box," through a minimal number of tests (i.e., measured input-output data sets). The algorithm co-evolves populations of candidate networks and actuation tests sequentially such that more informative (as opposed to random) tests can be applied to the hidden system. This helps to evolve networks using a minimum number of tests. For problems involving large deformations, gradient-based methods—being point-to-point searches—will stall when the deformed string configurations are non-unique (i.e., simulations do not converge within specified tolerance), and function derivatives cannot be computed.

The algorithm is initialized with a random test consisting of a force input on the target and its functional response (force output). A pre-specified number of candidate networks are evolved from divided subpopulations to satisfy this input-output test. The evolved candidate networks usually vary in their simulated output force response to the same set of input forces. An input force set that causes more discrepancy in functional response (output forces) between the networks is considered more informative. We employ the variances of output forces in the candidate networks to find the most informative set of input forces to be applied to the target system next. Once identified, the new input forces are applied to the target system to procure its output force response, the experimental data is augmented by it, and then the networks are evolved to satisfy those cumulative data sets. The procedure of co-evolving networks and actuation tests continues until no further improvement in the functional behavior of the candidate networks when compared with the target is observed. Cross-validation is performed against an independent set of data extracted at the beginning of the evolution procedure.

RESULTS AND DISCUSSION

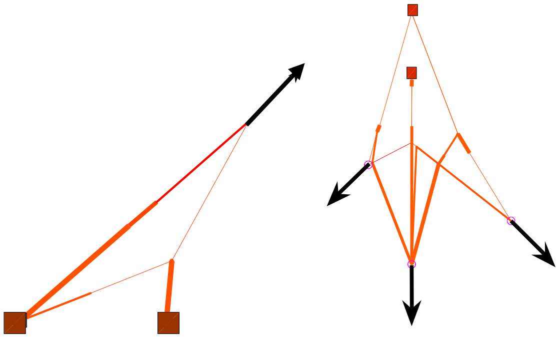
We illustrate the extraction of network topology and parameter values using the two target networks shown in Figure 1. The arrows show the directions of input forces, "squares" depict grounded nodes where reaction (output) forces are measured.



(a) (b)

Figure 1: (a) The 'A' target network, (b) The Winslow's target network.

Using the exploration-estimation algorithm described above and in detail in (Bongard & Lipson 2004), the respective networks evolved from the informative sparse data sets are shown in Figure 2. Note that the networks are functionally equivalent (Figure 3) and topologically very similar to their respective targets (cf. Figures 1 & 2).



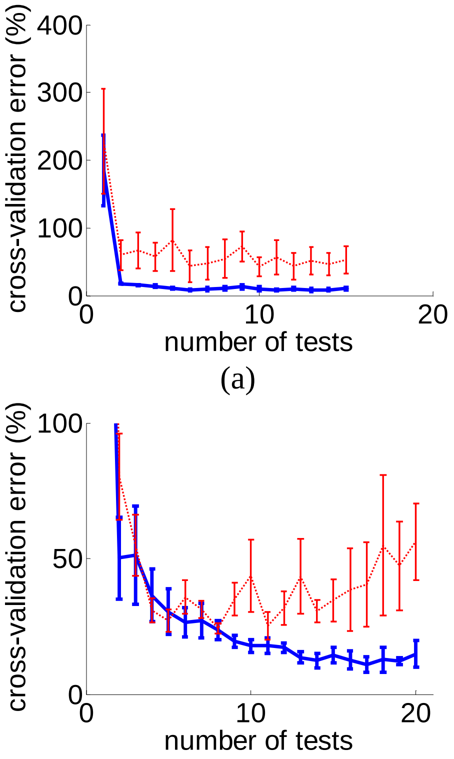
(a) (b)

Figure 2: The best evolved network obtained via minimal testing (a) of the 'A' target network; (b) of the Winslow's target network.

The cross validation errors for the two networks are shown in Figure 3, as a function of tests applied to the target system. Figure 3 compares two cases, one in which informative sets are used (solid/blue) and the other wherein random tests are employed (dashed/red). Informative tests perform statistically better than random tests on two counts (a) the cross validation errors are much smaller and (b) they converge much earlier. For the 'A' target, about 5% cross validation error is achieved using only three tests while the evolution of Winslow's rhombus takes only about 15 tests.

SUMMARY/CONCLUSIONS

We demonstrate feasibility, in simulation, in extracting tendon networks from informative sparse data, with lower cross validation errors than random tests. As a next step, we will validate our novel methods in anatomical specimens.



(a)

(b)

Figure 3: (a) Cross-validation error for the 'A' target network (b) the same for the Winslow's target network.

REFERENCES

1.- Valero-Cuevas FJ, Anand V, Saxena A, and Lipson H. *IEEE Trans Biomed Eng*. In Press
2.- Bongard JC and H Lipson, (2004) *Genetic and Evolutionary Computation Conference*, (GECCO '04), pp. 333-345.

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