

Network of anatomical texts (NAnaTex), an open-source project for visualizing the interaction between anatomical terms

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Abstract Anatomy is the science and art of understanding the structure of the body and its components in relation to the functions of the whole-body system. Medicine is based on a deep understanding of anatomy, but quite a few introductory-level learners are overwhelmed by the sheer amount of anatomical terminology that must be understood, so they regard anatomy as a dull and dense subject. To help them learn anatomical terms in a more contextual way, we started a new open-source project, the Network of Anatomical Texts (NAnaTex), which visualizes relationships of body components by integrating text-based anatomical information using Cytoscape, a network visualization software platform. Here, we present a network of bones and muscles produced from literature descriptions. As this network is primarily text-based and does not require any programming knowledge, it is easy to implement new functions or provide extra information by making changes to the original text files. To facilitate collaborations, we deposited the source code files for the network into the GitHub repository (<https://github.com/ryusukemomota/nanatex>) so that anybody can participate in the evolution of the network and use it for their own non-profit purposes. This project should help not only introductory-level learners but also professional medical practitioners, who could use it as a quick reference.

Keywords Anatomical terms · Cytoscape · GitHub · Network analysis · Open source

Introduction

Network analysis is an area of mathematics which examines the structure of the relationships and complex interactions among multiple components. Such analyses have been used in many fields, such as the social sciences, and have often revealed unexpected aspects of the issues and helped developing new strategies (Manrique et al. 2016). In biology, network analyses of molecular interactions have been carried out to find molecules or pathways that could potentially be exploited for pharmaceutical purposes (Chen et al. 2016; Zhang et al. 2016). Anatomical network analysis (AnNA) has recently been introduced for use in gross anatomical studies. The resulting detailed regional anatomical observations have demonstrated the modularity of the musculoskeletal system and have allowed the morphological changes that have occurred over the course of evolution to be elucidated, as well as the morphological changes associated with a particular pathological condition (Esteve-Altava et al. 2015; Diogo et al. 2015).

Due to the availability of advanced information technology, text-based anatomical information has become abundant. Indeed, there is so much of this information that it can overwhelm introductory-level learners of anatomy. Therefore, we attempted to integrate information on the bone and muscular interactions of the human body that is available in literature descriptions using Cytoscape, a network visualization software platform. Cytoscape was originally created to visualize biological molecular interactions, but it has since evolved to become a platform for performing any network analysis due to its user-friendly interface and

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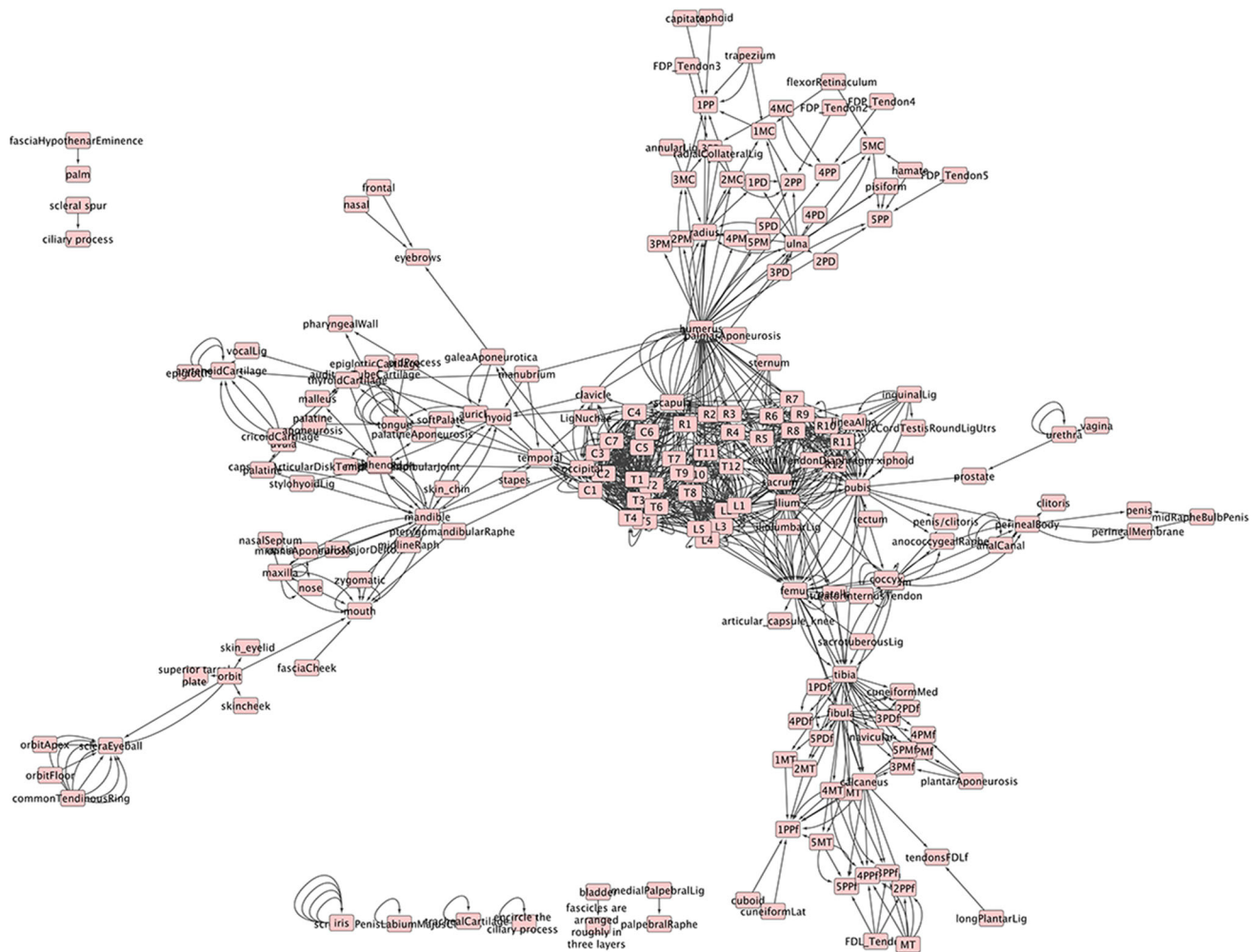


Fig. 1 An overview of the network displayed in the “Organic” style of yFiles Layouts. Muscles (edges) are indicated by *directed arrows*; body components with muscle attachment sites, mainly constituted by

bones, are shown as *pink nodes*. Abbreviations used to label nodes are defined in the ESM

the ability to extend its functionality with many apps (Ono 2016; Bader et al. 2017; Shannon et al. 2003). In our analysis, we obtained a network consisting of 196 nodes with 1048 muscular interactions. Important components in the network were identified. Combined with the functions of Cytoscape, this network can be employed as a very useful learning resource and a quick graphical reference by simply adding more text information. To encourage contributions to this network and thus promote its development, we deposited the relevant files in the GitHub repository (<https://github.com/ryusukemomota/nanatex>).

Materials and methods

We found that the tables in the webpages of the University of Michigan Medical School were a very good resource, as they were packed with succinctly summarized anatomical

information (<http://www.med.umich.edu/lrc/coursepages/m1/anatomy2010/html/anatomytables/>). Therefore, we obtained the permission of Dr. Thomas Gest (Texas Tech University Health Sciences Center, Paul L. Foster School of Medicine) to use that information in this project. To prepare the data set, the tabulated data were extracted from the HTML files and transferred to Excel 2016 (Microsoft) for further manipulation. The “Origin” and “Insertion” columns were duplicated and renamed to create “Origin1” and “Insertion1” nodes, respectively. We used a simplified model in which each body part is assumed to represent a single node, so we extracted names of body parts and removed detailed descriptions of muscle attachment sites. We then unified terms by removing synonyms (e.g., “C1 for atlas” and “C2 for axis”). For muscles with multiple origins/insertions such as “rotatores” or “splenius,” we visually confirmed multiple “origin–insertion” relationships using a MeAV Anatomie 3D system (Panasonic

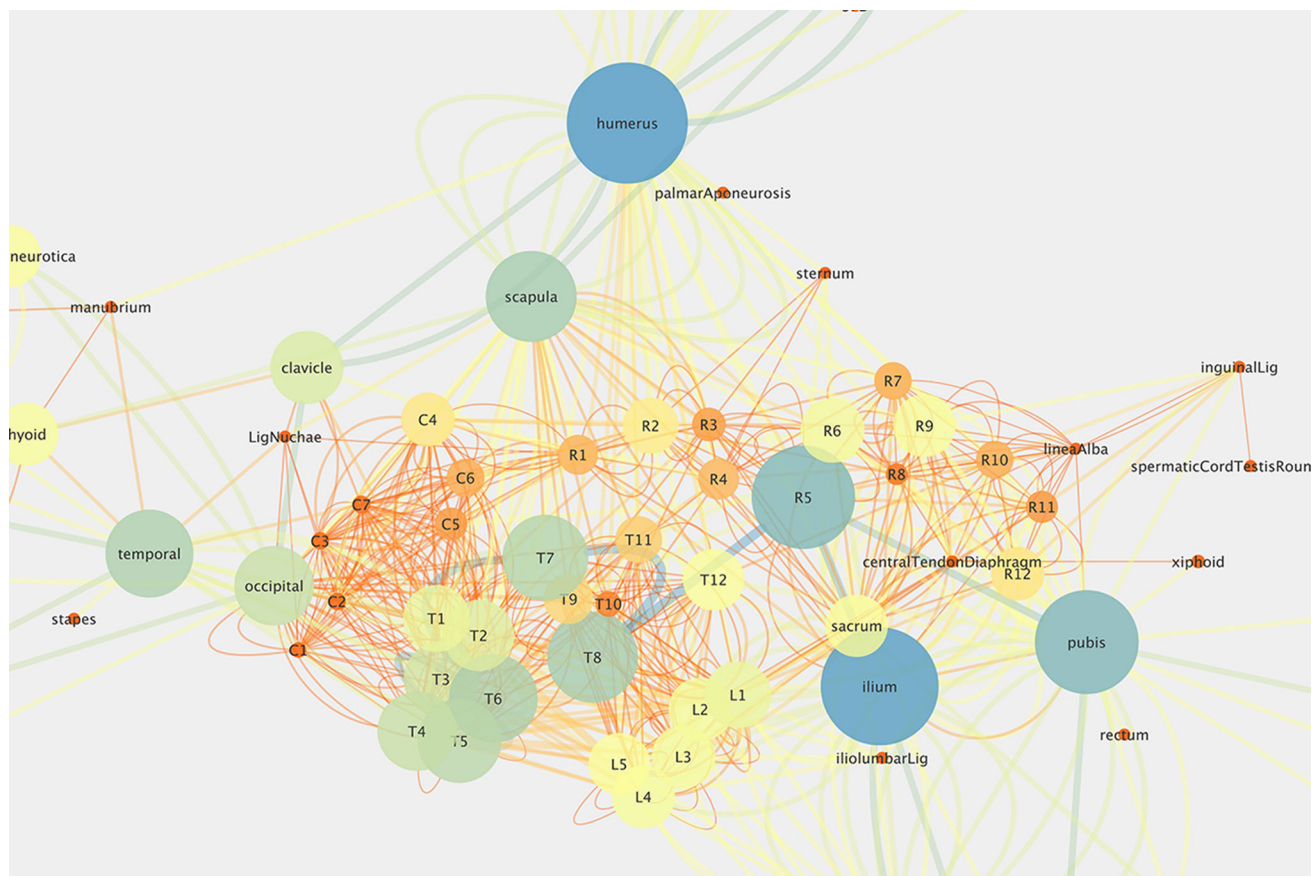


Fig. 2 Betweenness of nodes and edges. Betweenness is an index which describes how the network would be structurally affected if the node/edge was removed. The value of betweenness for a particular node

is indicated by both the size (small indicates a low value) and the color (which ranges from *dark red*, corresponding to a low value, to *dark blue*, corresponding to a high value) of the circle marking that node

Corporation and Okayama University), and generated a new row for each “origin–insertion” interaction. Thus, we obtained a table with 1048 muscles defined by “origin–insertion” interactions. The resulting *xlsx* file was imported and visualized by Cytoscape 3.5. We assumed that each muscle was defined by a record (row) defined by fields (columns). The fields “Origin1,” “Insertion1,” and “Muscle” were used as “Source Node,” “Target Node,” and “Edge,” respectively. The unmodified “Origin” and “Insertion” columns as well as the other columns, such as “Innervation,” “Artery,” and “Notes,” were also included as “Source Attribute,” “Target Attribute,” and “Edge Attribute,” respectively (see the Electronic supplementary material, ESM: NAnaTex.xlsx).

Results and discussion

Figure 1 shows a screenshot of the network displayed in the “Organic” style of yFiles Layouts. The central dense part mainly consists of vertebrae and ribs, suggesting that the bones and muscles of the trunk are tightly connected.

As expected, network analyses performed with NetworkAnalyzer (release 2.7) (Assenov et al. 2008) revealed that this dense region is a network consisting of 43 nodes with 612 edges and a higher average number of neighbors (16.23) than that for the whole network (6.71), indicating that the bones and muscles of the trunk are tightly connected and form a closed network. According to betweenness analysis, the ilium, humerus, pubis, and fifth rib showed the highest values in the whole network (Fig. 2 and the ESM). In the trunk network alone, the nodes for the ilium, fifth rib, and the muscle between them showed the highest values, indicating that these components are important in the trunk network.

We used the same labels as listed in the Wikipedia human skeleton section. Users can access Wikipedia for more information through “External Links.” In addition, users can look up words using the search window, which can be used to query not only the items on the screen but also the “Edge Attribute” descriptions hidden in the original text. For example, if a user looks for muscles innervated by the “radial nerve,” the muscles of interest are highlighted on the screen (Fig. 3), as well as other nerves,

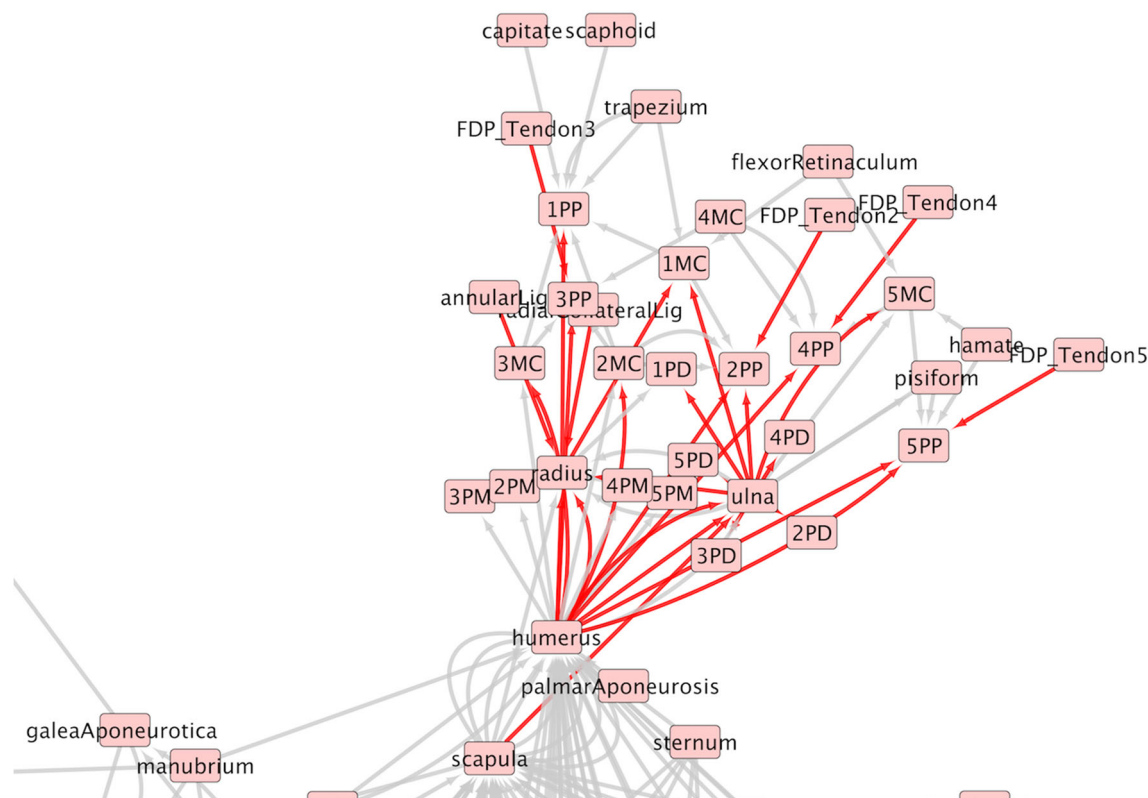


Fig. 3 An example of a query performed via the search window. Muscles innervated by the radial nerves are highlighted in *red*. The T8 node is shifted slightly to the left to show the edge from scapula to ulna (triceps brachii muscle)

arteries, and actions of the muscles. The graphical presentation of information helps users to grasp anatomical terminology; this is especially beneficial to introductory-level learners. Furthermore, since this network can be easily enhanced by adding more fields or text, it could be utilized as a platform for collaborative learning in anatomical curricula in order to promote active learning and understanding of anatomy; for instance, by encouraging students to implement new categories of related information such as diseases or physiology. As an example of how the contents of the network can be enhanced, we generated a JSON network file with information on the Foundational Model of Anatomy identifiers (FMA ID) and links to the FMA ontology data in Ontobee, a resource that integrates anatomical information based on terms and concepts (<http://www.ontobee.org/ontology/FMA>) (Rosse and Mejino 2003; Ong et al. 2017). Currently, we are in the process of evolving this preliminary network into a more informative one with a more attractive appearance, with the aim being to start a web service. We welcome you to use it and to develop it for your own projects. To this end, we deposited the relevant files and started an open-source project called NAnaTex (Network of Anatomical Texts) in the GitHub repository. Contributions to NAnaTex from other anatomists are encouraged, as they will cause NAnaTex to evolve.

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Compliance with ethical standards

Conflict of interest The author declares no conflict of interest.

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