LSO Pelvis/Scapula Activity

Activity 1: Pelvis and Scapula Anatomy

1.   Use the diagrams below to investigate the pelvis and scapula models and identify anatomical structures.

<table>
<tr><td>Articulated Pelvis
(anterior view)</td><td>Scapula
(posterior view)</td></tr>
</table>
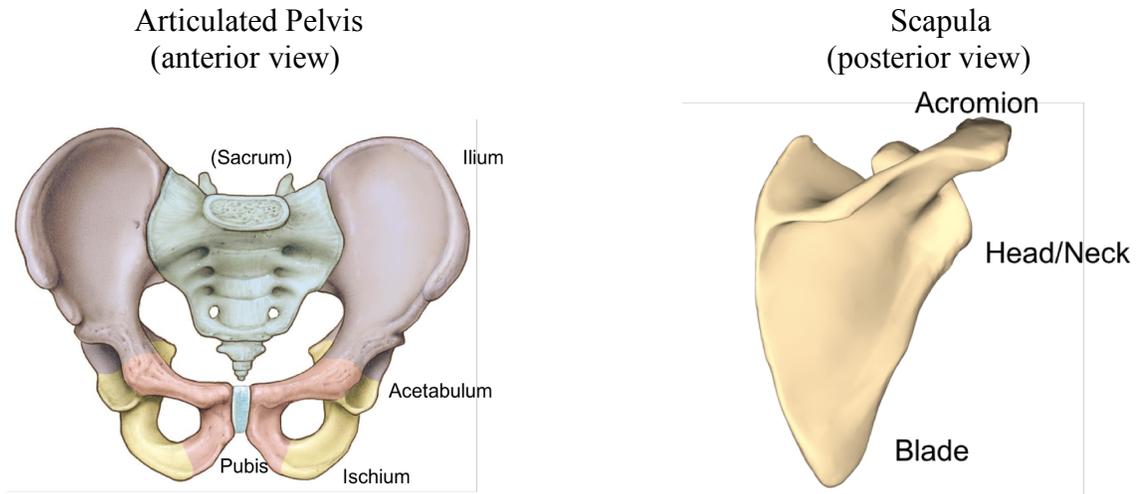
2.   Compare the pelvis and scapula. Although they share the same basic function of anchoring the limbs to the body's trunk, their morphologies are quite different. The pelvis is more robust and directly connects to the vertebral column via the sacrum, while the scapula is less robust and has no body connection to the vertebral column, among other differences. Can you hypothesize about why these differences are present?

The two bones emphasize different functions in the human body. The scapula prioritizes flexibility and mobility because we use our arms for many different activities, but it has very little involvement in locomotion. The pelvis prioritizes stability and power since it's supporting our entire upper body weight and has a much more significant role in locomotion through our legs.

3. Your group has been given either a male or female articulated pelvis (one that is connected in an anatomically accurate way to the sacrum, as well as fused at the pubic symphysis so that you have a right/left side together). Using the CER method, identify the sex of the pelvis in front of you and provide evidence and reasoning supporting your claim. *Hint: Try to determine this by looking at only the pelvis in front of you first. But if you're uncertain, comparing with a neighboring group can lead to further insight.*

Claim (*is the pelvis male or female*):_____

Evidence (*anatomical features that led you to this claim*):

Reasoning (*Why are these features different in a male/female pelvis*):

A female pelvis looks much more like a human baby could fit through it! A wider sub-pubic angle, a less curved sacrum, and other details make for a wider birth canal in the female pelvis than the male pelvis.

Activity 2: Investigating Hominin Fossils

For this activity, we will divide into four groups. Each group will be given a small selection of hominin fossils representing a single extinct species related to (*and possibly ancestral to!*) modern humans. Because of our limited time and limited supply of fossils, you will only interact with the fossils in your group for now. However, after the talk and activity, all fossils from the different species will be available for you to see and investigate.

1. Investigate the skull, pelvis, and (if applicable) the femur given to your group. Based on their characteristics and the review sheet at your table, match the fossil material to one of the four species listed: *Australopithecus afarensis, Homo erectus, Homo floresiensis, and Homo neanderthalensis.*

Claim (*what species do you have?*):_____

Evidence (*what features of the fossils suggest this species?*):

Reasoning (*why do these features support your claim on what species it is?*):

2. Once you have identified your species, confirm your identification with an instructor. Once we confirm your identification is correct, we will provide you with a model of another important trait of the species: its brain size. Whatever species you have, its brain is larger than a species it was closely related to, the chimpanzee. So as hominins were becoming better at walking on two legs, their brain size also increased. Why is this the case? And how would you frame the "cause and effect" here---did hominins begin walking on two legs because they had bigger brains, or did they evolve bigger brains because they became more efficient at walking on two legs?

As they became better at walking on two legs, they were able to travel further and more efficiently between food patches, so they could take in more food--and some of the calories from this food could go toward supporting a very expensive organ, the brain. With these extra calories in their diet, they could afford to have larger brains--and larger bodies as well. Thus, locomotion/brain size/body size/diet form a positive feedback loop in human evolution.

3. Now that you have identified your species and thought about how its brain size, locomotion, and diet are connected, let's take a deeper dive into a further link between its anatomy and behavior or environment. **Choose your group's species below and consider the question posed below with your group.** (If you finish early, feel free to peruse the questions related to other species and try your hand at them!)

Australopithecus afarensis: The locomotor strategies of Australopithecus species has been hotly debated in the paleoanthropology community. Its pelvis certainly suggests that it at least had the capability to walk on two legs efficiently, but it's uncertain how much it also climbed in trees. What other skeletal features would you like to investigate in order to determine whether or not it still climbed in trees? What would these features look like depending on if it was more bipedal or more arboreal?

A few examples:
- *Abducted/Adducted big toe: if the big toe is more in line with the others, it is more likely often bipedal (this is the case)*
- *Limb length: if the hind limbs are much longer than the forelimbs, it is more likely often bipedal (forelimbs and hindlimbs are roughly equal in this species)*
- *Reinforced knee: A more robust knee joint suggests that its knees bore more weight because it was more often bipedal (true)*
- *Other possible answers as well*

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Homo erectus: The ilium of *Homo erectus* is broader than in the hominin species that came before it and is much more similar to modern humans. Specifically, the region where the gluteus maximus inserts is newly enlarged in this species compared to others. We previously discussed the role of the other gluteals, the medius and minimus, in walking efficiently upright. The gluteus maximus is much less important in walking, but it does play a significant role in another form of locomotion. What type of locomotion would this be, and why might it have been selectively advantageous for *Homo erectus* to be able to move in this way?

The gluteus maximus is used much more in a running gait than a walking gait--so Homo erectus *could run much more efficiently than previous hominin species! This was advantageous because it opened up a new way of procuring food: hunting. Hunting provided calorie-rich food to support large brains, large body sizes, and larger groups of individuals.*

Homo floresiensis: This is a small-bodied species that lived until quite recently in evolutionary time in a very specific habitat—only on the island of Flores in Indonesia. Can you hypothesize about why the species was so small in adulthood, as well as so long-surviving? (*Hint: think about the challenges associated with living on an isolated island.*)

It's likely a case of island dwarfism! The species was isolated on the small island, where resources were more limited than if they had a huge geographical area in which to find food. Bigger bodies and brains require more energy, and without all the excess food to supply that energy, it became selectively advantageous for Homo floresiensis to reduce its body size.

Homo neanderthalensis: Neanderthals' pelves are actually broader than most modern humans' pelves. With your group, form a hypothesis about why their pelves were so broad (*hint: their entire bodies were generally broader than most modern human populations—not just their pelvis. And while birthing larger brained infants may have played a role, it is not the full story*).

Neanderthals lived farther north than most other hominins. Because they lived at much colder climates, heat retention would be a stronger selective force for them. According to principles such as Bergman and Allen's Rules, a shorter, broader body is more efficient for heat conservation. Therefore, it would be selectively advantageous for Neanderthals to be shorter and broader overall, which is likely why they had a broader pelvis.

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Activity 3: Bioinformatics Exploration of ATAC-seq Data

In this activity, you will use a popular bioinformatics program, BEDtools, to identify genomic regions that are either shared or unique to specific datasets. The computers provided have been pre-loaded with all the data and software you will need (please do not try to use your own computers for this—the program and data can be time-consuming to download). Opening the window, running the program, and viewing the results can be confusing, so please raise your hand if you need any help!

Running the Intersection

1. Each computer should have a terminal window open and navigated into the Desktop folder, where we'll be keeping all the files for ease of access.
   - If your computer is not already open to this window, find the terminal icon in the dock at the bottom of the desktop and click to open a window.

<div align="center">Terminal Icon (black box)</div>
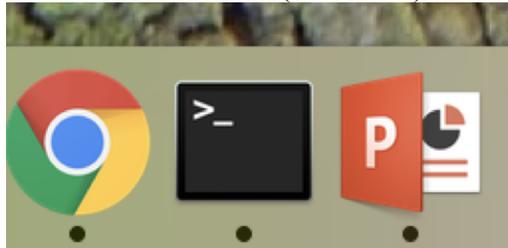
   - In the terminal window, type: "cd Desktop". This command brings you to the Desktop folder, where all the files you need are located.
   - Your Terminal window will look like this:


```
Last login: Thu Nov  1 22:22:41 on ttys000
Mariels-MacBook-Pro:~ marielyoung$ cd Desktop
```

2. BEDtools has many functions for exploring BED files, which are a type of file that lists the chromosome, start site, and end site for a number of genomic regions. Here is an example (they usually consist of thousands of lines like this):

```
chr1    3042867 3043304
chr1    3515098 3515149
chr1    3670726 3671049
chr1    3671351 3672153
```

- We will be using the "intersect" function, which compares two BED files and finds genomic regions that are shared by the two files, as shown below:
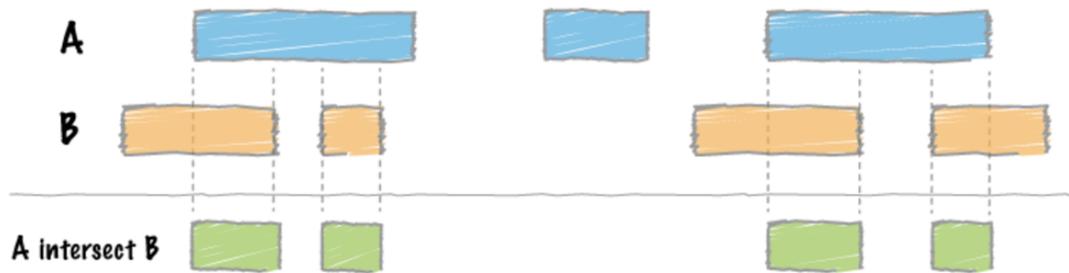
- Using the "intersect" function, we will input two BED files (from Mariel's ATAC-seq data), and the program will tell us which genomic regions the two have in common.
  - Each BED file represents regions of open chromatin in a specific part of the pelvis or scapula, or regions of human acceleration in the human genome. By "intersecting" the two BED files, we can find regions of open chromatin that are shared between the two files.

- Your group has been given a card telling you which two BED files you will be intersecting. Each group will perform a different comparison, and then we will report our results back to the entire group.

- To perform the intersection, simply type in the command below in your Terminal window, substituting [First_Bed_File] and [Second_Bed_File] for the names of files on your card:

```
bedtools intersect –a [First_Bed_File].txt –b
[Second_Bed_File].txt > [Output_File].txt
```


- Here is a breakdown of what this command is doing:
  - "bedtools" tells your computer you want to access the BEDtools program that has been downloaded.
  - "intersect" is the specific function within the BEDtools program you want it to run.

- o The "-a" followed by the first .txt file is telling the program what the first file is, while what follows the "-b" is giving it the second file.
  - o At the end of the command, you'll enter the > symbol, followed by whatever you wish to name the output file (for instance, "Pelvis_Scapula_CommonRegions.txt"). The output file can be called anything, but should end with ".txt". After you input this command, the output file will appear in the Desktop and can be opened

- After you have typed in the command, simply press "enter" and it will run.
- Your output file will appear on your Desktop.

Viewing the Results

3. To view the results of your intersection, find the output file you created in the Desktop.

4. Right click on your output file and select, "Open File in TextWrangler."
   - TextWrangler is a simple application for viewing and manipulating text files like BED files.

5. Once the output file is open in TextWrangler, scroll to the bottom of the file to view how many genomic regions were found to be overlapping between your two original files.

6. Record your results below, and be ready to share them with the group!

Number of Genomic Regions in File A:_____

Number of Genomic Regions in File B:_____

Number of Genomic Regions Shared Between Files A and B:_____

If you finish your intersection early, feel free to play with the tool and perform other intersections! Below is a list of all the files loaded on each computer that you could intersect:
Acetabulum.txt
Ilium.txt
PubisIschium.txt
ProximalFemur.txt
All_Pelvis.txt
All_Scapula.txt
Blade.txt
Acromion.txt
HeadNeck.txt
Human_Accelerated_Regions.txt