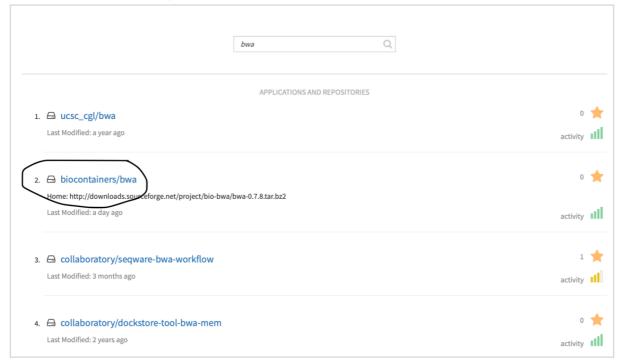
Using biocontainers

The best place to search for biocontainers at the moment is at Quay - use the containers from the biocontainers account. They have a website but it's super buggy and the search functionality is terrible.

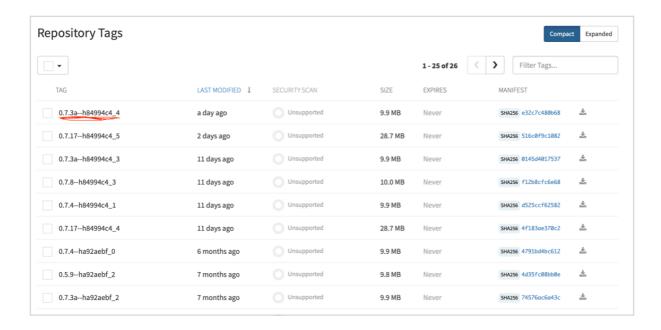
Click the biocontainers package.



Take note of the quay.io address for the container. Then click on on the tags.



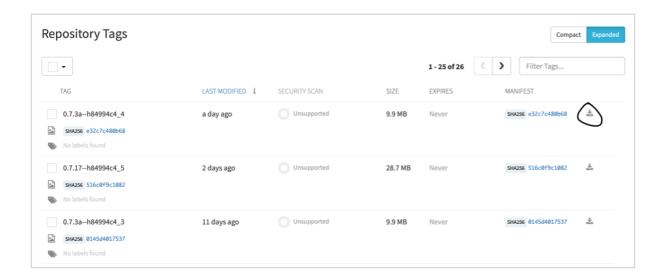
Find the version you want. Sometimes these tags will also specify versions of python within the container too.



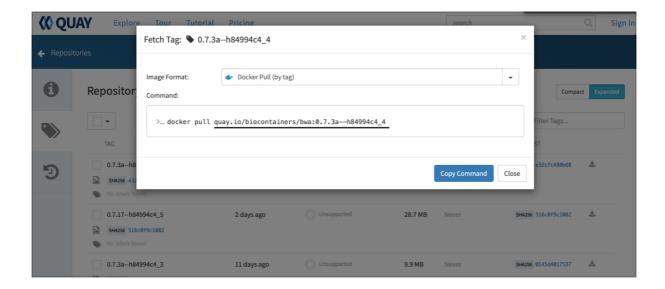
Put it all together into a docker hub URL and pull it into Singularity.

The way to construct these URLS is docker://quay.io/biocontainers/<tool>:<tag> So for this example of bwa the URL would be docker://quay.io/biocontainers/bwa:0.7.3a—h84994c4_4

Another way of fetching this URL is by clicking the fetch tag



Select "Docker Pull (by tag)" from the "Image Format" drop-down and copy the URL and add docker:// to the beginning of it.



With out URL in-hand we can use it in place of a singularity simg file when running singularity commands.

singularity exec docker://quay.io/biocontainers/bwa:0.7.3a--h84994c4_4 bwa mem