

COMP3850 Scripts/Model Execution Guide

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Revision history

Revision Number	Date	Person(s)	Changes
1.0	16/05/2024	Group 23	Initial version

Intended audience

This script and model execution guide is intended for use by individuals who need to build and run a computer vision model for animal posture estimation using the SLEAP framework. It is assumed that the user is using Microsoft Windows as their operating system and has a basic level of computer literacy, including an understanding of how to navigate through the file system, download and run files from the Internet, and launch applications from the Start Menu, but otherwise has no in-depth technical expertise.

System Requirements

Recommended minimum hardware requirements

- Processor: Intel i5
- RAM: 16GB
- Graphics card: Nvidia Geforce RTX 2060

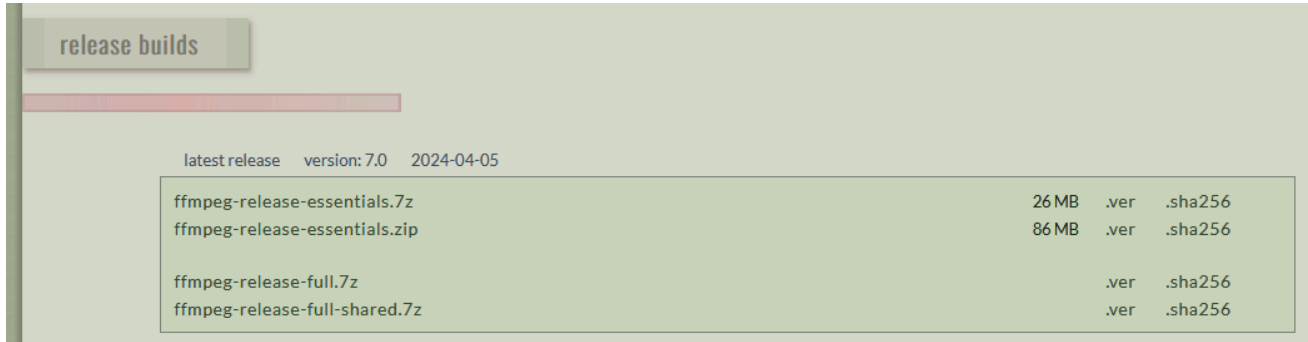
Software requirements

- Operating System: Microsoft Windows 10 / 11
- Internet Browser: Mozilla Firefox or Google Chrome

Installation

ffmpeg

1. Navigate to <https://www.gyan.dev/ffmpeg/builds/> in your web browser.
2. Scroll down to the 'release builds' section and click on 'ffmpeg-release-essentials.zip' to download the latest release of ffmpeg for Windows.

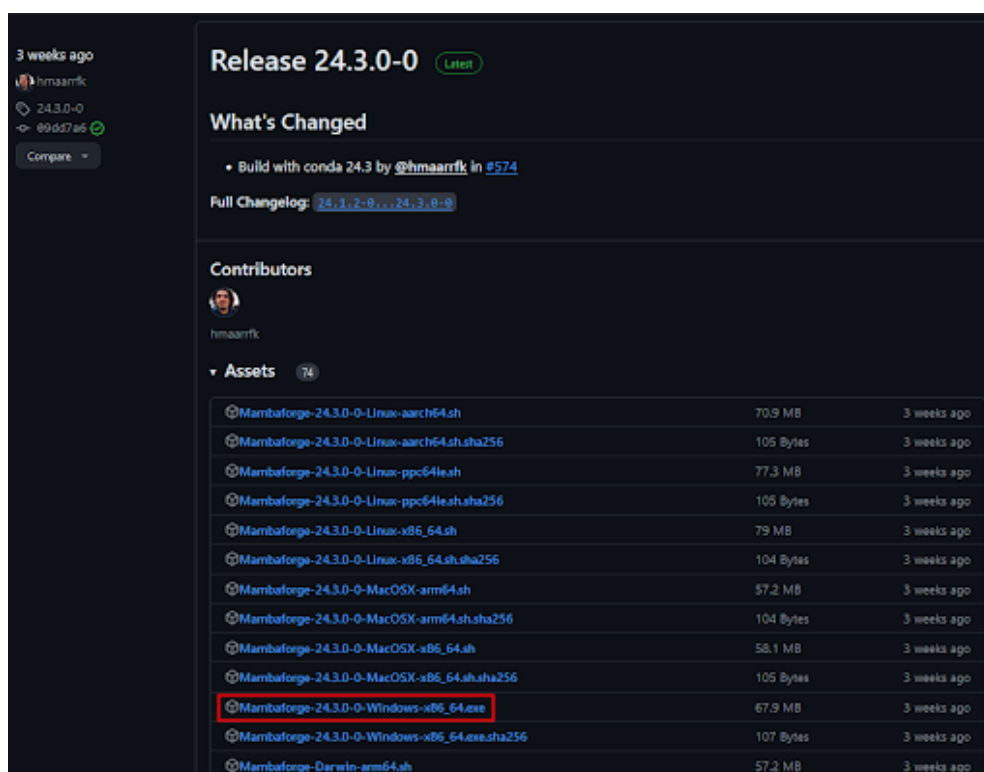


release builds			
latest release	version: 7.0	2024-04-05	
ffmpeg-release-essentials.7z	26 MB	.ver	.sha256
ffmpeg-release-essentials.zip	86 MB	.ver	.sha256
ffmpeg-release-full.7z		.ver	.sha256
ffmpeg-release-full-shared.7z		.ver	.sha256

3. Extract the contents from the downloaded file.

Mamba

1. Navigate to <https://github.com/conda-forge/miniforge/releases> in your web browser.
2. Download the latest version of Mambaforge (not Miniforge) for Windows in the 'Assets' section of the most recent release.
 - a. The name of the file to download should be in the format "Mambaforge-<version number>-Windows-x86_64.exe"
 - b. You may need to click 'Show all <number> assets' at the bottom of the list to locate the Windows version.



3 weeks ago
himaarrfk
24.3.0-0
09d37a6
Compare

Release 24.3.0-0

Latest

What's Changed

- Build with conda 24.3 by @himaarrfk in #574

Full Changelog: [24.1.2-0](#)...[24.3.0-0](#)

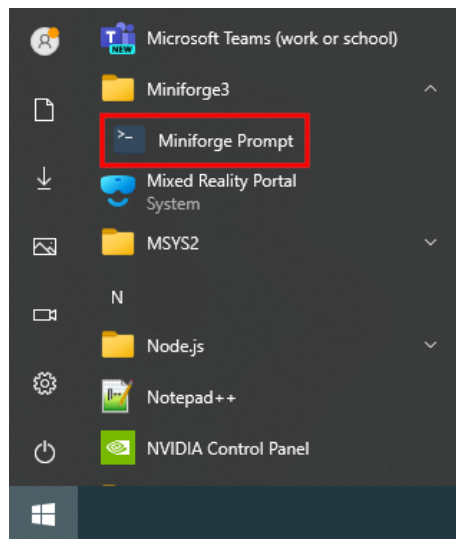
Contributors

himaarrfk

Assets 74

Mambaforge-24.3.0-0-Linux-aarch64.sh	70.9 MB	3 weeks ago
Mambaforge-24.3.0-0-Linux-aarch64.sh.sha256	105 Bytes	3 weeks ago
Mambaforge-24.3.0-0-Linux-ppc64le.sh	77.3 MB	3 weeks ago
Mambaforge-24.3.0-0-Linux-ppc64le.sh.sha256	105 Bytes	3 weeks ago
Mambaforge-24.3.0-0-Linux-x86_64.sh	79 MB	3 weeks ago
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Mambaforge-24.3.0-0-MacOSX-arm64.sh	57.2 MB	3 weeks ago
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Mambaforge-24.3.0-0-MacOSX-x86_64.sh	58.1 MB	3 weeks ago
Mambaforge-24.3.0-0-MacOSX-x86_64.sh.sha256	105 Bytes	3 weeks ago
Mambaforge-24.3.0-0-Windows-x86_64.exe	67.9 MB	3 weeks ago
Mambaforge-24.3.0-0-Windows-x86_64.exe.sha256	107 Bytes	3 weeks ago
Mambaforge-Darwin-arm64.sh	57.2 MB	3 weeks ago

3. Run the downloaded file and follow the installation steps.
 - a. It is recommended that you select the 'All users (requires admin privileges)' option for who to install for. Other settings may be set per your preferences.
 - b. Note that Mamba will appear as 'Miniforge' in the Start Menu once the installation completes.



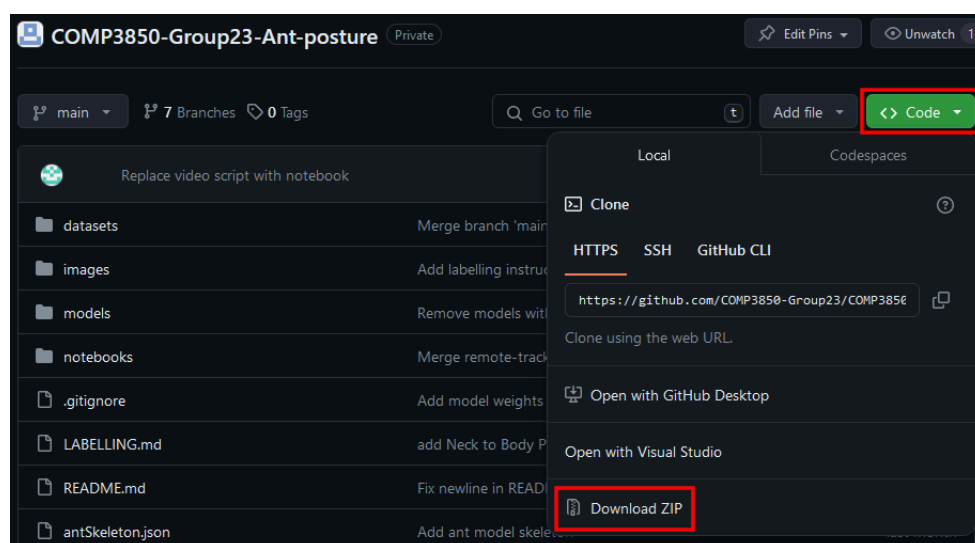
The Miniforge shortcut as it appears in the Windows 10 Start Menu

SLEAP and Jupyter

1. Open 'Miniforge' from the Start Menu.
2. Type `mamba create -y -n sleap -c conda-forge -c nvidia -c sleap -c anaconda sleap=1.3.3 jupyterlab` into the command prompt and press the Enter key.

Project resources

1. Navigate to <https://github.com/COMP3850-Group23/COMP3850-Group23-Ant-posture> in your web browser.
2. Click on the green 'Code' drop-down menu and select the 'Download ZIP' option.



3. Extract the contents from the downloaded file.

Startup

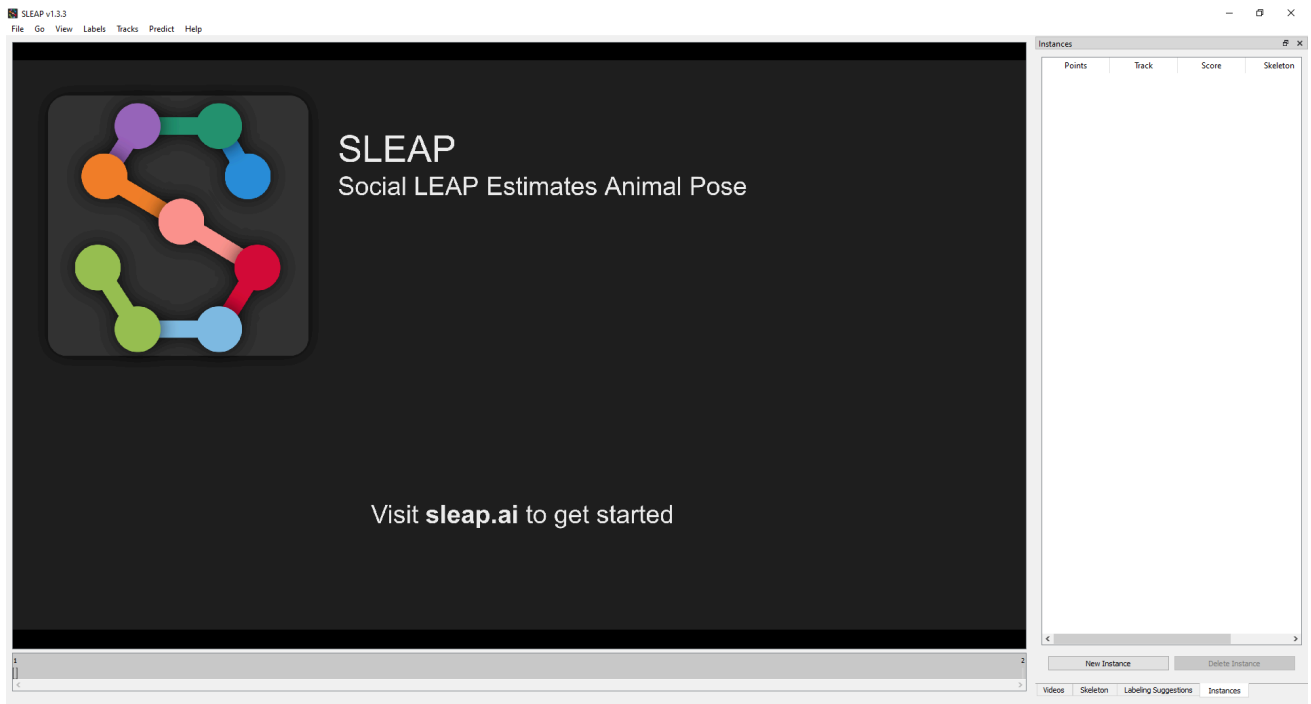
Starting the SLEAP or Jupyter applications requires using the command-line interface as per the following instructions.

SLEAP

1. Open 'Miniforge' from the Start Menu.
2. Type `mamba activate sleap` into the command prompt and press the Enter key.
 - a. If done correctly, the command prompt will change to show you are now using the 'sleap' environment

```
(sleap) C:\Users\Owner>
```

3. Type `sleap-label` into the command prompt and press the Enter key. This will open the SLEAP application in a new window.



Jupyter

1. Open 'Miniforge' from the Start Menu.
2. Type `mamba activate sleap` into the command prompt and press the Enter key.
 - a. If done correctly, the command prompt will change to show you are now using the 'sleap' environment

```
(sleap) C:\Users\Owner>
```

3. Type `cd /d` followed by the drive letter for the hard drive containing the Jupyter notebooks into the command prompt followed by a colon (:) and press the Enter key.
 - a. For example, if the Jupyter notebooks are stored in the "C:\Documents\Ant-posture\notebooks" folder, then type `cd /d c:` into the command prompt and press the Enter key.
4. Type `jupyter notebook` into the command prompt and press the Enter key. This will open the Jupyter Notebook interface in your default web browser.

The screenshot shows the Jupyter Notebook web interface. At the top, there's a 'jupyter' logo and 'Quit' and 'Logout' buttons. Below that, there are tabs for 'Files', 'Running', and 'Clusters'. The 'Files' tab is active, showing a file browser view. The path is 'Documents / COMP3850-Group23-Ant-posture / notebooks'. There are buttons for 'Upload', 'New', and a refresh icon. A table lists the files in the directory:

	Name	Last Modified	File size
<input type="checkbox"/>	..	seconds ago	
<input type="checkbox"/>	Data export.ipynb	a day ago	2.61 kB
<input type="checkbox"/>	Dataset merging.ipynb	9 days ago	3.56 kB
<input type="checkbox"/>	Label analysis.ipynb	9 days ago	7.79 MB
<input type="checkbox"/>	Model analysis.ipynb	a day ago	1.02 MB
<input type="checkbox"/>	Model evaluation.ipynb	2 days ago	118 kB
<input type="checkbox"/>	Test.ipynb	Running 2 hours ago	1.71 kB
<input type="checkbox"/>	Training config generator.ipynb	11 days ago	7.68 kB
<input type="checkbox"/>	Video generator.ipynb	5 days ago	3.67 kB
<input type="checkbox"/>	Video pre-processing.ipynb	2 days ago	3.38 kB

Workflow

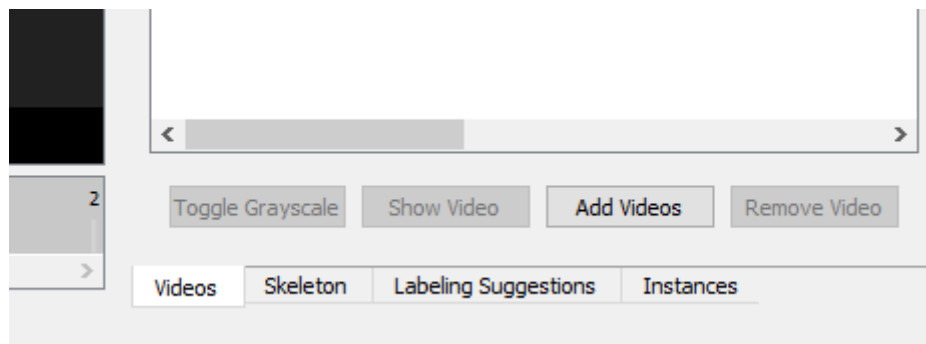
The following steps represent the recommended workflow for training and running a model using SLEAP. More advanced features and options for SLEAP are documented on the [official website](#).

Video pre-processing

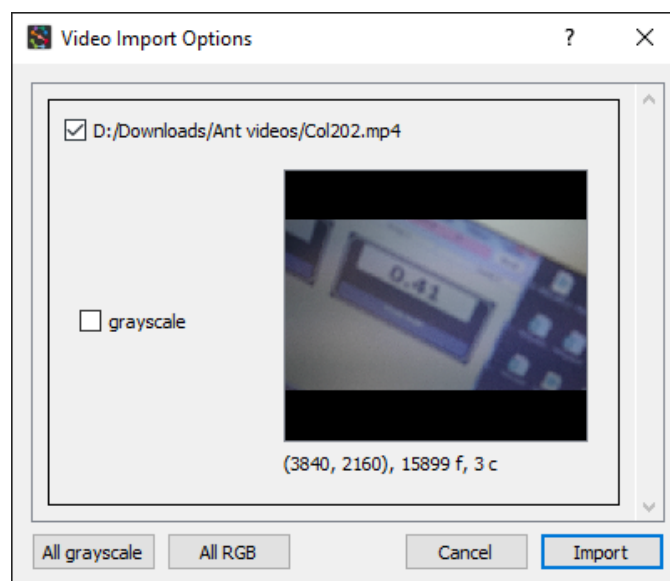
1. Create an output folder to store the processed videos if one does not already exist.
2. Copy or move all of the videos that you want to process into a single input folder.
3. Follow the instructions for using the [Video pre-processing](#) Jupyter Notebook.

SLEAP project setup

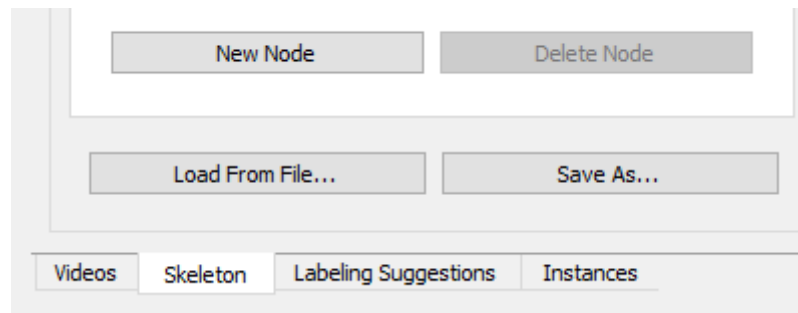
1. Follow the instructions for starting up the [SLEAP](#) application.
2. Select the 'Videos' tab at the bottom-right side of the SLEAP window.



3. Click the 'Add Videos' button.
4. Select one or more video files in the file picker dialogue window that opens, then click the 'Open' button.
5. In the 'Video Import Options' window that appears, click the checkbox for 'grayscale' next to each video that you want to convert to black-and-white, or leave it unchecked for colour videos.
 - a. This can be changed after importing the videos by selecting the video(s) in the 'Videos' tab and clicking the 'Toggle Grayscale' button.



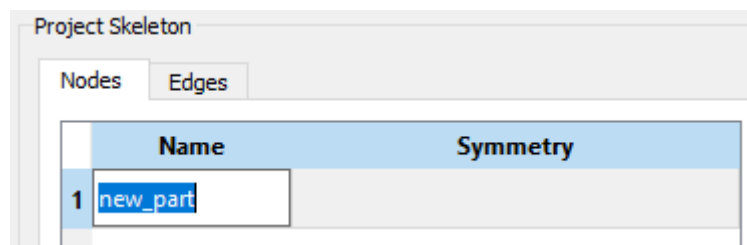
6. Click on the 'Skeleton' tab at the bottom-right side of the SLEAP window.



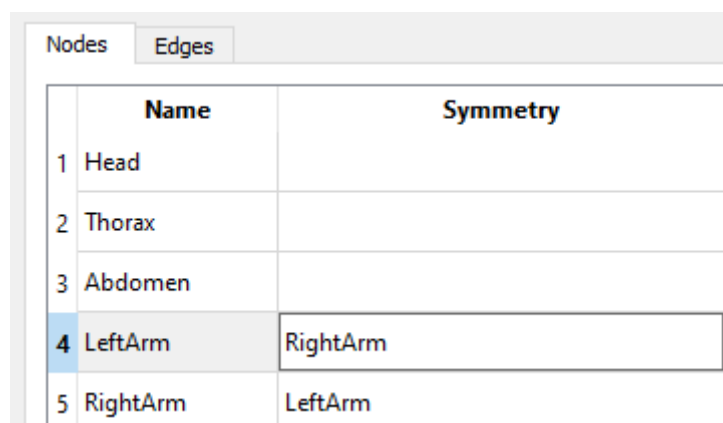
7. Create or import a skeleton as follows,

a. To create a new skeleton for the model,

- i. Click the 'New Node' button.
- ii. Double-click on the name of the newly created node and type in a new name for the body part that the node relates to.

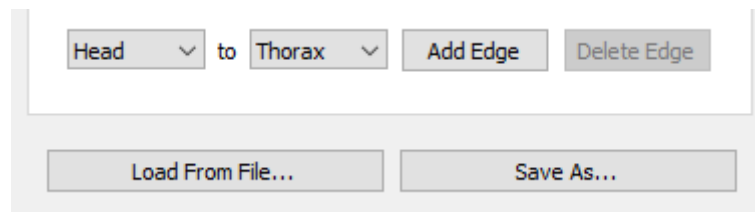


- iii. Repeat for each point on the animal(s) that needs to be tracked in the imported videos.
- iv. For body parts that are symmetrical with another body part (e.g. left front leg and right front leg), double-click on the space under 'Symmetry' next to the node and type in the name of the corresponding symmetrical node.



- v. Once all nodes have been named and any symmetrical nodes have been configured, click on the 'Edges' tab near the top-right side of the SLEAP window.

- vi. Add edges to indicate adjacent body parts by selecting the parent node in the left drop-down menu at the bottom of the window and selecting the child node in the right drop-down menu, then clicking the 'Add Edge' button.



- vii. Ensure that there is only one root node (i.e. one node that is the ancestor of all other nodes) in the skeleton.
 - Go to [Skeleton Design](#) in the SLEAP documentation for more information about designing skeletons.
- b. To open a saved skeleton file,
 - i. Click on the 'Load From File...' button.
 - ii. Locate and select a JSON (.json) file containing a skeleton then click the 'Open' button.

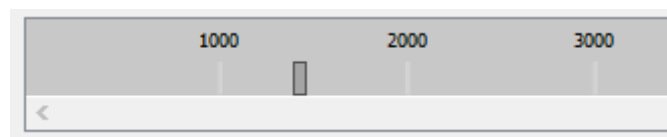
Labelling

Initial labelling

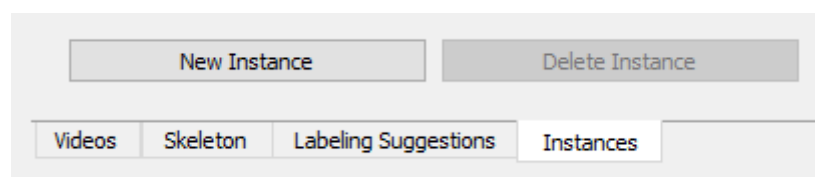
1. Select a video by double-clicking the entry for it in the 'Videos' tab.

Videos				
	Filename	Frames	Height	Width
1	...os/Col202.mp4	15899	2160	3840
2	...os/Col210.mp4	74366	2160	3840

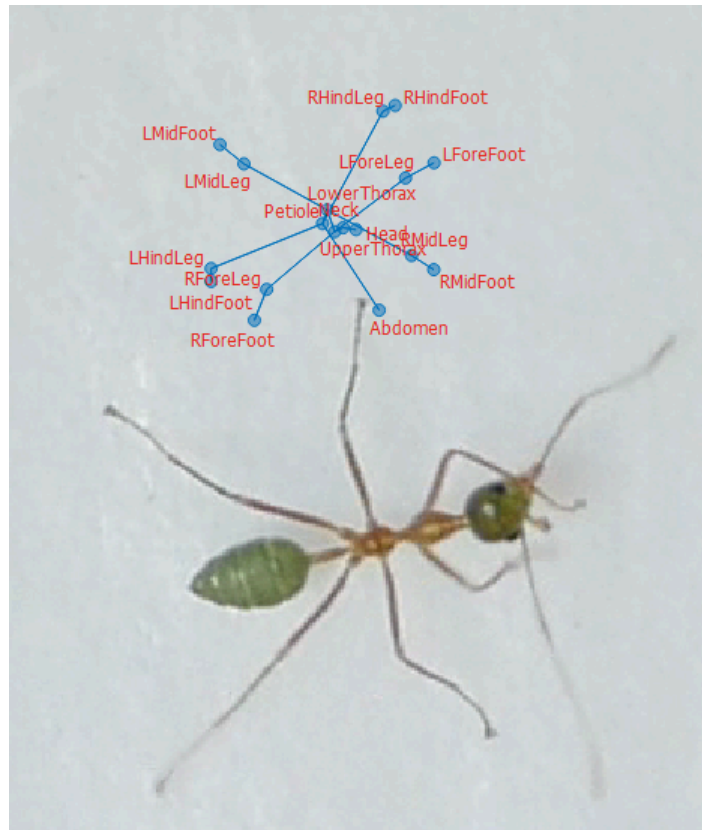
2. Select a frame using the timeline at the bottom of the SLEAP window.



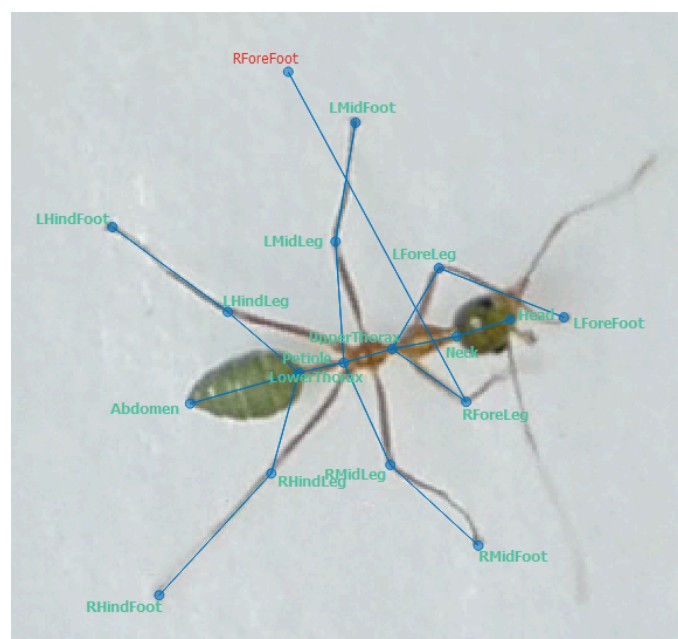
3. Click on the 'Instances' tab.



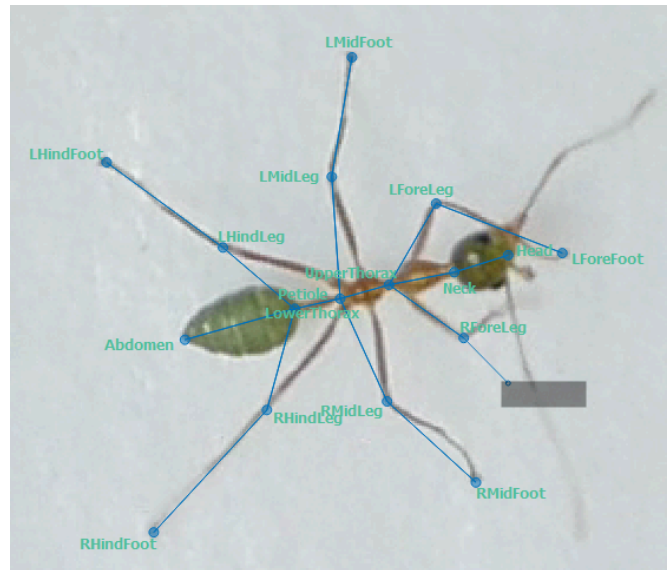
4. Click on the 'New Instance' button. A new instance of the skeleton will be added to the frame, with each point coloured red to indicate that the points have not yet been verified by the labeller.



5. Click and drag each point to the corresponding body part visible in the frame. The point will turn light blue to indicate that the point has been verified by a labeller.
 - a. The mouse scroll wheel can be used to zoom in and out of the frame. Clicking and then dragging the mouse on the frame while zoomed in will pan around the frame.
 - b. Holding the Alt key before clicking and dragging will move the entire skeleton instead of a single point.



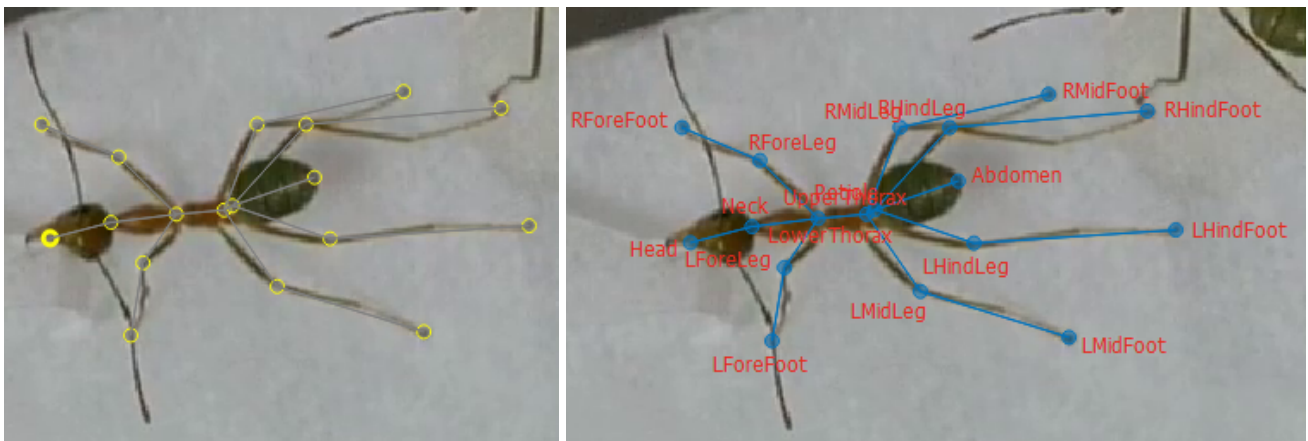
6. If a body part is not visible in the frame, right-click on the point to mark it as not visible, which will change the point colour to grey. The position of non-visible labels does not affect the training.



7. Repeat for each instance of an animal present in the frame.
 - a. It is recommended but not required to label each instance in a frame, as this will generally make the model more robust and accurate.

Prediction-assisted labelling

1. Select a frame containing a predicted animal instance.
2. Double-click on the instance to convert it into a user-labelled instance.

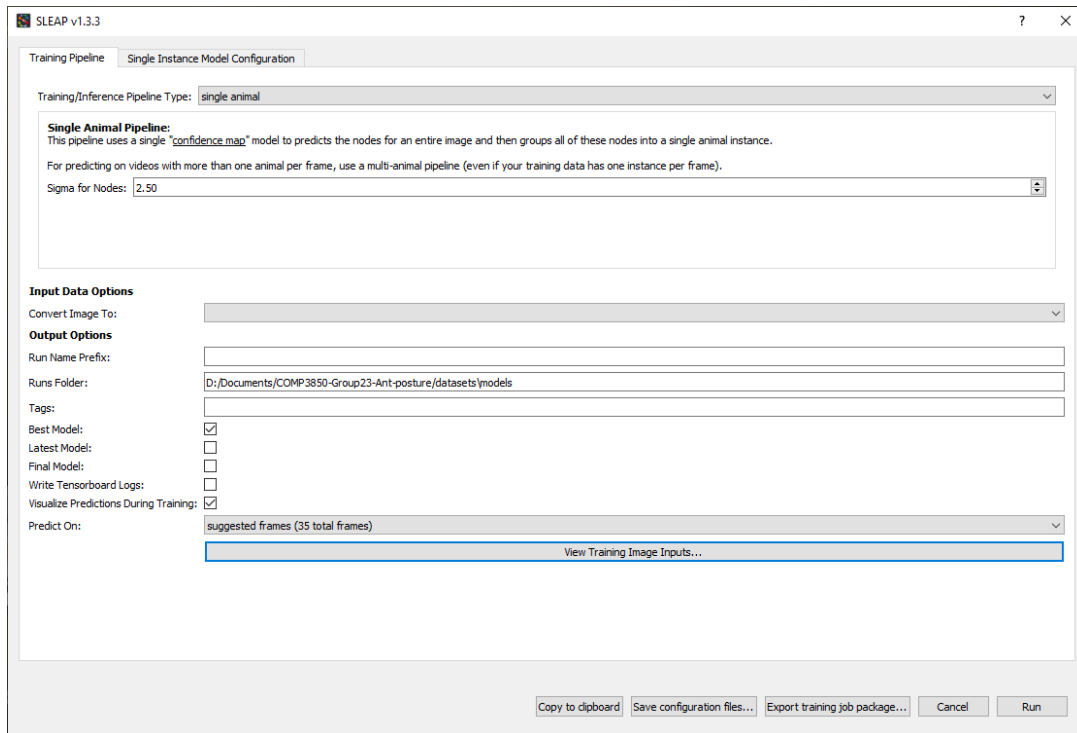


A predicted ant posture before (left) and after (right) being converted into a user-labelled instance

3. Click and drag all points in the instance skeleton onto the correct location in the frame.
 - a. It is recommended that you verify all points in the instance by clicking them, even if the predicted location is correct. This will make it easier to check that no incorrect predictions have been inadvertently left in their predicted position, which will cause trained models to be less accurate as these points are still included in the training data.
4. Repeat as many times as required or until all predictions have been corrected.

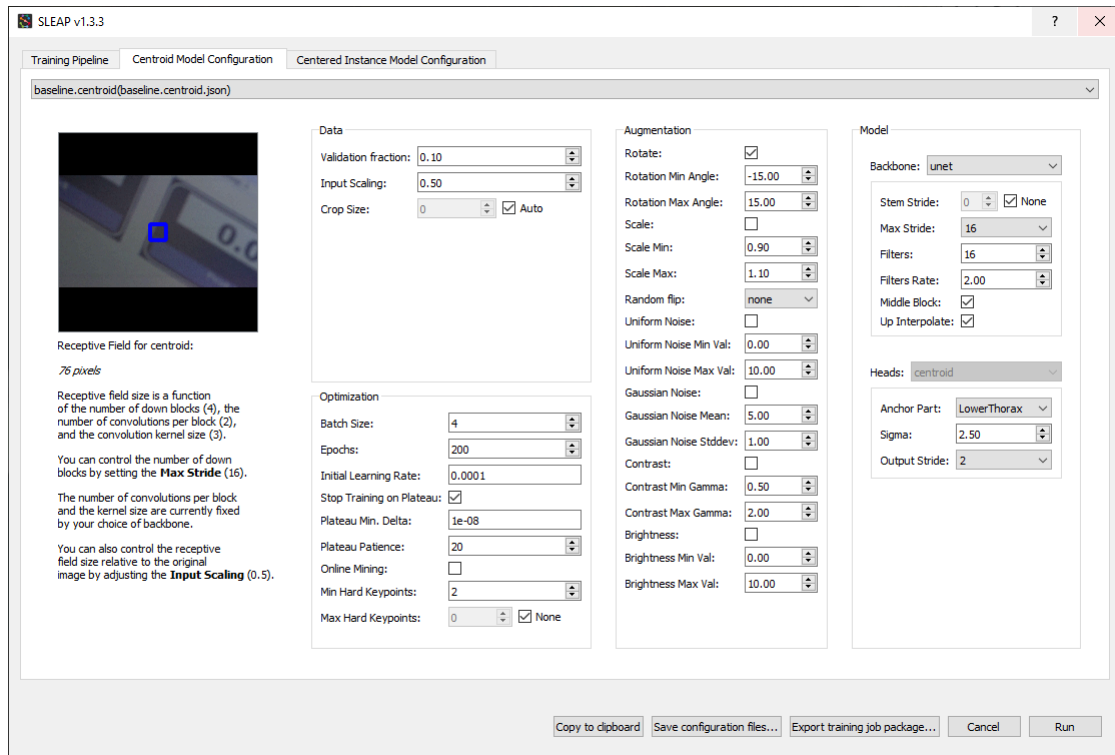
Training

1. In the SLEAP application window, go to File > Open Project... in the top menu bar.
2. Select a SLEAP dataset containing labelled video frames from the [Labelling](#) stage and click the 'Open' button.
3. In the top menu bar, go to Predict > Run Training... which will open the training configuration window.



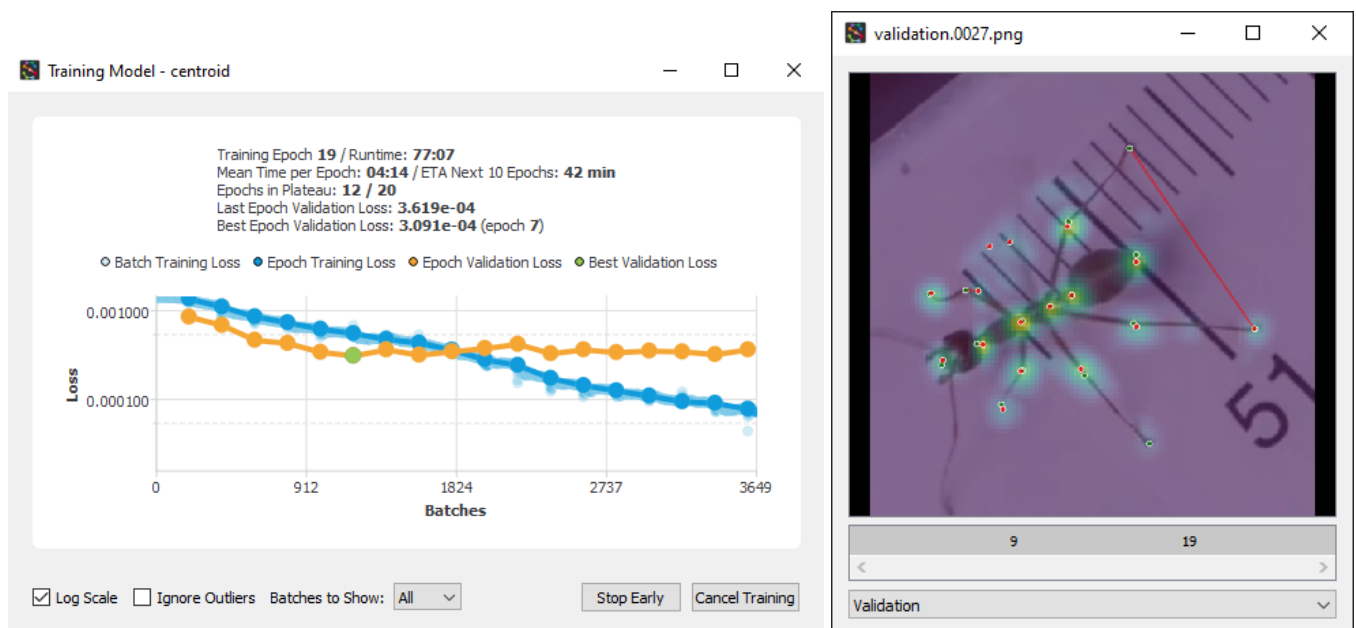
The training configuration window

4. Select 'multi-animal top-down' from the 'Training/Inference Pipeline Type'.
 - a. Other model pipeline types can be used, however it was found that this setting provided the most ideal balance of accuracy and memory use for the ant videos used during the project.
5. Under 'Output Options', set the 'Runs Folder' to the location where the trained model should be saved and provide a value for 'Run Name Prefix' if required.
 - a. It is recommended that the 'Run Name Prefix' has a value that briefly describes the settings used, as the default model folder name only uses the timestamp for when training started.
6. In the 'Centroid Model Configuration' and 'Centered Instance Model Configuration' tabs at the top of the window, select the settings that you want to use for each model.
 - a. See the [Training settings and model hyperparameters](#) section in the Appendix for an explanation of each setting.



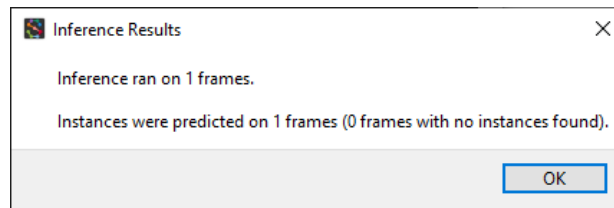
The centroid model configuration tab. The centred instance model configuration tab has the same options.

7. If the configuration is needed for future use, click the 'Save configuration files...' button at the bottom of the window and select a folder location in the file selection window to save the configuration files.
8. Click the 'Run' button at the bottom of the window when you are ready to begin training.
9. During training, a window showing the training progress will appear as well as a window showing a sample of the model's current prediction performance and confidence map.
 - a. Note that for top-down pipeline types, the training may appear to restart halfway through the process. However, this is actually because the process has switched to training the second model (centred instance).



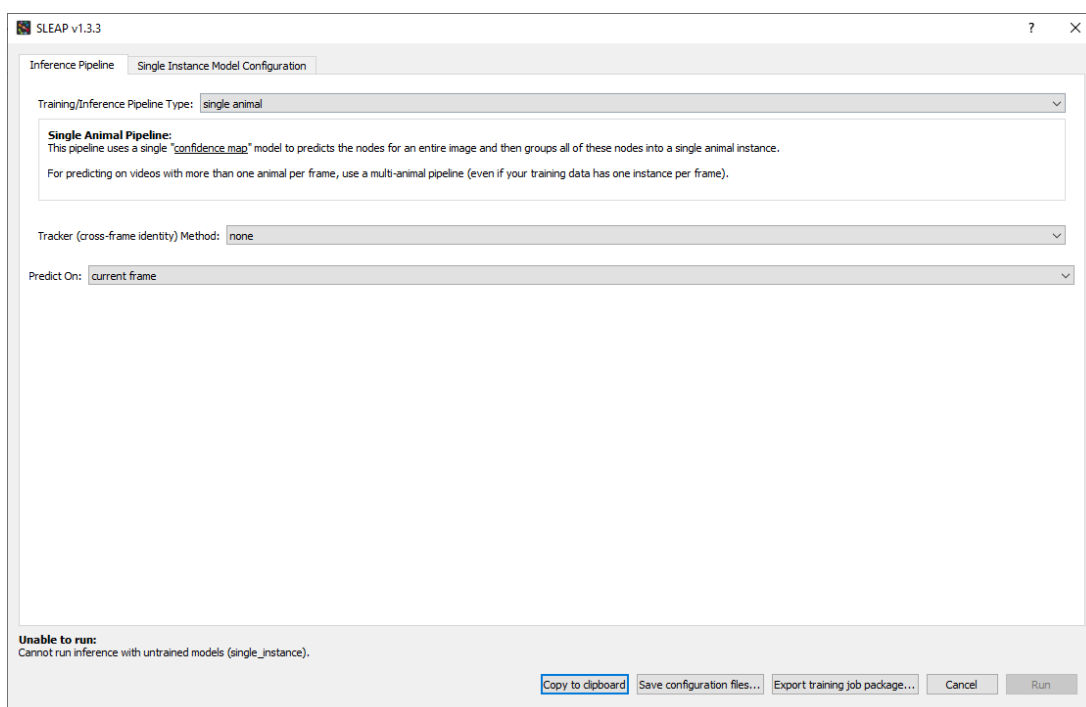
The training progress window (left) and a sample of the current model performance for a single instance (right)

10. After training has finished, the number of post-training predictions will be displayed and the trained model(s) can be used for inference.



Inference and Tracking

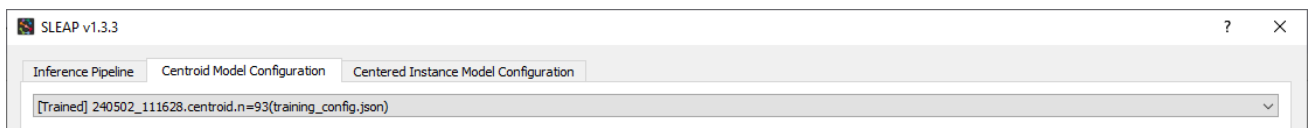
1. Follow the instructions for starting up the [SLEAP](#) application if it is not already running.
2. In the SLEAP application window, go to Predict > Run Inference... in the top menu bar, which will open the inference configuration window.



The inference configuration window

3. Select 'multi-animal top-down' from the 'Training/Inference Pipeline Type'.
4. Select the type of frames that you want to run inference on under the 'Predict On' drop-down menu.
 - a. You can Shift-click and drag to select a region in the timeline before opening the inference window to specify a range of frames, which then appears as an option in the 'Predict On' menu. This is recommended when tracking instances between frames when not running inference for entire videos.
5. To track animal instances between frames, select either 'flow' or 'simple' in the 'Tracker (cross-frame identity) method' drop-down menu.
 - a. The 'simple' option tracks instances by matching the nearest instance in a subsequent frame to a previous frame, while the 'flow' option shifts instances from their position in the previous frame based on their apparent movement before matching it to the nearest instance in the subsequent frame.
6. Select 'instance', 'centroid', or 'iou' in the 'Similarity Method' drop-down menu.

- a. The 'instance' option matches instances between frames based on the distances between corresponding nodes in the previous and subsequent frames.
 - b. The 'centroid' option matches instances based on the distance between instance centroids.
 - c. The 'iou' option matches instances based on the overlap between instance bounding boxes.
7. Select 'greedy' or 'hungarian' in the 'Matching Method' drop-down menu.
 - a. The 'greedy' option matches instances between frames in order of instances with smaller to larger distances in previous and subsequent frames.
 - b. The 'hungarian' option matches instances by minimising the overall cost of matching, based on the distances between each corresponding instance in previous and subsequent frames.
8. Enter a window size for the 'Elapsed Frame Window' setting.
 - a. This setting controls how many frames that an instance can be missing for before a reappearance is considered a new instance. An instance is considered missing for a frame if there is no prediction for it, even if it is visually present.
 - b. This value should be large enough to cover any prediction gaps, otherwise, multiple tracks may be generated for the same instance which cannot be joined in SLEAP and are harder to manage in the exported data.
9. Click the 'Centroid Model Configuration' tab at the top of the window, then select a model from the drop-down menu at the top of the window or click 'Select training config file...' in the menu to select a 'training_config.json' file for the model you want to use for centroid inference.



10. Repeat the previous step for the 'Centered Instance Model Configuration' tab.
11. Click the 'Run' button at the bottom of the window.
12. Wait until inference and tracking (if selected) are completed for the frames selected previously.
 - a. When the inference progress window closes and the tracking begins, SLEAP may stop responding and appear frozen. However, the program is still running so do not close it when this happens.
13. Once the inference and tracking are complete, the predictions and tracks will be added to the relevant frames.
 - a. Predicted instances are not included in subsequent training unless converted to user-labelled instances as per [Prediction-assisted labelling](#).
14. Predicted instances can be removed individually by selecting them in the 'Instances' tab and clicking the 'Delete Instance' button, or multiple predicted instances can be deleted using the options at the bottom of the 'Labels' menu in the top menu bar.

Data Export

1. If instance tracking data is needed in the data export file, check that all tracks are continuous and have not been split into multiple tracks for the same animal instance.
 - a. If this has occurred, this may be fixable by [re-running the inference](#) with a larger 'Elapsed Frame Window' setting
2. Follow the instructions for using the [Data Export](#) Jupyter Notebook.

Tools

Jupyter Notebooks

The Jupyter Notebook files are located in the `notebooks/` folder in the [project resources](#) repository.

Video pre-processing

1. Open the 'Video pre-processing' notebook.
2. Enter values for the `ffmpeg_path`, `input_folder`, `output_path`, and `output_suffix` variables in the first cell.
3. Go to Cell > Run All in the top menu bar.
4. Once the notebook finishes running, the processed videos will be saved in the output folder specified.

Dataset merging

1. Open the 'Dataset merging' notebook.
2. Enter values for the `input_folder` and `output_filename` variables in the first cell.
3. Go to Cell > Run All in the top menu bar.
4. Once the notebook finishes running, the merged dataset file will be saved to the input folder with the output filename specified.

Labelled dataset analysis

1. Open the 'Label analysis' notebook.
2. Enter a value for the `filename` variable in the first cell.
3. Go to Cell > Run All in the top menu bar.
4. Once the notebook finishes running, check the output of each cell for information about the labelled dataset specified.

Model comparison and analysis

1. Open the 'Model analysis' notebook.
2. Enter a value for the `model_folder` variable in the first cell.
3. Go to Cell > Run All in the top menu bar.
4. Once the notebook finishes running, check the output of each cell for comparisons of the models in the folder specified.

Data export

1. Open the 'Data export' notebook.
2. Enter values for the `dataset_path`, `output_path`, and `predictions_only` variables in the first code cell.
3. Go to Cell > Run All in the top menu bar.
4. Once the notebook finishes running, the data export file will be saved to the output path specified.

Frequently Asked Questions

Running the Miniforge Start Menu shortcut opens a command prompt window with the error message “The system cannot find the path specified”

This is likely due to a corrupted or incomplete Mamba installation which is causing the shortcut to point to a non-existent location. Uninstall any previous installations of Mamba and delete any Mamba shortcuts from your Start Menu, then re-install Mamba.

Running the ‘mamba create’ command when installing SLEAP and Jupyter gives the error “Could not open lockfile”

This may be resolved by running the command `mamba clean --locks` and then re-running the full ‘mamba create’ command as per the [installation instructions](#) for SLEAP and Jupyter. If this does not work, delete the entire ‘cache’ folder containing the lock file by following the file path in the error message, then re-run the ‘mamba create’ command. Note that you may need to display hidden files and folders in Windows Explorer to find the cache folder, which can be done by typing “hidden files” in the Start Menu which should provide a link to the Settings window where the option to display hidden files and folders is located.

Running the ‘sleap-label’ or ‘jupyter notebook’ commands in Miniforge gives the error “<command name> is not recognized as an internal or external command, operable program or batch file”

The ‘sleap-label’ and ‘jupyter notebook’ commands are only available once the SLEAP working environment has been activated in Miniforge. This can be confirmed by checking if the command prompt text contains “(sleap)”, including the parentheses. If the environment has not been activated, follow the [startup](#) instructions to activate it.

The trained models are not very accurate or are accurate on the training data but not when used for inference on unseen data

Model performance is highly dependent on the quantity and consistency of the labelled data and it is recommended to have labelled at least 100 instances before training a multi-animal pose estimation model with the goal of using it for inference. Setting the ‘Input scaling’, ‘Max stride’, and ‘Filters’ values too low in the training configuration will also negatively affect model accuracy so increasing these values may improve accuracy, though this will also increase the amount of time and memory required to train the model. If the model performs well on the training data but not on other data, it could be that “overfitting” is occurring where the model is memorising the training data so it cannot generalise to other inputs. Increasing the ‘Validation fraction’ value in the training configuration and/or labelling more instances may reduce the impact of this issue.

A single ant instance is being split onto multiple tracks during tracking despite being visible for the entire duration

A single ant may have multiple tracks generated for it if it disappears from the video for a certain number of frames. For tracking purposes, an instance is considered to have disappeared if there are no predictions for it, which may be due to poor model performance. This can be corrected by improving the model performance as above and/or by increasing the ‘Elapsed Frame Window’ value during the [tracking](#) process.

After opening Jupyter Notebook, the file selection interface is in the wrong folder and I’m not able to change drives/go up to previous folders

The starting point for the Jupyter Notebook file selection interface is based on the working directory in Miniforge at the time that the ‘jupyter notebook’ command was run. The current working directory in Miniforge is shown by the folder path in the command prompt. To fix that, follow Step 3 in the [Jupyter](#)

[startup](#) instructions to change the current working directory before starting Jupyter Notebook.

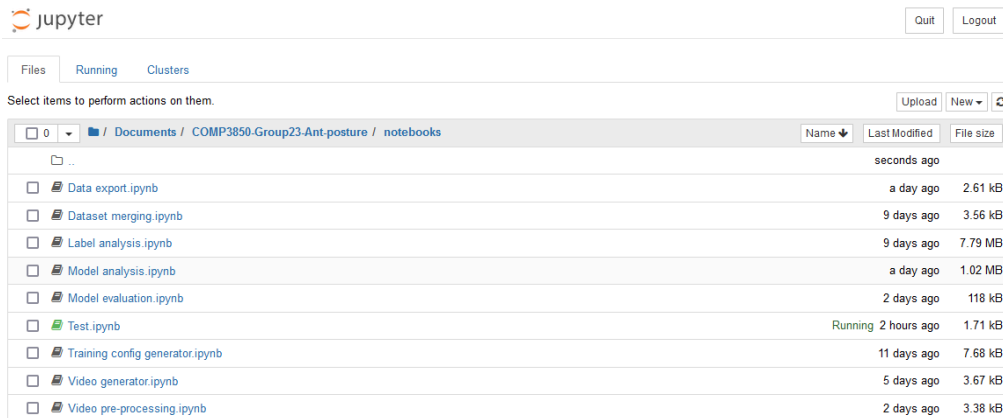
When running the Jupyter Notebook files, it gets stuck at one of the cells and does not run all the way to the end

One of the cells may have encountered an error (called an 'exception' in Python terminology) while running the code in the cell. There are many reasons that an error may occur but the most likely reason is that one or more of the input variables that require a folder path has a path that does not exist. Check the error message immediately below the cell that caused the error as it often provides important information about the error that occurred and what can be done to fix it.

Appendix

Using Jupyter notebooks

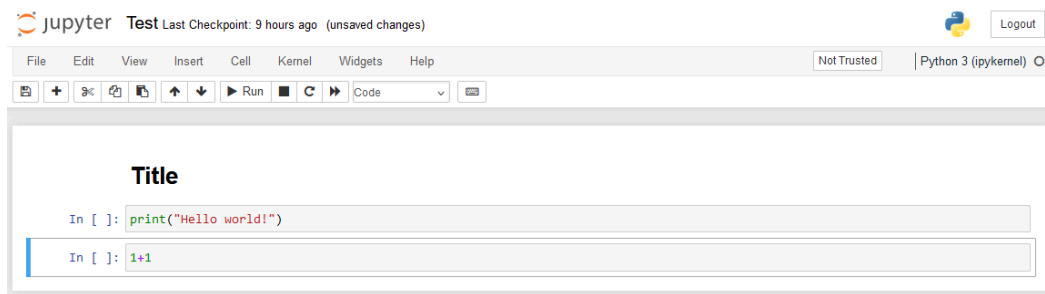
After running the `jupyter notebook` command as per the instructions for [starting Jupyter](#), a new page will be opened in the default web browser showing the Jupyter file selection interface.



The Jupyter file selection web interface

The file system can be navigated similarly to using Windows Explorer. Jupyter notebooks have the file type '.ipynb' and can be opened by clicking on them in the web interface. A new Jupyter notebook can be created by clicking on the 'New' drop-down menu in the top-left side of the window and clicking on 'Python 3 (ipykernel)'.

Opening a Jupyter notebook will initiate a Python 'kernel', which is a Python process that will be used to run all of the code in the notebook. Notebooks consist of a series of cells that can either contain Python code or text written in Markdown, which is a markup language used for formatting text.



Example of a basic Jupyter notebook

Individual cells can be selected by clicking on the left side of the cell, outside of the text box. The currently active cell will have a blue outline when it is not being modified. The contents of cells can be edited by clicking inside the text box for the cell or by double-clicking on a Markdown cell. The outline of the cell will turn green to show that it is being modified.



Example of a cell when selected (left) and being edited (right)

To run the code in a cell, select the cell and go to Cell > Run Cell in the top menu bar or press Ctrl+Enter. The contents of the cell will be executed and any output will be displayed below the cell. The number in square brackets will also be updated to show the sequence number for the command (1 for the first command executed, 2 for the second etc.).

All of the cells can be run in order by selecting Cell > Run All in the top menu bar. Running the cells out of order may result in errors, particularly if a cell uses a variable declared in a previous cell that has not been executed. To restart the underlying Python process for the notebook and clear all variables that have been declared so far, go to Kernel > Restart in the top menu bar. Finally, the title of the notebook can be renamed by clicking on the title and typing in the new name for the notebook.

Training settings and model hyperparameters

Data

- **Validation fraction:** Fraction of training data to use for validation after each epoch.
 - Recommended value: 0.20
- **Input scaling:** Factor to scale inputs by before training and inference (e.g. 0.5 for half the height and width of the original image dimensions).
 - Reducing this value can reduce video memory consumption at the cost of reduced accuracy.
- **Crop size:** Size in pixels of the height and width of the frame section to be cropped from the frame, mostly relevant for centred instance models.
 - Must be a multiple of the Max Stride setting value.

Optimisation

- **Batch size:** Number of images to include in each batch.
 - Higher values improve model generalisability but require more video memory.
- **Epochs:** Maximum number of epochs to run for training a single model.
 - One epoch equates to one cycle where each training image has been seen at least once.
- **Initial Learning Rate:** The initial rate of change used by the optimiser to update the model parameters during training.
 - Higher values will cause the model to learn faster but risk not finding the parameters that produce the most accurate model, lower values may result in a more accurate model but generally result in a longer training time.
- **Stop Training on Plateau:** Stop training early if the validation loss fails to improve after a configurable number of epochs.
- **Plateau Min. Delta:** Minimum decrease in validation loss required for an epoch not to be considered in a plateau.
- **Plateau Patience:** Number of epochs that validation loss must plateau for before training is stopped early.
- **Online Mining:** Enable or disable Online Hard Keypoint Mining (OHKM)
 - OHKM identifies body parts that tend to be harder to predict accurately and increases the penalty for incorrect predictions on those parts. This generally results in models that more accurately predict the positions of these “hard” points.
- **Min Hard Keypoints:** Minimum number of body parts considered “hard” to predict.
- **Max Hard Keypoints:** Maximum number of body parts considered “hard” to predict.

Augmentation

- **Rotate:** Randomly applies a rotation to the input image.
- **Rotation Min Angle:** Minimum angle to rotate the image.
- **Rotation Max Angle:** Maximum angle to rotate the image.
- **Scale:** Randomly scales the input image.
- **Scale Min:** Minimum factor to scale the image by.

- **Scale Max:** Maximum factor to scale the image by.
- **Random flip:** Randomly flip the input image horizontally or vertically.
- **Uniform Noise:** Applies random visual noise to the input image based on a uniform distribution.
- **Uniform Noise Min Val:** Minimum value for the noise uniform distribution.
- **Uniform Noise Max Val:** Maximum value for the noise uniform distribution.
- **Gaussian Noise:** Applies random visual noise to the input image based on a Gaussian (normal) distribution.
- **Gaussian Noise Mean:** Mean value for the noise Gaussian distribution.
- **Gaussian Noise Stddev:** Standard deviation for the noise Gaussian distribution.
- **Contrast:** Randomly adjust the gamma for the input image.
 - Gamma is a factor that controls the brightness for each colour value in an image. Higher gamma values result in higher contrast between light and dark colours.
- **Contrast Min Gamma:** Minimum value for the image gamma.
- **Contrast Max Gamma:** Maximum value for the image gamma.
- **Brightness:** Randomly adjust the brightness of the input image.
- **Brightness Min Val:** Minimum value to adjust the brightness by.
- **Brightness Max Val:** Maximum value to adjust the brightness by.

Model

Backbone

- **Stem Stride:** Determines the number of stem blocks to use before the downsampling section of the model.
 - Using stem blocks can downsample large input images while retaining spatial information.
- **Max Stride:** Determines the number of downsampling layer blocks in the model.
 - Increasing this value will increase the receptive field of the model, which allows the model to include more of the image during training and inference and may improve accuracy.
- **Filters:** Number of filters to use in the first layer block of the model.
 - Increasing this value improves the model's performance on complex images but increases the risk of overtraining.
- **Filters Rate:** Factor that the number of filters should be increased by for each layer block.
 - For example, a value of 2 will multiply the number of filters by 2 for each subsequent layer block.
- **Middle Block:** Include an additional layer block between the downsampling and upsampling sections of the model.
- **Up Interpolate:** Use bilinear upsampling instead of transposed convolutions during the upsampling section of the model.
 - This may reduce video memory requirements at the cost of model accuracy.

Heads

- **Anchor Part:** The body part (if any) to use as the anchor point for the rest of the skeleton.
 - If configured, the part should be located centrally to the animal's body.
- **Sigma:** The standard deviation of the Gaussian distribution used for calculating the confidence map.
 - Smaller values may improve model accuracy but require a longer time to train.
- **Output Stride:** The stride length for the confidence maps relative to the input image size.
 - Increasing this value reduces the video memory required for training but may produce a less accurate model.
- **Loss weight:** Relative value that the loss for each head in the model should be weighted by, for bottom-up model pipelines only.