

General knowledge

GenICam provides a standardized interface for accessing camera devices. Users must supply a CTI file, which is a compiled binary representing the transport layer, enabling the **Harvesters** library to manage the device effectively.

Below is a script demonstrating the essential steps: importing Harvesters, adding a CTI file, listing and connecting to a device, adjusting settings, and initiating data acquisition.

```
def main(args=None):

    from harvesters.core import Harvester

    harvester = Harvester()

    harvester.add_file(CTI_FILE, check_existence=True, check_validity=True)

    harvester.update()

    device = harvester.create(

        {'serial_number': SERIAL_NUMBER})

    features = device.remote_device.node_map

    SetSettings(features)

    device.start()

    print("Starting acquisition")

    while (True):
        acquire(device, features)
```

Utilizing the provided script facilitates the configuration of a stereo camera system, enabling synchronized image acquisition from dual cameras.

The **GenICam Browser** by Stemmer Imaging is a valuable software tool that offers an intuitive interface for exploring GenICam-compatible cameras. It is particularly useful for identifying camera settings and their ranges prior to capturing images.

For the GenICam Browser to recognize CTI files, these must be placed in the program files directory on the C drive. This step is crucial; if the CTI files are not located in the specified directory, the browser will not be able to connect using the designated transport layer.

By following these guidelines, users can efficiently set up their stereo camera systems and adjust settings using the GenICam Browser, ensuring a smooth and effective image acquisition process.