# Cello API

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***Cello API Documentation: http://www.cellocad.org/Cello-1.html***
There are 2 ways you can connect to Cello. You could use curl commands or use the Cello Python API.

## 1 Curl Commands

- **Simple curl test:**
  curl -u "username:password" http://cellocad.org:8080
- **Get a netlist:**
  curl -u "username:password" http://cellocad.org:8080/netsynth -X POST --data-urlencode "verilog_text@demo_verilog.v"
- **Design a circuit:**
  curl -u "username:password" -X POST http://cellocad.org:8080/submit \
  --data-urlencode "id=demo001" \
  --data-urlencode "verilog_text@demo_verilog.v" \
  --data-urlencode "input_promoter_data@demo_inputs.txt" \
  --data-urlencode "output_gene_data@demo_outputs.txt"
- **Get a list of your completed jobs:**
  curl -u "username:password" -X GET http://cellocad.org:8080/results
- **Get a list of result file names from a job result:**
  curl -u "username:password" -X GET http://cellocad.org:8080/results/demo001
- **Get the contents of a specified file. For example, the file specifying the top-scoring assignment::**
  curl -u "username:password" -X GET\
  http://cellocad.org:8080/results/demo001/demo001_A000_logic_circuit.txt
- **Post a UCF:**
  curl -u "username:password" -X POST http://cellocad.org:8080/ucf/test.UCF.json --data-urlencode "filetext@myName.UCF.json"

- **Validate a UCF file:**
  curl -u "username:password" -X GET http://cellocad.org:8080/ucf/myName.UCF.json/validate
- **Delete a UCF file:**
  curl -u "username:password" -X DELETE http://127.0.0.1:8080/ucf/myName.UCF.json
- **Run Cello using a very specific UCF file:**
  curl -u "username:password" -X POST http://cellocad.org:8080/submit \
  --data-urlencode "id=demo001" \
  --data-urlencode "verilog_text@demo_verilog.v" \
  --data-urlencode "input_promoter_data@demo_inputs.txt" \
  --data-urlencode "output_gene_data@demo_outputs.txt" \
  --data-urlencode "options=-UCF myName.UCF.json -plasmid false -eugene false"

# 2 Using the Python API

The Cello Python API is contained in the "**pycello**" folder.

- To use the API, you must install Python and pip.
- Set environment variables:
  - Mac and Linux users: Open a terminal and set the environment variables:
    export CELLOUSER=username
    export CELLOPASS=password
  - Windows Users can set environment variables by typing "Environment Variables" in 'Search' and adding the above two environment variables.
- Go to the pycello folder (in your terminal) and type:
  sudo pip install .
- Check if installation was successful by typing:
  cello
  If installation was successful, you should be able to see the welcome message
  Usage: cello_client.py [OPTIONS] COMMAND [ARGS]...
  Along with a list of available python commands.

## Commands

- **Get a netlist:**
  cello netsynth --verilog demo_verilog.v
- **Design a circuit:**
  cello submit --jobid "pythonTest" --verilog demo_verilog.v --inputs Inputs.txt --outputs Outputs.txt
- **Get a list of your completed jobs:**
  cello get_results
- **Get a list of result file names from a job result:**
  cello get_results --jobid="pythonTest"
- **Get the contents of a specified file. For example, the file specifying the top-scoring assignment::**
  cello get_results --jobid="pythonTest" --filename "verilog.v"
- **Post a UCF:**
  cello post_ucf --name newJSON.UCF.json --filepath myJSON.UCF.json
  **Note :** If you are modifying the UCF file from cello (Eco1C1G1T1.UCF.json), please run the following:
  python exclude_cytometry_data.py Eco1C1G1T1.UCF.json > newUCF.UCF.json
- **Validate a UCF file:**
  cello validate_ucf --name newJSON.UCF.json
- **Delete a UCF file:**
  cello delete_ucf --name newJSON.UCF.json
- **Run Cello using a very specific UCF file:**
  cello submit --jobid "pythonTest2" --verilog demo_verilog.v --inputs Inputs.txt --outputs Outputs.txt --options="-UCF myName.UCF.json -plasmid false -eugene false"

## Using ucf_writer.py

To convert CSVs containing Cello Library specific information into UCF.json, you can use the ucf writer.py script. To use this, try:
python ucf_writer.py gates_Eco1C1G1T1.csv > newJSON.UCF.json