Access and usage of the IGBMC HPC cluster

First you need to verify that your environment is properly set.

```
>ssh login@surf
```

The sbatch command allow you to submit a script with commands to the cluster

```
>sbatch -p surf cmd
```

- The command then gives a job execution number.
-
  ```
  >scontrol show job <job-number>
  ```

  allows you to follow the execution of the job
-
  ```
  >scontrol show job <job-number>
  ```

  allows you to kill the job

The job will generate output files:

- *slurm-<job-number>.out* in the directory from which the sbatch command was executed
- *slurm-<job-number>.e* in case of errors

In case of necessity the debug line

```
sbatch -p debug
```

allows you to use two additional lames (16 procs with 24GB memory)

There are options to:

- specify the memory required

  ```
  >sbatch -p surf --mem=xxMB
  ```
- specify the number of processors required

  ```
  >sbatch -p surf --cpus--per-task=24
  ```

  (if you specify more than 24, the number of available lames for your job will be very limited)

The cmd script must start with

```
#!/bin/bash
```

and should set the necessary environement. All alias can be checked with the command

```
>alias
```

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Last update: **2023/11/01 20:17**