# MR\_ACR installation instruction

* Download factory tools:   
    
  git clone https://bitbucket.org/MedPhysNL/wadqc.git <<TOOLSDIR>>
* Clone repository to local machine:  
    
  git clone http://gitlab.nki.nl/m.barsingerhorn/mr\_acr.git <<REPODIR>>
* Make factory module zip file:  
    
  cd <<REPODIR>>  
  pipenv sync   
  pipenv shell   
  cd ..   
  mkdir <<FACTORY\_OUTPUT\_DIR>>  
  cd <<TOOLSDIRS>>/Tools  
    
  python .\make\_factory\_module.py -m zip -i <<REPODIR>>\manifest.json -d <<FACTORY\_OUTPUT\_DIR>>
* SSH to WAD server and install Docker daemon:  
    
  sudo apt install docker   
  usermod -a -G docker <<user>>
* Reboot server
* WINSCP to WAD server. Copy contents of <<REPODIR>> directory to wad server.
* SSH to WAD server, cd to directory containing <<REPODIR>>. Build docker container:  
    
  docker build –t mr\_acr .
* In the WAD management interface:
  + Select: “Import modules/selectors”, select “browse” and select created zip file from <<FACTORY\_OUTPUT\_DIR>>. Then press “Import”
  + Select: “Module configs”, scroll down if required and press: “new“
    - Add a name and description, these can be anything.
    - For module select: MR\_ACR
    - For datatype select: dcm\_study
    - Browse to config file name: <<REPODIR>>\config\module\_config.json
    - Browse to meta config file name: <<REPODIR>>\config\meta\_config.json
    - Finally press: Submit
  + Select: “Selectors”, scroll down if required and press: “new“
    - Add name and description, these can be anything.
    - Check “isactive” checkbox
    - In “config” listbox, select config with name you created earlier
    - Press “Submit”
  + In the overview with selectors, go to the just created selector and press “edit”
    - In “extra rules to add” enter ‘1’ and press enter
    - In the new rule enter “Modality” for tag and “MR” for value. (Don’t enter the parenthesis)
    - Press: “Submit”
* Send a dataset to the WAD server and test functionality