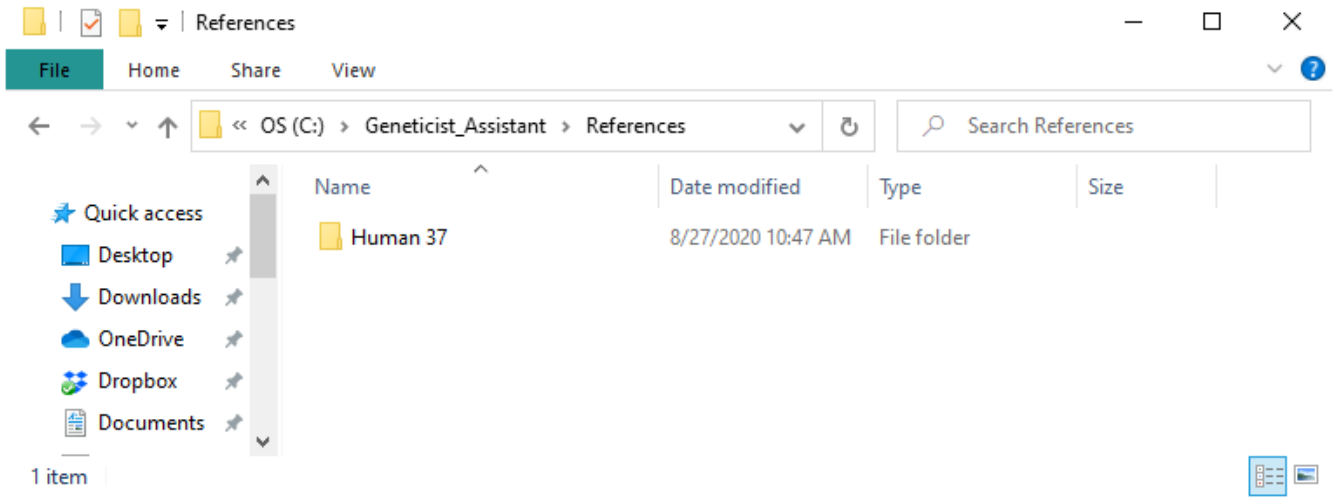
Geneticist Assistant Quick Start Guide

- ## Download
  - Download GeneticistAssistantSetup_*.exe from the SoftGenetics ftp server.
  - Download references_minimal.zip from SoftGenetics ftp server.
  - Contact tech_support@softgenetics.com for download information if you don't have it.

- ## Create Reference folder
  - Create a folder anywhere on your computer for the Geneticist Assistant reference files.
  - Extract the downloaded references_minimal.zip file and copy the resulting Human 37 folder into the reference folder created.



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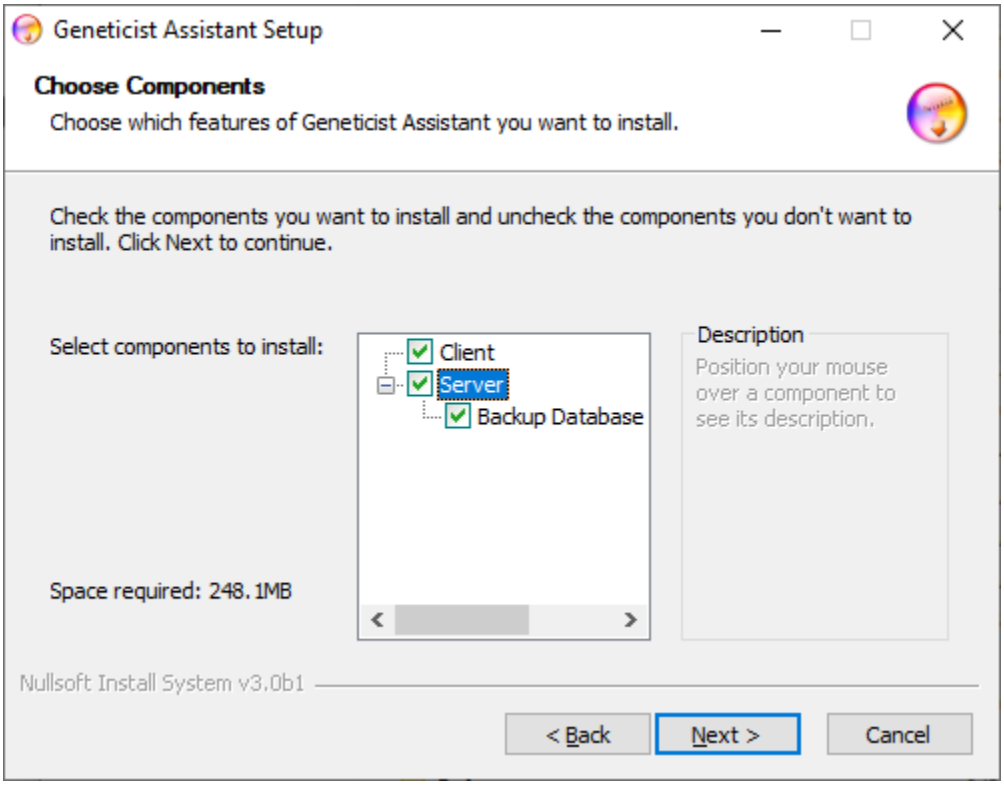
- Install
  - Run GeneticistAssistantSetup_*.exe
  - Install the server and client on the computer you wish to run the server from.
  - Install just the client on other computers



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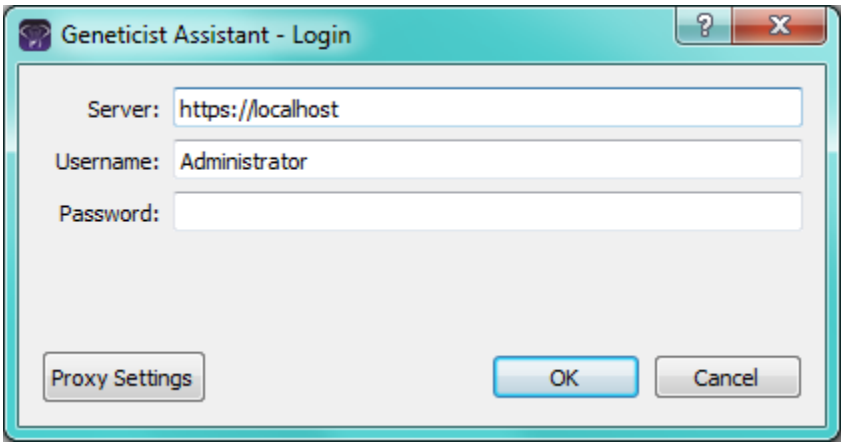
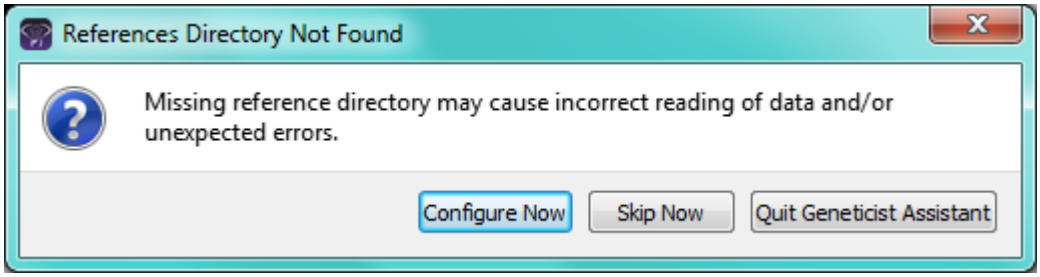
- Log in
  - Server: Name of the computer running the server
  - Username: The user name you set up during install
  - Password: The password you set up during install



- Configure Reference Directory
  - After opening Geneticist Assistant, you will be prompted to configure the reference directory - Click “Configure Now”



  - Browse to and select the directory you created containing the Human 37 reference folder.

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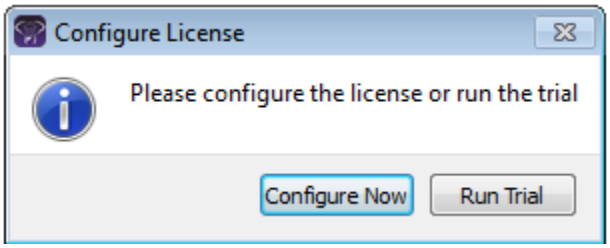
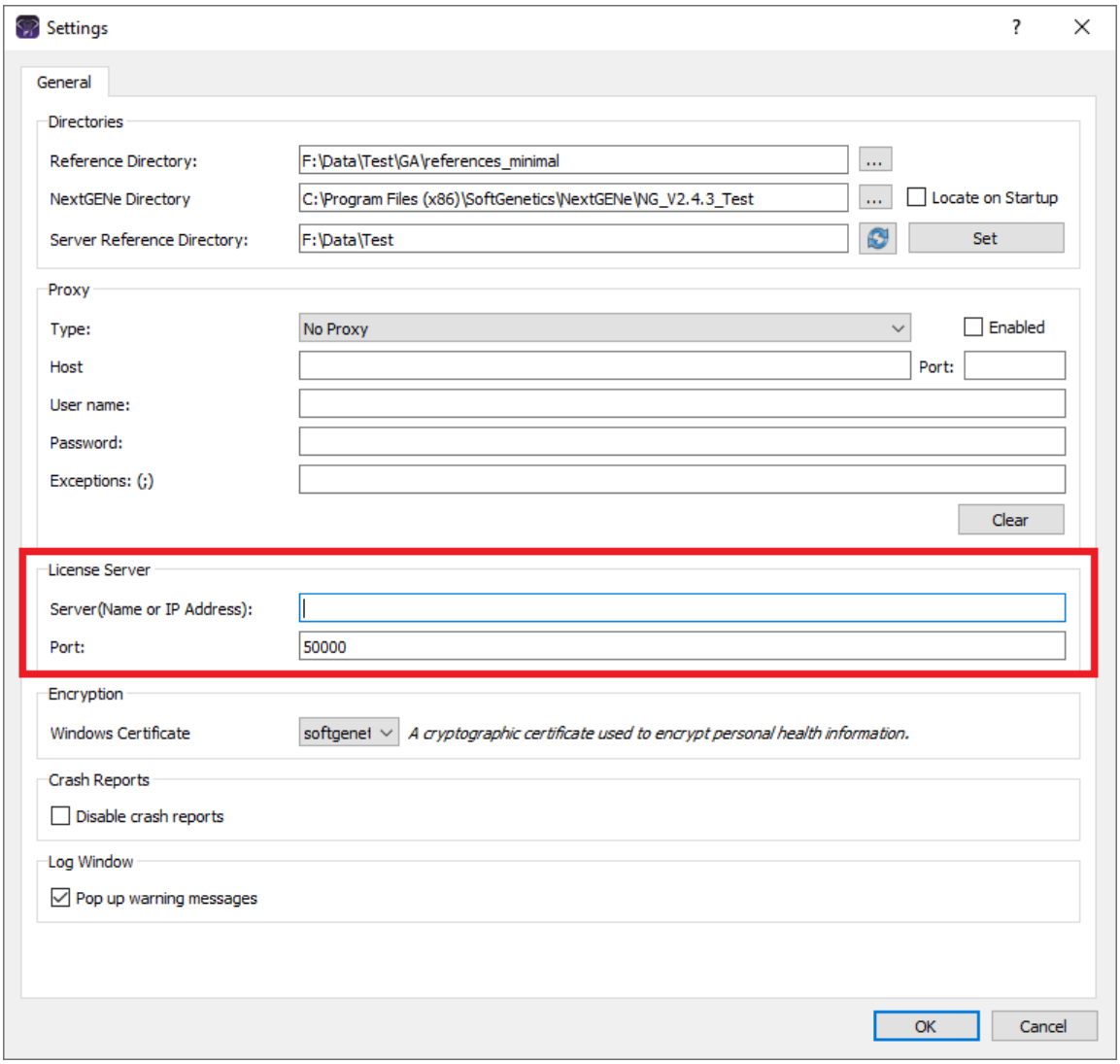
- Configure License
  - Registered user click "Configure Now". All others click "Run Trial"



  - Set the server to the computer with the License Server installed
    - The default port is 50000
    - License Server installation is described in a separate guide. Contact SoftGenetics to obtain this if needed.



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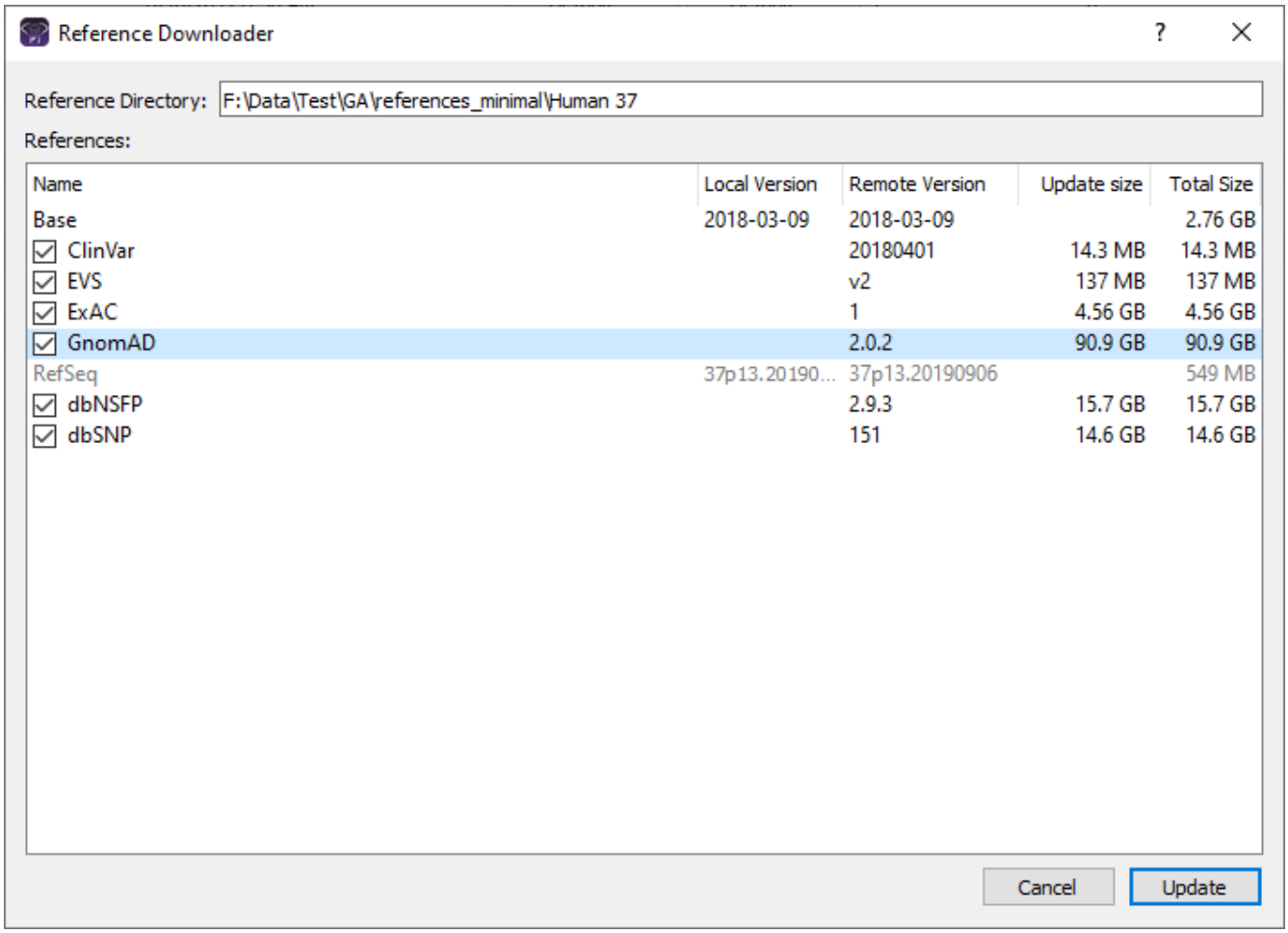
- ## Download Annotation Databases
  - Click the “Ref” button at the top right of Geneticist Assistant
  - Select databases to be downloaded and click “Update”



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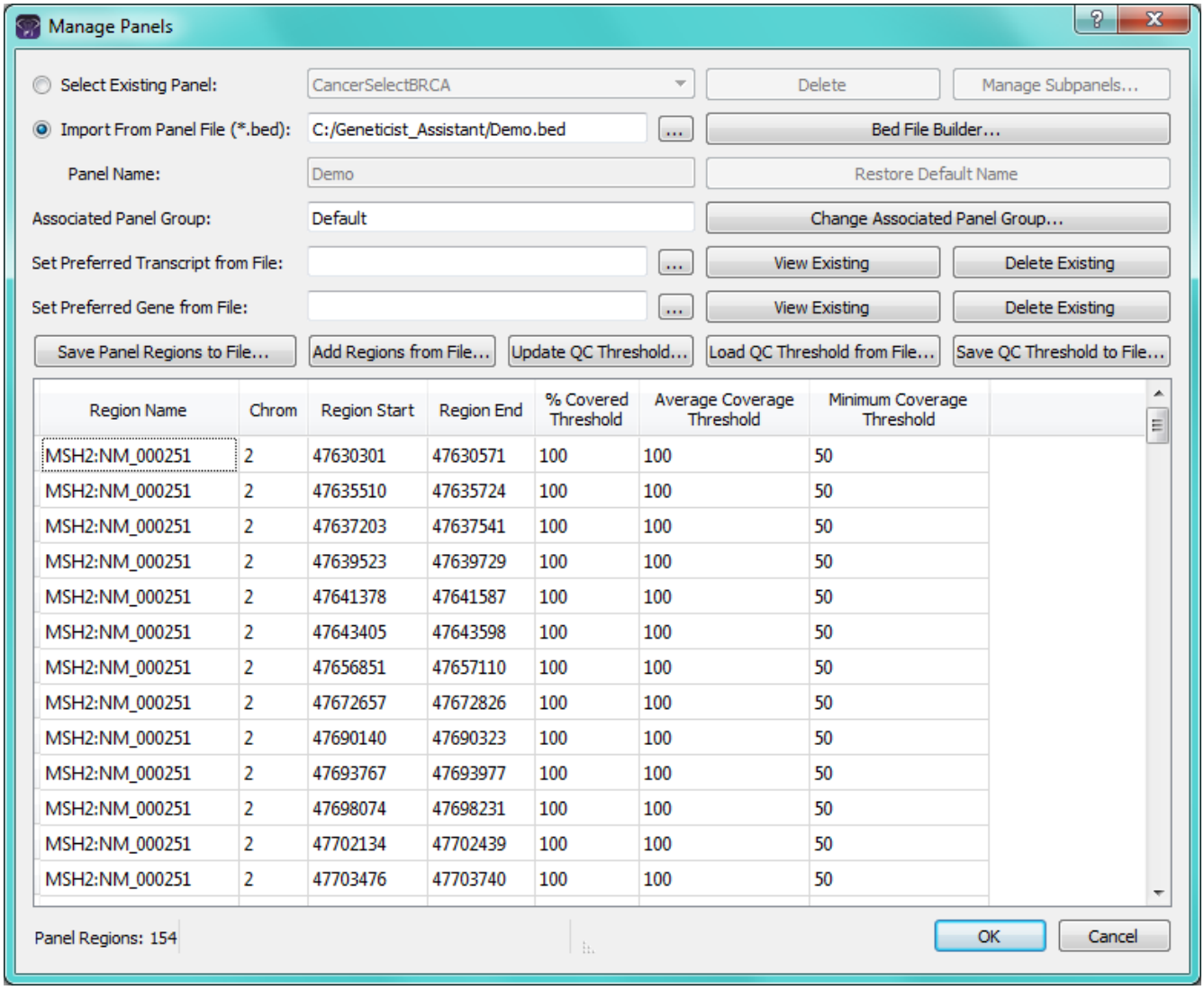
- ## Create Panel
  - Go to: Panels->Manage Panels
  - Select "Import From Panel File (*.bed)"
  - Click "…" to browse to and select a BED file to add as panel
  - Click "Import Panel" to load BED file regions
  - Click "OK" to import the panel



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- ## Submit New Run
  - File > New Run
  - Enter a name for the run
  - Click "Select Variant and/or Coverage Files" to browse to and select your data files.
    - You can select multiple BAM and VCF files at the same time. They will be automatically paired based on their filename.
  - Click "OK" to submit the samples.