

Step 1: Install the Standalone BAS program. Download and extract the files from <http://utopia.csis.pace.edu/cs691/2009-2010/team4/team3/> “Specific Deliverable 4” “biofeature.zip” to a scratch/temporary directory on your local disk. Locate the biofeature.bat file from the extracted files and move it into the “C:\it691\BAS” directory. This is the same directory you used for deliverable 1. **Only copy the biofeature.bat file.** The Refactored-BAS.bat and Refactored-BAS.jar are older versions than the one you setup in deliverable 1.

After extracting the files, you should have in the c:\it691\BAS directory the following files. Additionally, the directory will contain metadata, dichotomy, and results files created in deliverable 1:

- Calculator.bat
- Refactored-BAS.bat
- Refactored-BAS.jar
- Biofeature.bat

Step 2: Download the Raw Data Files

Download the raw data files for this experiment from Utopia. The raw data can be found in the following location:

sftp://utopia.csis.pace.edu/2009-2010/team4/rawdata/FableLaptop.zip

*180 text files should be downloaded.

The “C:\it691\rawdata” directory will be used for this deliverable.

Step 3: Download the demographics file

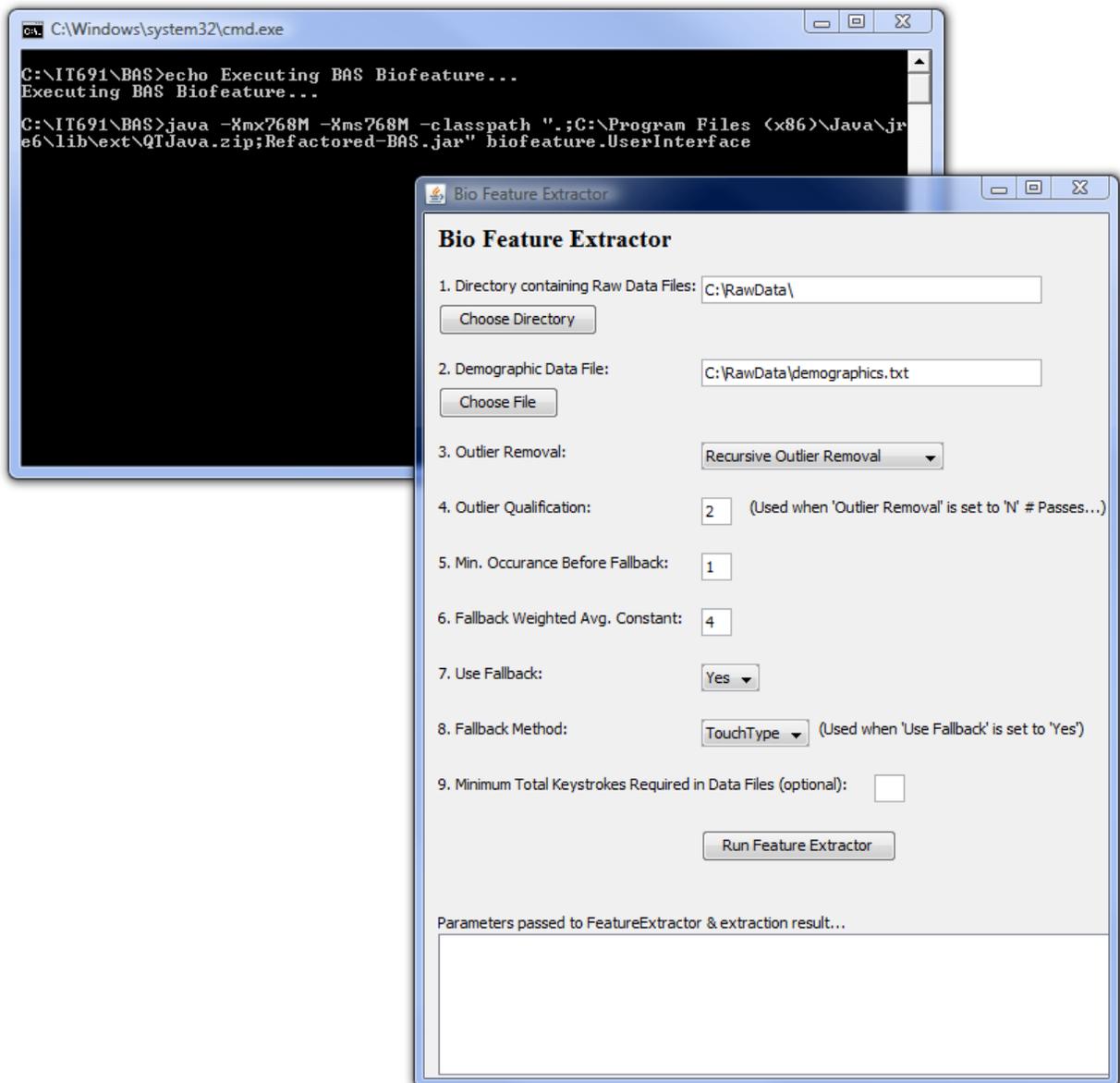
From the same Utopia location detailed in the previous step, download the demographics.txt file to your local disk. This file should be moved to the “C:\it691\demographics” directory.

Step 4: Create the results directory for the processed feature file

- **Create the following directory:**
“C:\it691\BAS\features”

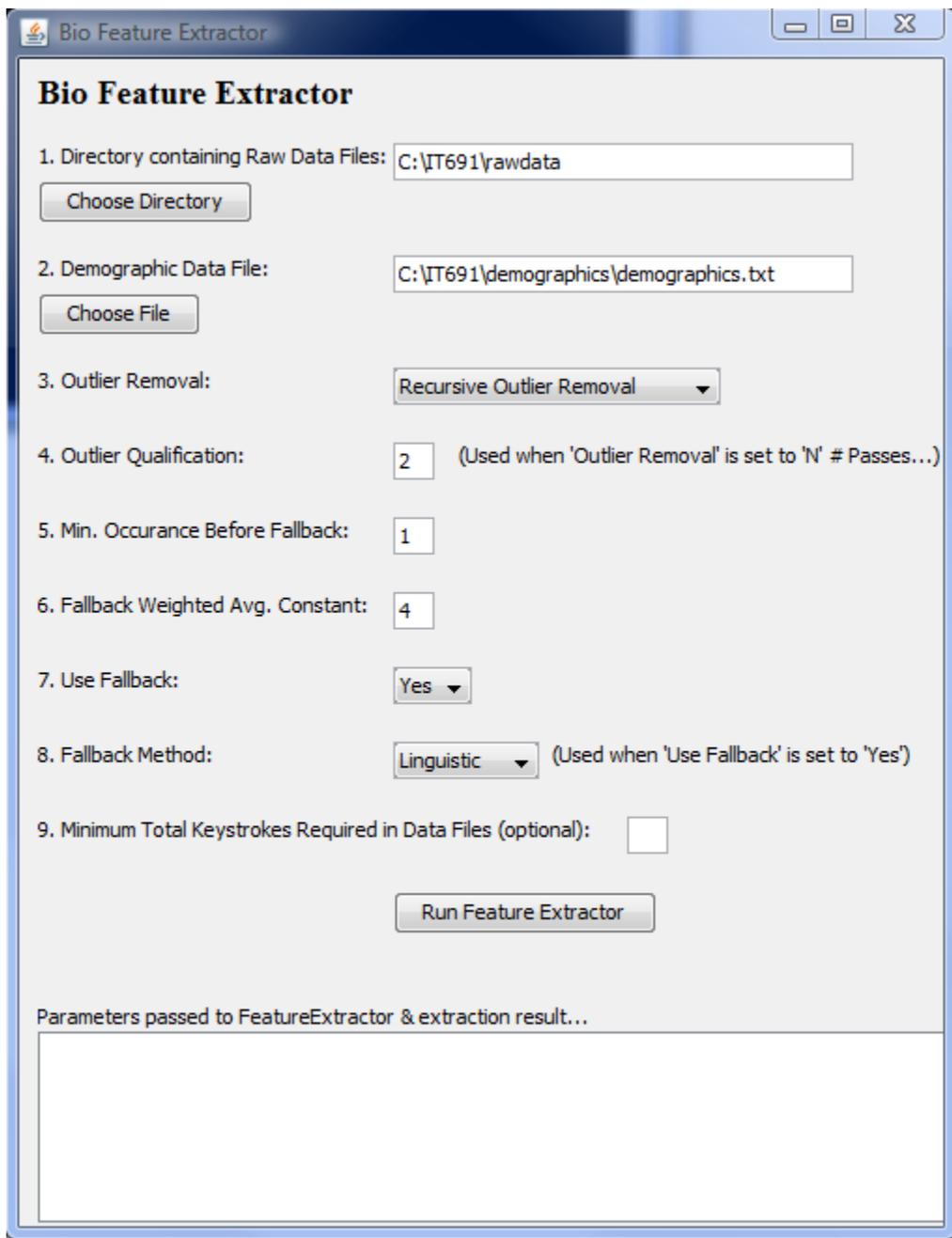
Step 5: Launch the Bio Feature Extractor

Run the Biofeature Extractor application from Windows Explorer or the command prompt. The following screen should display if you launched BAS successfully:



The command window can be minimized if desired, but must not be closed.

- Fill in the Raw Data File location and Demographics File location fields. All other fields should remain at their default values. You can also use the Choose Directory button to navigate to the desired paths.
- Change the default fallback method from TouchType to Linguistic.

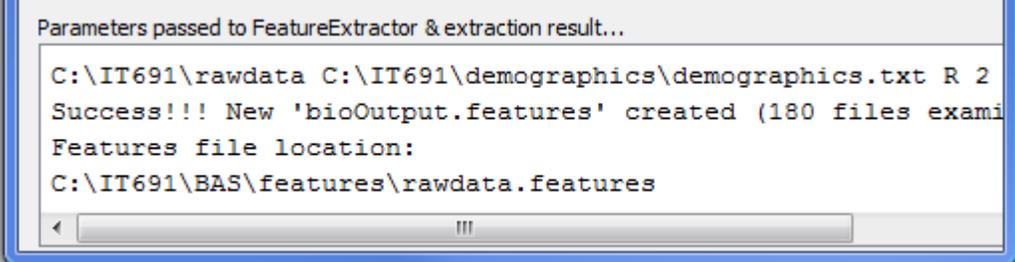


The screenshot shows the 'Bio Feature Extractor' application window. The title bar reads 'Bio Feature Extractor'. The main window has a title 'Bio Feature Extractor' and contains the following configuration options:

1. Directory containing Raw Data Files:
2. Demographic Data File:
3. Outlier Removal:
4. Outlier Qualification: (Used when 'Outlier Removal' is set to 'N' # Passes...)
5. Min. Occurance Before Fallback:
6. Fallback Weighted Avg. Constant:
7. Use Fallback:
8. Fallback Method: (Used when 'Use Fallback' is set to 'Yes')
9. Minimum Total Keystrokes Required in Data Files (optional):

Parameters passed to FeatureExtractor & extraction result...

- Click on the Run Feature Extractor button. While the application is running, messages will scroll in the command window. After processing completes, a success message displays in the results window at the bottom of the application window:



```
Parameters passed to FeatureExtractor & extraction result...
C:\IT691\rawdata C:\IT691\demographics\demographics.txt R 2
Success!!! New 'bioOutput.features' created (180 files examined)
Features file location:
C:\IT691\BAS\features\rawdata.features
```

- If the processed feature file does not exist in the feature results directory: “C:\it691\BAS\features\rawdata.features”, you likely did not create it in Step 4 above. To correct this problem, check to make sure all parts of Step 4 are complete, and run the feature extractor again.
- After the rawdata.features file is created, you can exit the Bio feature Extractor application window by clicking on the “X” in the top right of the window. The command window will close automatically.

Step 6: Check the Features File

- You will need a file manager, such as Windows Explorer and a text editor for this step. Navigate to “C:\it691\BAS\features”. Check for the existence of the “rawdata.features” file. It should be 816 KB in size.
- Using a text editor, open the file. Be sure to turn word wrap OFF so the file is readable.
- The top portion of the file should look similar to this:

```
Keystroke biometric data, Unknown/Unknown, created 1/26/2010
180
ANCEY VARGHESE/Female/20 - 29, Right, LAPTOP, FABLE 1, 230, 0.7266667491162182, 0.727104133131765, 0.6369769516470855,
ANCEY VARGHESE/Female/20 - 29, Right, LAPTOP, FABLE 1, 230, 0.7630007359389196, 0.7743209305003186, 0.644236238161651,
ANCEY VARGHESE/Female/20 - 29, Right, LAPTOP, FABLE 1, 230, 0.7684780204670636, 0.7639645139271874, 0.6928610271156311,
ANCEY VARGHESE/Female/20 - 29, Right, LAPTOP, FABLE 1, 230, 0.7833716752003784, 0.6794804639616254, 0.5479103453949666,
ANCEY VARGHESE/Female/20 - 29, Right, LAPTOP, FABLE 1, 230, 0.787878446293536, 0.8018513936972236, 0.5831567092775979,
ANNIE GRENCI/Female/30 - 39, Right, LAPTOP, FABLE 1, 230, 0.7359144654574524, 0.5593334132141434, 0.33217605305386816,
```

- It is important that the number 180 appear on the second row of the file. The file should contain 182 rows (180 data rows plus the file header).