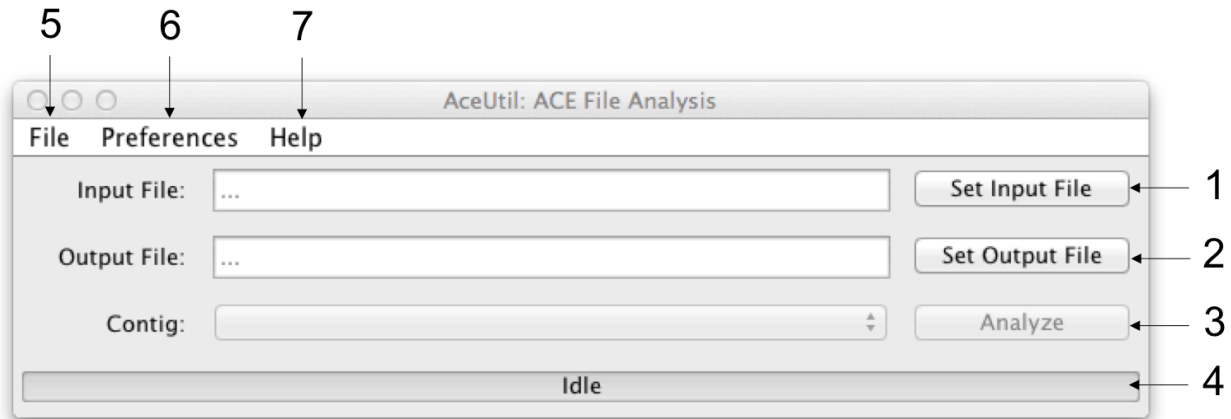**Main Window Quick Reference**

To Run AceUtil:

1. **Click "Set Input File"** to select a properly formatted ACE sequence assembly file.
    - Contig headers should not contain logical separators: | , / \ etc.
2. **Click "Set Output File"** to select where the output is saved. If the file exists, it will be overwritten. This field is automatically populated in incremental format after setting input.
3. **Click "Analyze"** to start your analysis. This option is not available until file options are set. Upon completion the file is written and a summary printout is available in the command line window.
4. **The Progress Bar** keeps you updated on progress of assembly parsing, building, and analysis.

Other Helpful Features:

5. **All controls** are available through the file menu.
6. **The Preferences Menu** allows you to customize analyses and cutoffs.
    - **Analyses Version:** Always use the most recent unless you have issues. Newer is faster!
    - **Included Analyses:** Allows you to toggle certain analysis on or off – all on by default!
        o **Discfind:** Flag discrepancies across the entirety of coverage in the genome
        o **DistStrand:** Flag strand-based discrepancies in the genome
        o **LowCov:** Flag areas of low coverage in the genome
        o **LowStrand:** Flag strand-based discrepancies in the genome
    - **Write Output:** Not writing output is useful for diagnostic purposes, especially when run through a command line. Use this option to save time during troubleshooting.
    - **Settings:** Launches a dialogue that allows you to customize settings in the program
        o **Default AceUtil Directory**
        o **Cutoff Adjustment for Analyses**
            - **Percentage cutoffs for discrepancies**
            - **Read count cutoffs for coverage**
        o **Ability to Save settings for repeated use**
7. **The Help Menu** lets you report the current version.