**Table S1**. Integrated Biomedical System command line utilities for data loading. These extract, transform, and load (ETL) modules provide administrator tools capabilities for bulk loading of data files. Tools are run with the prefix “rails runner lib/utilities/<ETL loader.rb> <parameters>.

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| **Data** | **Command line data loader** |
| Actigraph sleep | actigraph\_sleep\_loader.rb |
| EPA air data | air\_loader.rb <filename> |
| Intel Basis B1 | basis\_file\_loader.rb <filename> <user id> |
| NCBI gene | drug\_gene\_loader.rb <filename> |
| Empatica | empatica\_zip\_loader.rb <filename> <user id> |
| Food list | food\_loader.rb <filename> |
| NCBI gene | gene\_info\_loader.rb <filename> |
| PharmGKB  | genes\_loader.rb <filename> |
| Hexoskin | hexoskin\_ecg\_loader.rb <filename> <user id> |
| Vocal Matlab  | mat\_loader.rb <filename> <user id> |
| MyTracks | my\_tracks\_loader.rb <filename> <user id> |
| Moves | moves\_file\_loader.rb <filename> <user id> |
| Pathways | pathway\_loader.rb <filename> |
| Basis Peak | peak\_file\_loader.rb <filename> <user id> |
| RCSB PDB | pdb\_loader.rb <filename> |
| Equivital SEM | sem\_hr\_loader.rb <filename> <user id> |
| Equivital SEM | sem\_persisted\_loader.rb <filename> <user id> |
| SwissProt | swiss\_loader.rb <filename> |
| VCF variants | vcf\_loader.rb <filename> <user id> |
| Vocal | vocal\_loader.rb <filename> <user id> |
| Zephyr Bioharness | zephyr\_loader.rb <filename> <user id> |