1. ~~Re-run join of egg takes table with new fields added by brian (Year, Brood code, Number of unmarked spawners, Number of marked spawners)~~
   1. ~~add stock ID (done; code already does this)~~
   2. ~~add pHOS from SPI~~
   3. ~~calculate pNOB~~
   4. ~~calculate pHOB~~
   5. ~~calculate PNI~~

Caveats

* caveat: this PNI calc is only correct for brood codes released in the basin the pHOS came from (and the wild spawners)
* pHOS calculated only for “mixed” or “wild” origin\_desc brood\_codes, meaning if there are two programs in basin pNI is wrong
* PNI may be biased even for integrated programs if some crosses in integrated program were HxX and origin\_desc was hatchery
* Could explore redo-ing by release location somehow

NOTES

1. Spatial join release locations from releases table to stock\_id; add in the NOAA pop name