Stock\_run\_species-based 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

Release\_location -based pNI caveats

* Uses pHOS of NOAA designated species, run at release site; if no match, uses species only (e.g., winter steelhead pHOS in elochoman for winter run releases)
* pNOB is calculated across all releases in that noaa-defined population (even if a mix of segregated and integrated—no ability to differentiate the two reliably anyway since program is not a field in fishbooks, and hxh crosses, even if integrated, will not be differentiable from hxh seg crosses if stock name is same (e.g., beaver creek vs. deep river coho).
* When releases occur out of basin but adults are returned to basin (tilton coho), we had to manually “change’ the smolt release location to be tilton so the mapping based match of noaa pop would be correct
* Cases like lower Cowlitz fall chinook are even weirder since broodstock is actually tilton now but is being matched to lower Cowlitz because released there…

NOTES:

1. Why are we missing some brood codes from unique spawn events?
   1. Often because there is a plant record for the brood code but there is not egg take event so the brood code was “immaculately conceived via a transfer from Olympia HQ record” in fishbooks
2. No co-op releases are included in fishbooks (e.g., Coweeman steelhead).