① Species A — TBlastX (1) → Species B → Sub-set of B — TBlastX (2) → Species A → Sub-set of A

② A1 ──────────→ B1 ──────────→ AX

AX=A1 or AX similar to A1?

Yes

No

Discard

Compare

③ Sub-set of Sub-set of A — BlastX → Swissprot/TrEMBL → Species B best hit

① Two reciprocal TBLASTX for comparing species A and species B transcript sequences

② We conserve only the pairs of transcript sequences originating consistent TBLASTX(1) and TBLASTX(2) results

③ We consider previously obtained pairs in order to limit erroneous assignment of orthologous pairs for paralogous ones