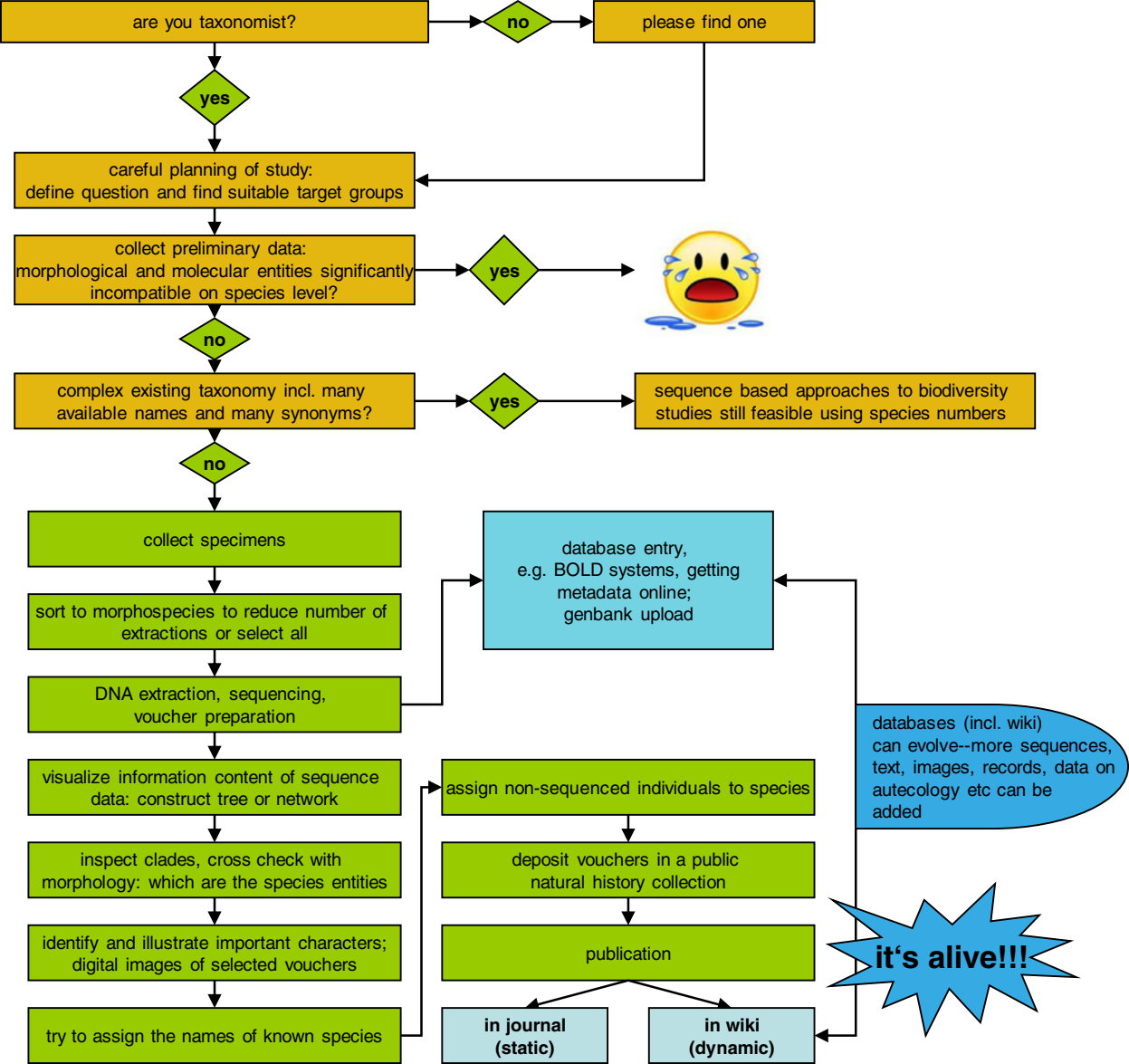
are you taxonomist?
no
please find one
yes
careful planning of study:
define question and find suitable target groups
collect preliminary data:
morphological and molecular entities significantly incompatible on species level?
yes
no
complex existing taxonomy incl. many available names and many synonyms?
yes
sequence based approaches to biodiversity studies still feasible using species numbers
no
collect specimens
sort to morphospecies to reduce number of extractions or select all
DNA extraction, sequencing, voucher preparation
visualize information content of sequence data: construct tree or network
inspect clades, cross check with morphology: which are the species entities
identify and illustrate important characters; digital images of selected vouchers
try to assign the names of known species
database entry,
e.g. BOLD systems, getting metadata online;
genbank upload
assign non-sequenced individuals to species
deposit vouchers in a public natural history collection
publication
in journal (static)
in wiki (dynamic)
databases (incl. wiki) can evolve--more sequences, text, images, records, data on autecology etc can be added
it‘s alive!!!