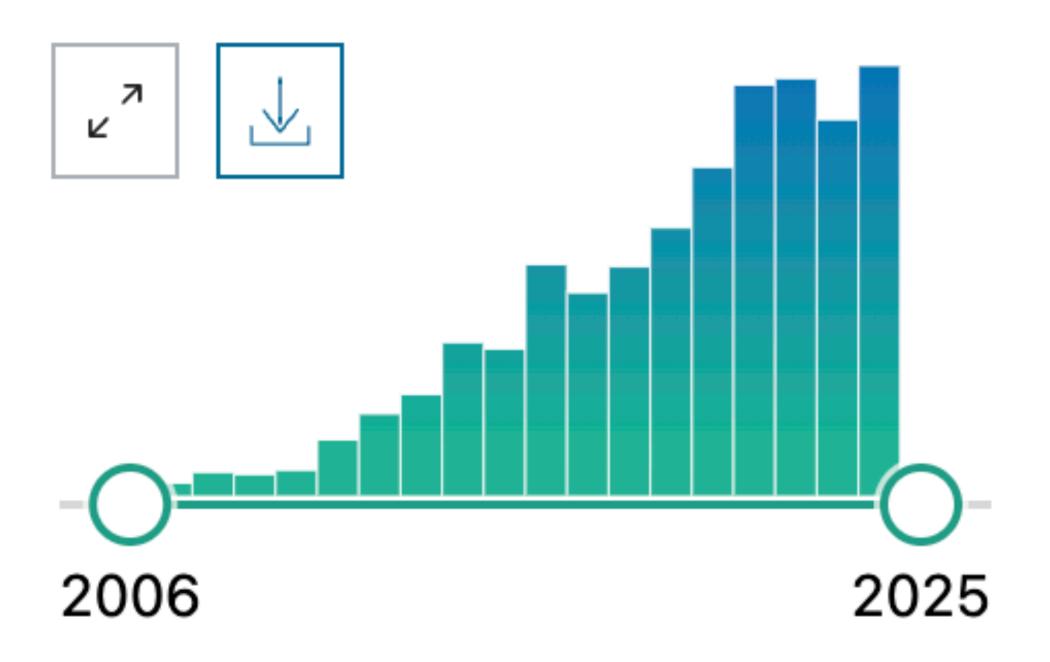
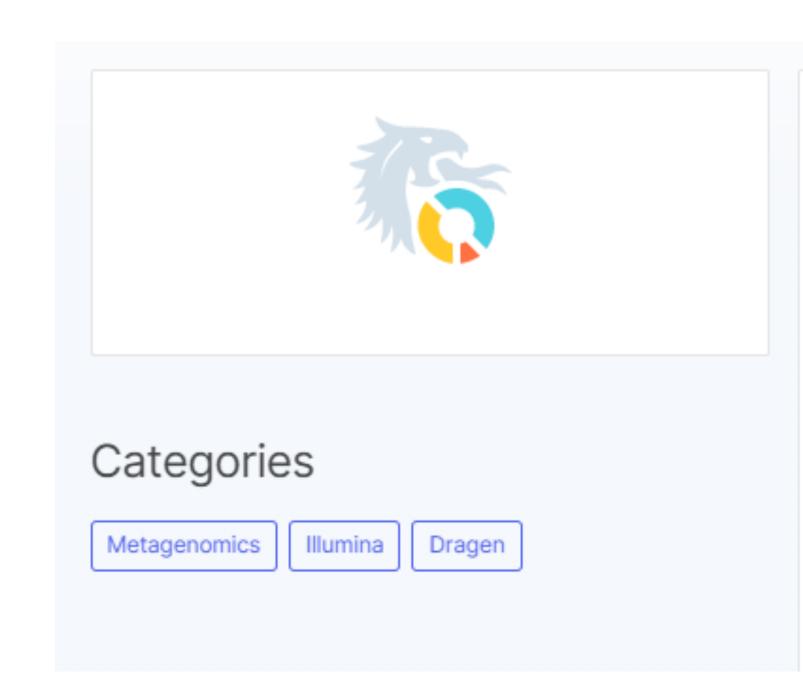
Bioinformatics tools and pipelines

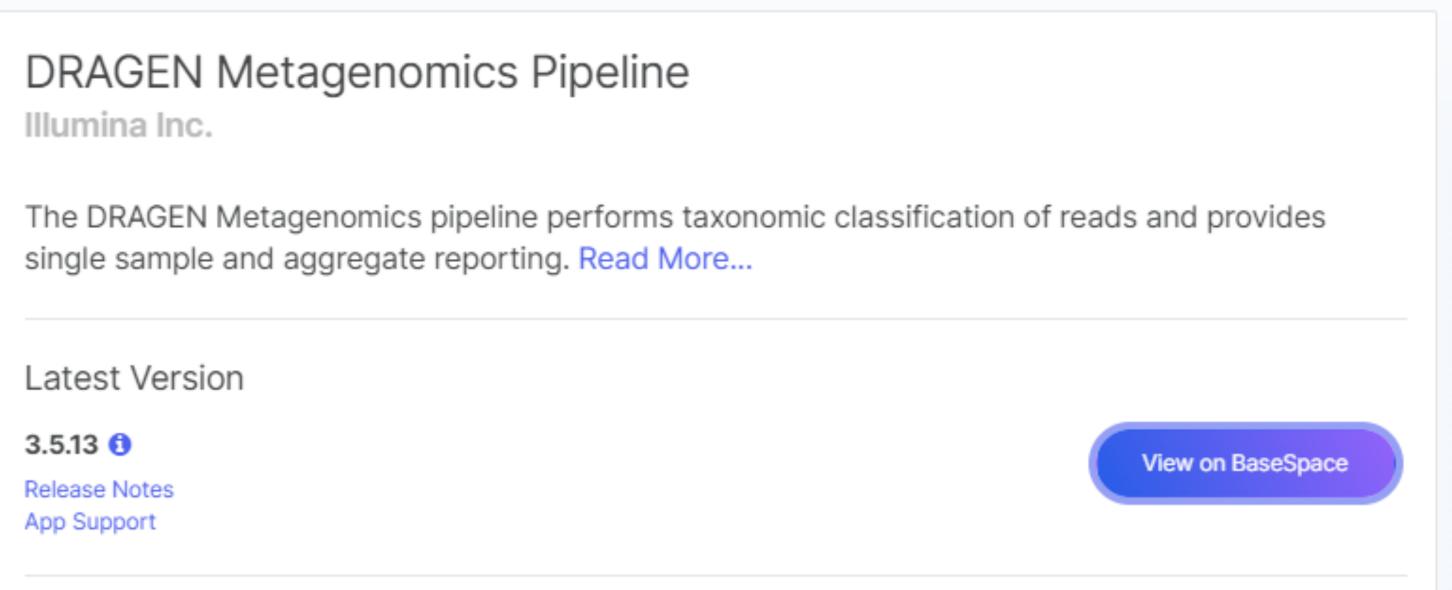
In Metagenomics

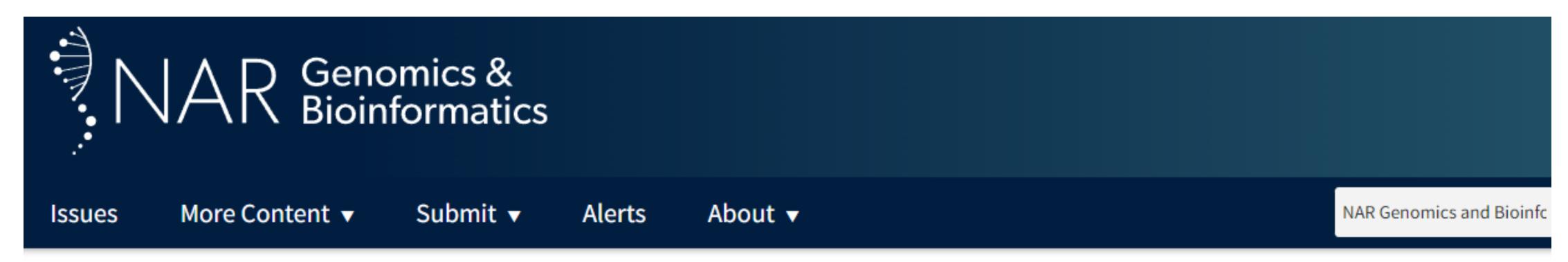
Past, present, and future

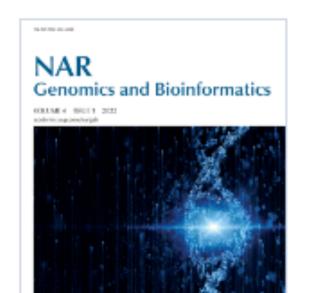
RESULTS BY YEAR











JOURNAL ARTICLE

nf-core/mag: a best-practice pipeline for metagenome hybrid assembly and binning 3

Sabrina Krakau ™, Daniel Straub, Hadrien Gourlé, Gisela Gabernet, Sven Nahnsen