Which overlap mode should I use?

When I wrote htseq-count, I was not sure which option is best and included three possibilities. Now, several years later, I have seen very few cases where the default union would not be appropriate and hence tend to recommend to just stick to union.
Usage and Options

htseq-count [options] <alignment_file> <gff_file>

- `-f <format>, --format=<format>`. (default is sam)
- `-r <order>, --order=<order>`. (default is name)
- `-s <yes/no/reverse>, --stranded=<yes/no/reverse>`. (default: yes)
- `-a <minaqual>, --a=<minaqual>`. (default: 10)
- `-t <feature type>, --type=<feature type>`. (3rd column in GFF file)
- `-i <id attribute>, --idattr=<id attribute>`. (default is gene_id)
- `-m <mode>, --mode=<mode>`. (default: union)
- `-o <samout>, --samout=<samout>`
- `-q, --quiet`
- `-h, --help`