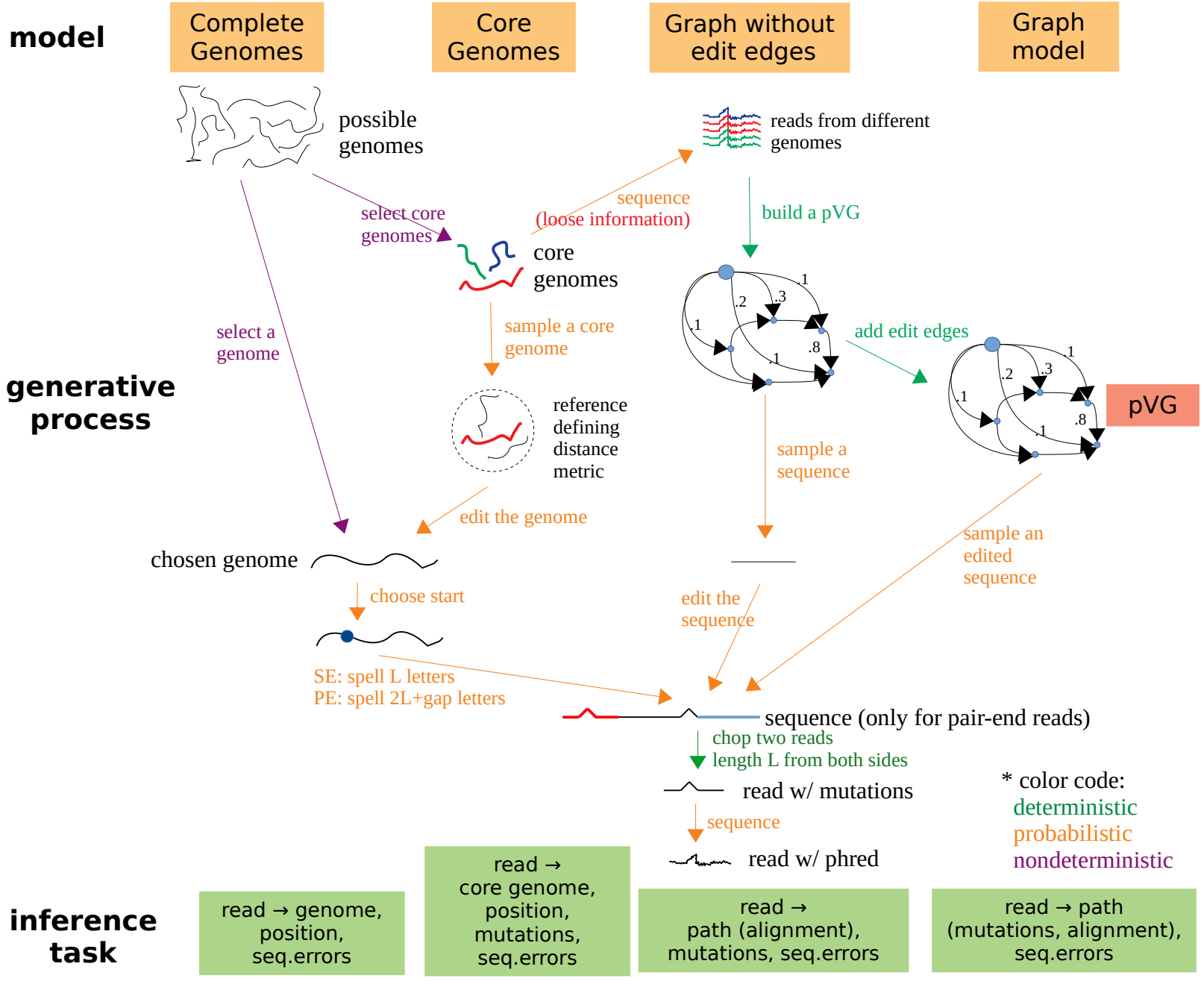
model
Complete Genomes
Core Genomes
Graph without edit edges
Graph model
possible genomes
reads from different genomes
select core genomes
sequence (loose information)
build a pVG
core genomes
select a genome
sample a core genome
add edit edges
generative process
reference defining distance metric
pVG
sample a sequence
edit the genome
chosen genome
sample an edited sequence
choose start
edit the sequence
SE: spell L letters
PE: spell 2L+gap letters
sequence (only for pair-end reads)
chop two reads length L from both sides
read w/ mutations
* color code:
deterministic
probabilistic
nondeterministic
sequence
read w/ phred
inference task
read → genome, position, seq.errors
read → core genome, position, mutations, seq.errors
read → path (alignment), mutations, seq.errors
read → path (mutations, alignment), seq.errors