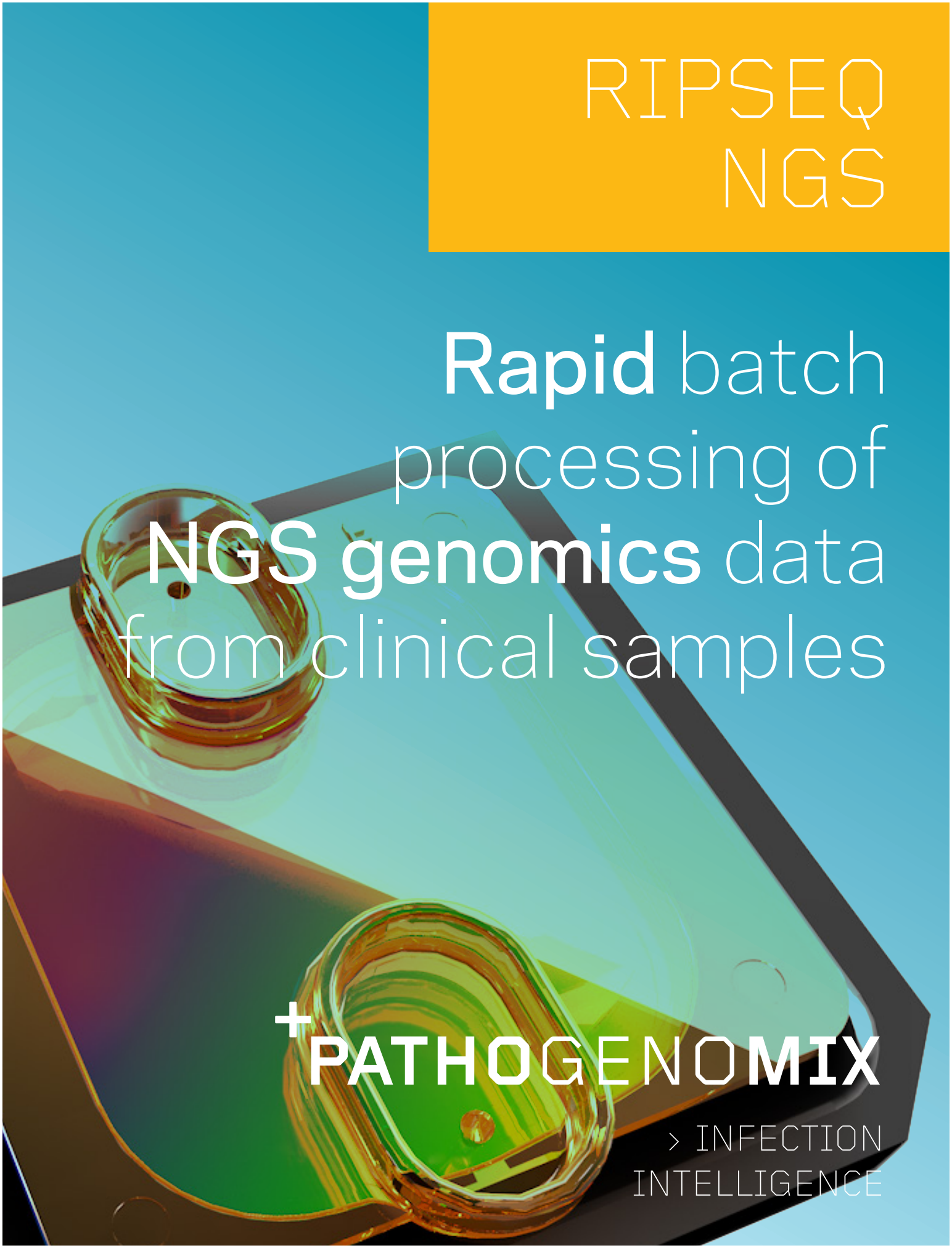
RIPSEQ NGS

Rapid batch processing of **NGS genomics** data from clinical samples



+PATHOGENOMIX

› INFECTION INTELLIGENCE

RipSeq® NGS is an online software tool for rapid bacterial identification, with focus on analyzing any clinical sample - **simple or complex**.

Through the use of advanced clustering algorithms, we remove the need for manual isolation and re-cultivation of colonies from poly-microbial samples prior to 16S rDNA sequencing. This makes direct sequencing using NGS relevant and usable in a clinical setting.

Compared to culture, the possibility to analyze mixed bacterial, fungi or virus populations with direct sequencing offers a significant reduction in time to identification, in particular for samples containing slow growing pathogens, or pathogens for which phenotypical identification is not readily available.

More importantly, it provides a powerful diagnostic tool for patients who have received antibiotics prior to sample collection. For this patient group, culture is unreliable and should never be trusted as the sole diagnostic approach.

Even if growth is obtained for some species, others can already be dead or too affected by anti-infectives to be cultured.

AND - there is no need for expensive bio-informatics resources. RipSeq NGS is as easy as RipSeq Sanger.

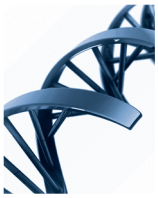
Identification time using traditional methods: **2-7 days or more**

Day 1
PATIENT SAMPLE

Day 2-4
CULTIVATION

Day 3-7
CHEMICAL TESTING

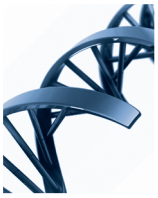
Last resort
SEQUENCING



RipSeq NGS identifies ALL bacteria in a sample in MINUTES!

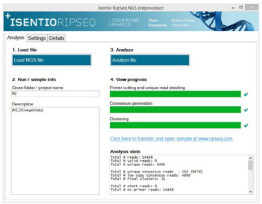
Day 1
PATIENT SAMPLE

Day 1
NGS SEQUENCING



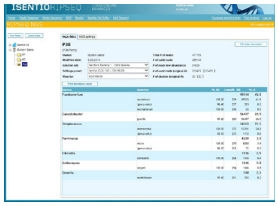
NGS sequencing using universal primers will with the latest NGS equipment result in nice long-enough reads for bacterial ID, without the need for further assembly.

Day 1
LOCAL PREPROCESSING



RipSeq Preprocessor will filter and cluster all reads in the big data NGS file, reducing the sequences needed for upload by a factor of 1000+. All in less than 2 minutes (for a 500K read file)

Day 1
RIPSEQ CLOUD ID



RipSeq NGS in the cloud will then analyze the uploaded reads using our advanced algorithms toghether with our curated Ripseq DB databases, and generate the abundance report. All in just over a minute.

W: www.ripseq.com
W: www.pathogenomix.com
M: contact@pathogenomix.com
P: +1 408 712 0550

PATHOGENOMIX

› INFECTION INTELLIGENCE