NGS - GAME CHANGING FOR SCIENCE AND HEALTH TECH

Next Generation Sequencing

NGS can be used for studying microbiomes, identifying bacteria, studying infectious disease, discovering novel pathogens, cancer research and investigating genetic diseases/disorders.

NGS easily explained in steps

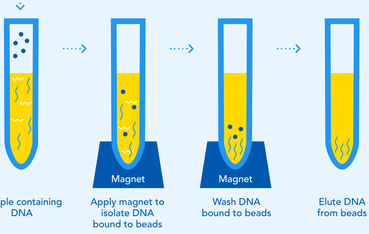
Step 1

LIBRARY PREPARATION

- Pipetting various reagents and buffers
- Transferring the sample DNA
- Transferring master mixes
- Sample normalization
- Adding index adapters to samples
- Bead-based purification with multiple washing steps

PRINCIPLE OF BEAD-BASED PURIFICATION

Add magnetic beads to DNA



Sample containing DNA | Apply magnet to isolate DNA bound to beads | Wash DNA bound to beads | Elute DNA from beads

Step 2

SEQUENCING

The libraries get loaded onto a flow cell and placed on the sequencer. DNA fragments binds to the surface of the flow cell and are then amplified , creating clusters of millions of copies of single-stranded DNA.

Step 3

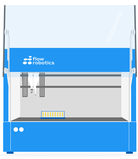
DATA ANALYSIS

The sequence reads are assigned to the appropriate samples and aligned to a reference genome.

More than **300 pipette tasks** per 96 well plate when using an 8-channel pipette.

That's around 2,500 when using a single-channel pipette. This is an **extremely heavy workload** to carry out manually.

flowbot® ONE can help



Automate your library preparation for:

- Greater accuracy
- Less cross contamination
- Better work environment

SIGN UP FOR A FREE DEMO

Go from manuel pipetting to an easy and flexible automated setup with flowbot® ONE

Contact us for a demo that fits your needs:
flow-robotics.com/demo

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