

# EBI ENA

## Introduction

The European Nucleotide Archive (ENA) is part of the European Bioinformatics Institute (EBI) and it's a **repository for experimental sequence data**.

## Using ENA for Metagenomics

### Uploading data

A first scenario is creating our own metagenomics project in the ENA database, and using it to upload and share our data. It is wise to upload data as soon as possible, as it will be automatically annotated with the Metagenomics pipeline from EBI.

### Metadata layers

Each sample can be modelled as a **sample object**, and the data can be attached to it. The sample objects are searchable using metadata, and then they will link to the downloadable sequencing data (after it has been publicly released). The **experiment** represents the sequencing library, while the **run** object is actually a container for reads files.

Sample ← Experiment ← Run

### Retrieving data

From:  
<https://seq.space/notes/> - **Bioinformatics Notes**

Permanent link:  
<https://seq.space/notes/doku.php?id=ena>

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