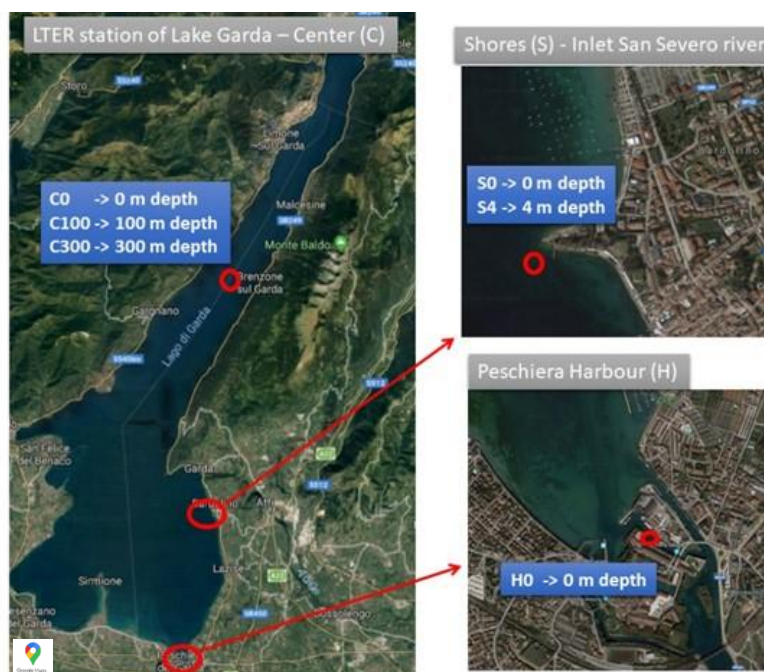


EAW FASTQ files for bioinformatic courses (18S rRNA genes)

Selection of 6 samples, with 6 Forward (R1) and 6 Reverse (R2) files, including primers. R1 and R2 reads are ca. 300 bp long, and were obtained by Illumina MiSeq technologies, at the FEM facility sequencing platform. The files refer to the 18S rRNA gene reads obtained from the analyses carried out on the samples collected and filtered (Sterivex™ 0.22 µm) in different areas and depths of Lake Garda on September 2018. Sampling and analyses were carried out in the framework of the project Eco-AlpsWater (ASP569), funded by the Interreg Alpine Space program, <https://www.alpine-space.eu/projects/eco-alpswater/en/home>

Forward (R1)	Reverse (R2)	MapCode
• ECOALPSWATER-18S-386-09-18-0stv_S145_L001_R1_001.fastq	• ECOALPSWATER-18S-386-09-18-0stv_S145_L001_R2_001.fastq	S0
• ECOALPSWATER-18S-386-09-18-4stv_S146_L001_R1_001.fastq	• ECOALPSWATER-18S-386-09-18-4stv_S146_L001_R2_001.fastq	S4
• ECOALPSWATER-18S-B0918D1stv_S141_L001_R1_001.fastq	• ECOALPSWATER-18S-B0918D1stv_S141_L001_R2_001.fastq	C0
• ECOALPSWATER-18S-B0918D4stv_S142_L001_R1_001.fastq	• ECOALPSWATER-18S-B0918D4stv_S142_L001_R2_001.fastq	C100
• ECOALPSWATER-18S-B0918D5stv_S143_L001_R1_001.fastq	• ECOALPSWATER-18S-B0918D5stv_S143_L001_R2_001.fastq	C300
• ECOALPSWATER-18S-Porto0918stv_S144_L001_R1_001.fastq	• ECOALPSWATER-18S-Porto0918stv_S144_L001_R2_001.fastq	H0



Location of the sampling stations included in the dataset. Codes, see table (MapCode).

The reads were obtained using the primers:

TAReuk454FWD1 (5' CCAGCASCYGC GGTAATTCC 3') (Stoeck et al., 2010), and
TAReukREV3_modified (5' ACTTTCGTTCTTGATYRATGA 3') (Stoeck et al., 2010; Piredda et al., 2017),

following the methods described in Salmaso et al. (2018, 2020).

The corresponding 16S rRNA gene reads, obtained from the same eDNA extracts, are saved in
<https://doi.org/10.5281/zenodo.5215815>

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