

# Combining multi-omics data to study in situ biosynthesis in natural plankton communities

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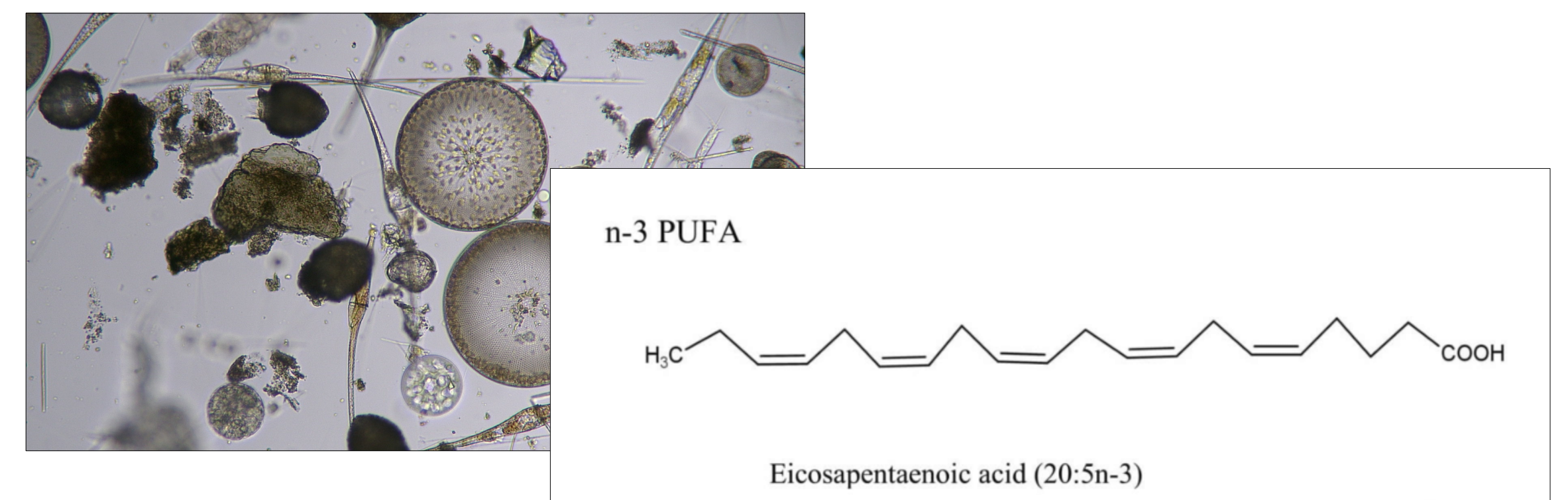
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## Introduction

Fatty acids include essential molecules for growth and development, e.g. omega 3 long-chain polyunsaturated fatty acids (n-3 LC-PUFA). Marine phytoplankton is rich in n-3 LC-PUFA and many consumers depend on it for their dietary requirements. Diatoms and other phytoplankton groups synthesize n-3 LC-PUFA through aerobic pathways involving desaturase and elongase enzymes. High-throughput sequencing technologies allow us to study *in-situ* metabolic activities of such communities at scale. In our study, we combined metatranscriptomic data with fatty acids compositional profiles of microplankton-enriched samples from the Belgian Part of the North Sea.

## Goals

Describing seasonal and spatial variation in fatty acid composition of microeukaryotic plankton ecosystems, together with biodiversity and expression of transcripts involved in fatty acid metabolism.



## Methods

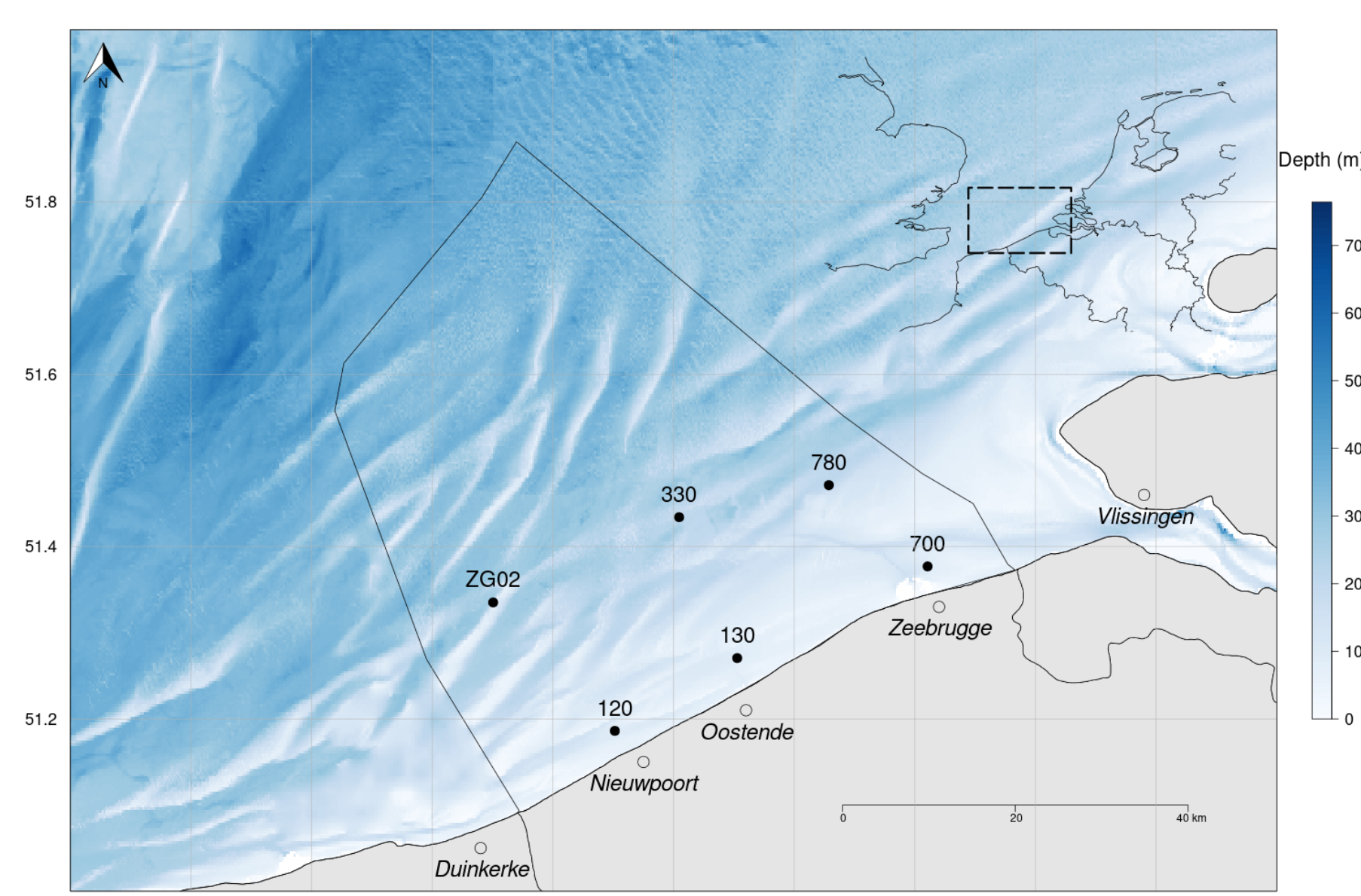
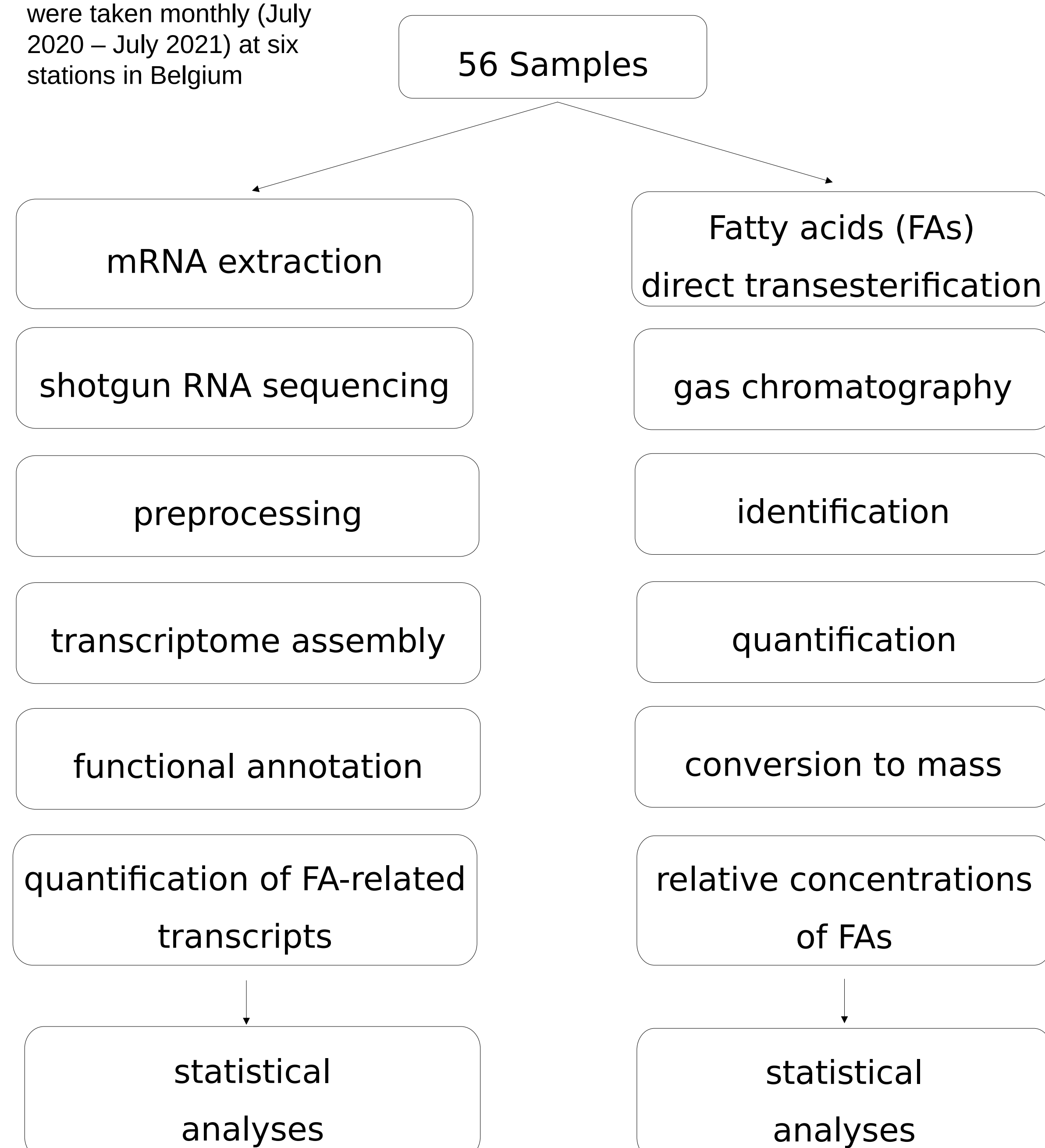


Fig. 1: Samples (50 L of sea surface water 50 - 250 µm) were taken monthly (July 2020 – July 2021) at six stations in Belgium



## Preliminary results

