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# Subject Section

# koios: machine learning for big biological data

# Simon Dirmeier 1 and Niko Beerenwinkel 1,\*

<sup>1</sup>Department, Institution, City, Post Code, Switzerland

\* To whom correspondence should be addressed.

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### **Abstract**

**Motivation:** Analysing biological data is becoming increasingly difficult due to its ever increasing volumnes and dimensionality. Since desktop solutions are not sufficient anymore to analyse big biological data sets comprising terabytes of data, such as features extracted from images or gene expression of millions of cells, we propose a novel machine learning command line tool for distributed highly-parallel analysis.

**Availability and implementation:** *koios* is available from Github (https://github.com/cbg-ethz/koios) and soon to be released on Bioconda.

Contact: niko.beerenwinkel@bsse.ethz.ch

#### 1 Introduction

$$\sum x + y = Z \tag{1}$$

## 2 Approach

#### 3 Methods

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 2 Sample et al.

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Table 1. This is table caption

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row2	row2	row2	row2
row3	row3	row3	row3
row4	row4	row4	row4

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Fig. 1. Caption, caption.

## 3.2 Test1

# 4 Discussion

Sample et al.

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- 3. this is item, use enumerate

## **Acknowledgements**

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