AG Algorithmic Bioinformatics
Biostore Project

Usability Improvement of the SeqAn Library

Björn Kahlert
Institut für Informatik
Freie Universität Berlin
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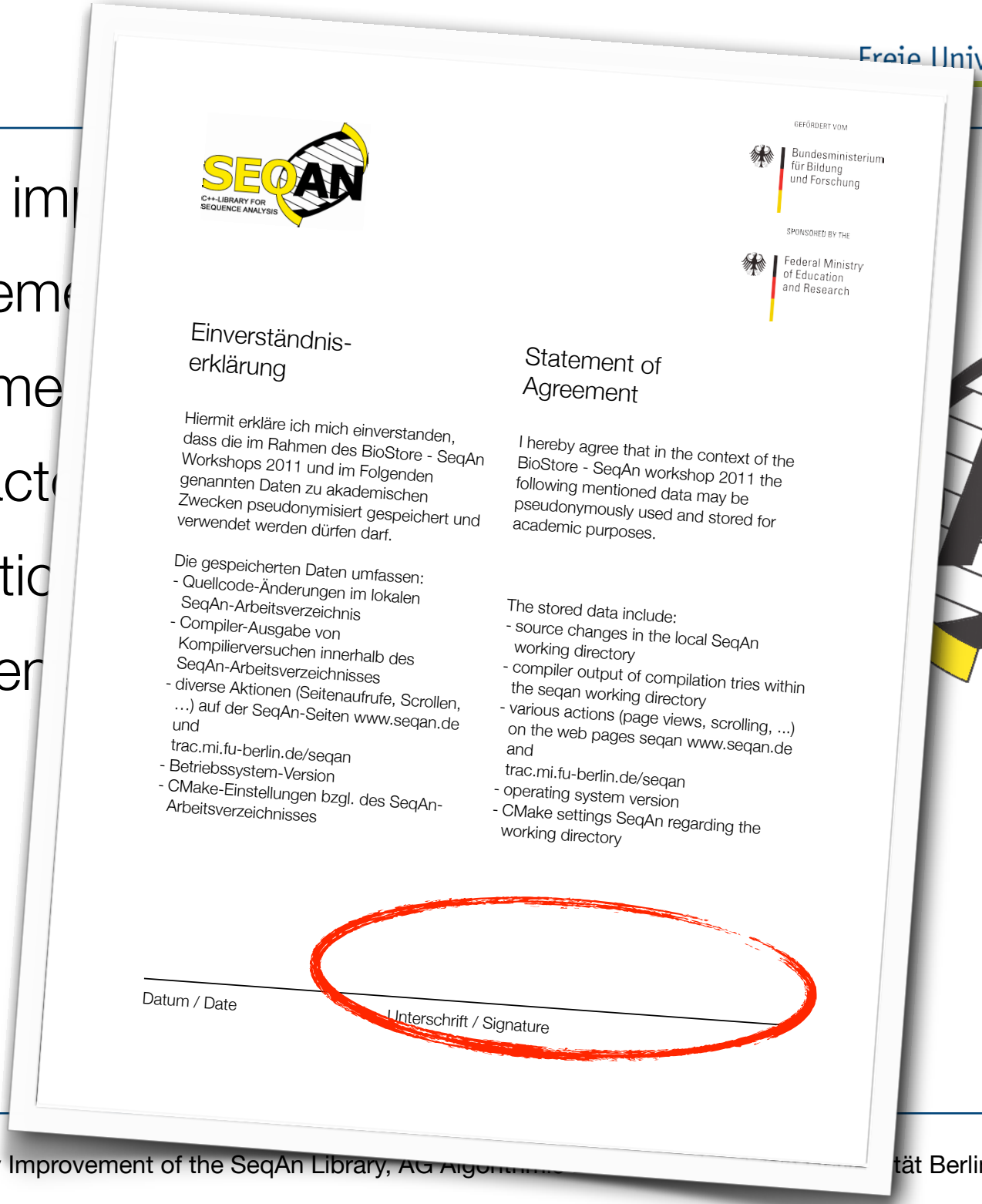
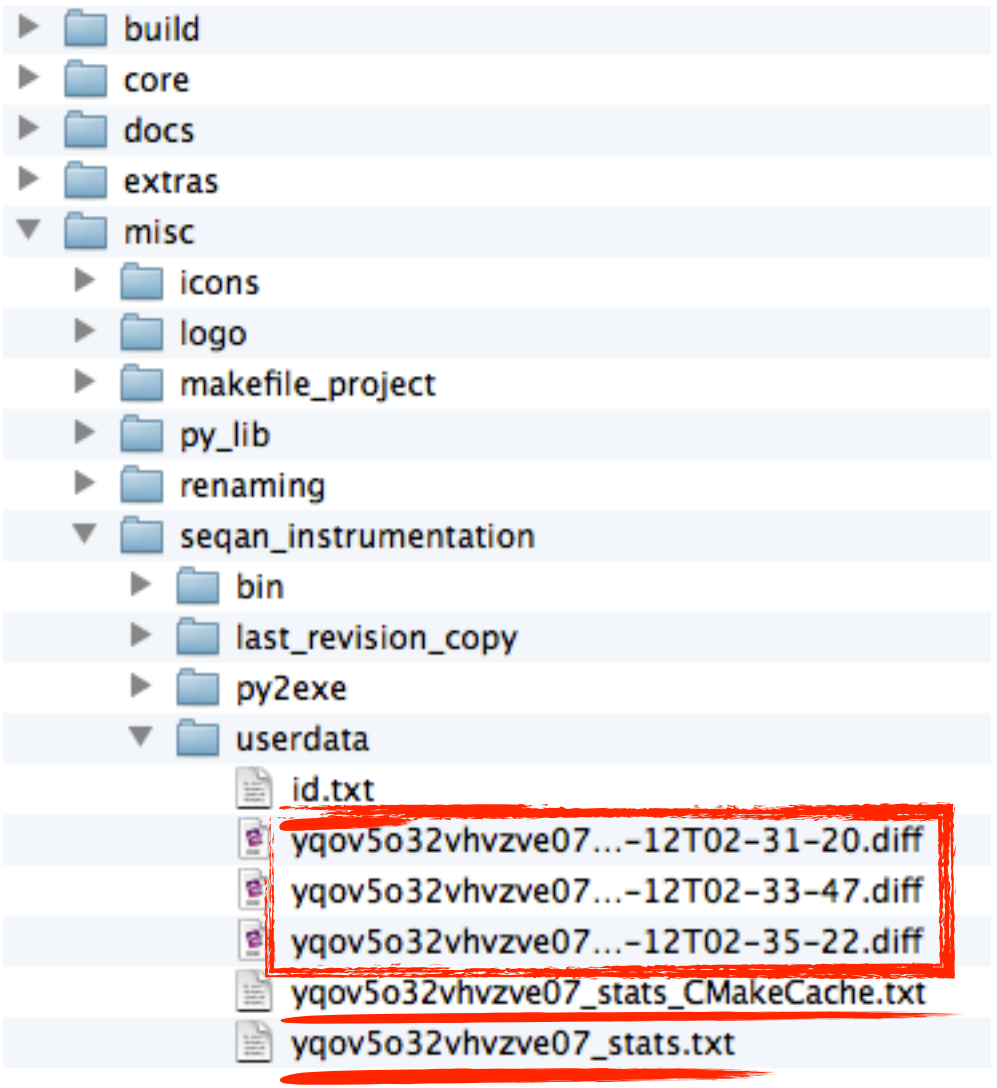
Goal

- Usability imp
  - requireme
  - less time
  - satisfact
- Observatio
- Experimen



Data Collection

Transmitted Data



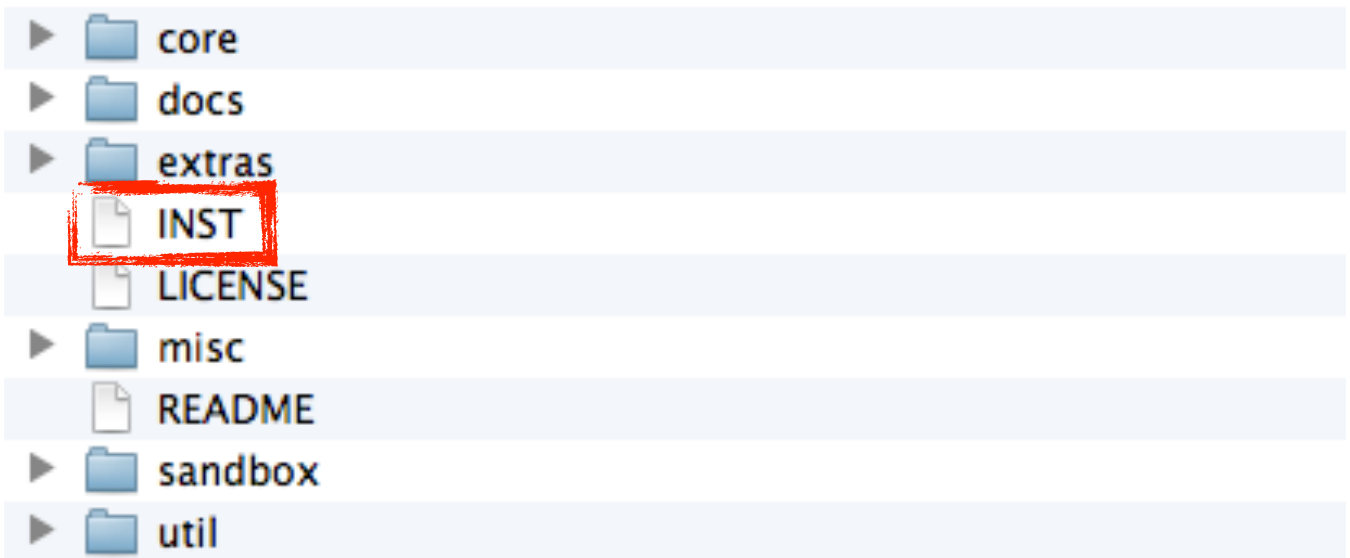

```
"machine": {
    "machine": "x86_64",
    "processor": "i386",
--- alignment.cpp    2011-09-12 02:26:03
    "architecture": "64bit" },
"devenv": {
+++ alignment.cpp    2011-09-12 02:35:17
    "CMAKE_CXX_COMPILER":
        "/usr/bin/g++",
@@ -1,4 +1,4 @@ yqov5o32vhvzve07
    "CMAKE_GENERATOR":
-///A tutorial about alignments.
        "Xcode",
+///A tutorial about global alignments.
    "CMAKE_BUILD_TYPE":
 #include <iostream>
        "Debug" },
 #include <seqan/align.h>
"os": {
 #include <seqan/graph_align.h>
    "system": "Darwin",
    "platform": "Darwin-11.1.0-64bit",
    "release": "11.1.0"    }
```

Privacy

- only pseudonymized data
  - no link to real person
- only SeqAn sites
  - www.seqan.de
  - trac.mi.fu-berlin.de/seqan
- activated **manually**

- activated **manually**

```
home$                cd seqan-trunk
seqan-trunk$         echo "" > INST
```



Summary

- diff and doc usage logged
- privacy
- create file INST in seqan-trunk
  - seqan-trunk$ **echo "" > INST**
- run cmake
- open seqan.de/?id=[YOUR ID HERE]
- please only use the online documentation

Have fun using SeqAn!

Thank you for taking part in the experiment!