STANDARD ST.26 AT EPO – A SUCCESSFUL JOURNEY

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FROM THE VISION TO THE BIG-BANG IMPLEMENTATION OF ST.26

- The problem to solve:

  - the need to improve search accuracy on life sciences patent field

  - The need to streamline SEQL workflows and improve automation (one SEQL fits all IPO's)

- 2010: the beginning of the journey – CWS approves EPO proposal and Task No 44 is created

- 2016: Standard ST.26 is approved by the CWS/4BIS

- 2020:   1st release of WIPO Sequence tool and EPO Strategic Plan (SP2023) at full steam

  Big-bang date set for ST.26 and adaptative mandatory development triggered at EPO

- 1/7/2022: all PCT offices ready to receive sequence listings in ST.26 format

- 2023: WIPO launches survey to access benefits/difficulties by the IPO's on transition to ST.26

- 2024: EPO and USPTO propose 2 substantive changes to improve ST.26

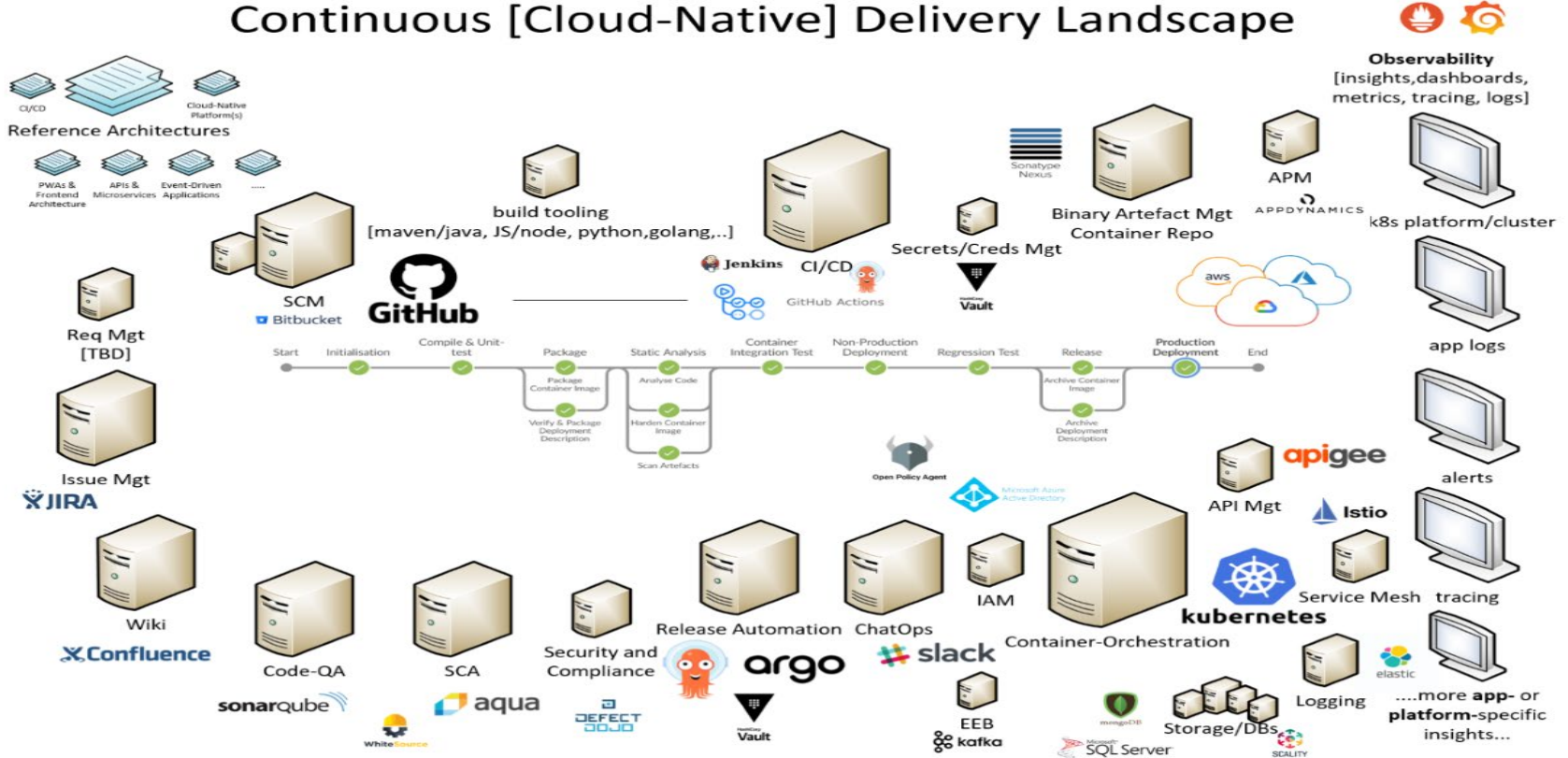# THE IMPLEMENTATION OF ST.26 AT EPO

- **The challenge:**

  - Use the new open source IT stack to drive the adaptation development as much as possible

  - Changes in the SEQL flow impact almost every IT system in Patent Grant Process and Search

  - Re-utilize existing IT components as much as possible

  - Streamline the SEQL flow and significantly reduce the manual tasks

  - Certified copy of Priority document
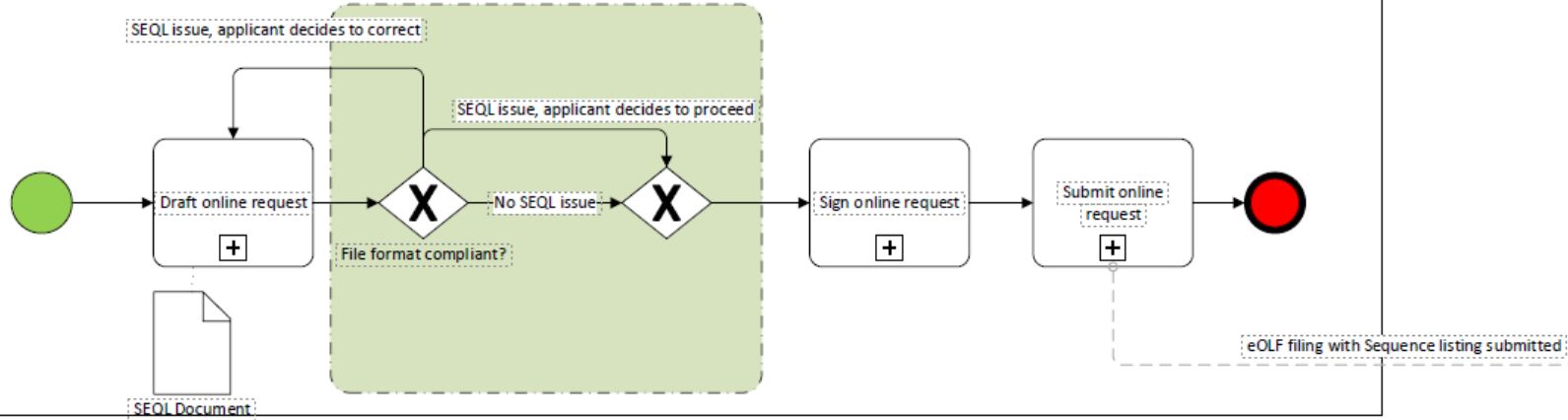
- **The objectives**

  - Solve the original problem – improve search accuracy, streamline and automate the SEQL flow

  - Improve efficiency on the Patent Grant Process for applications with SEQL's

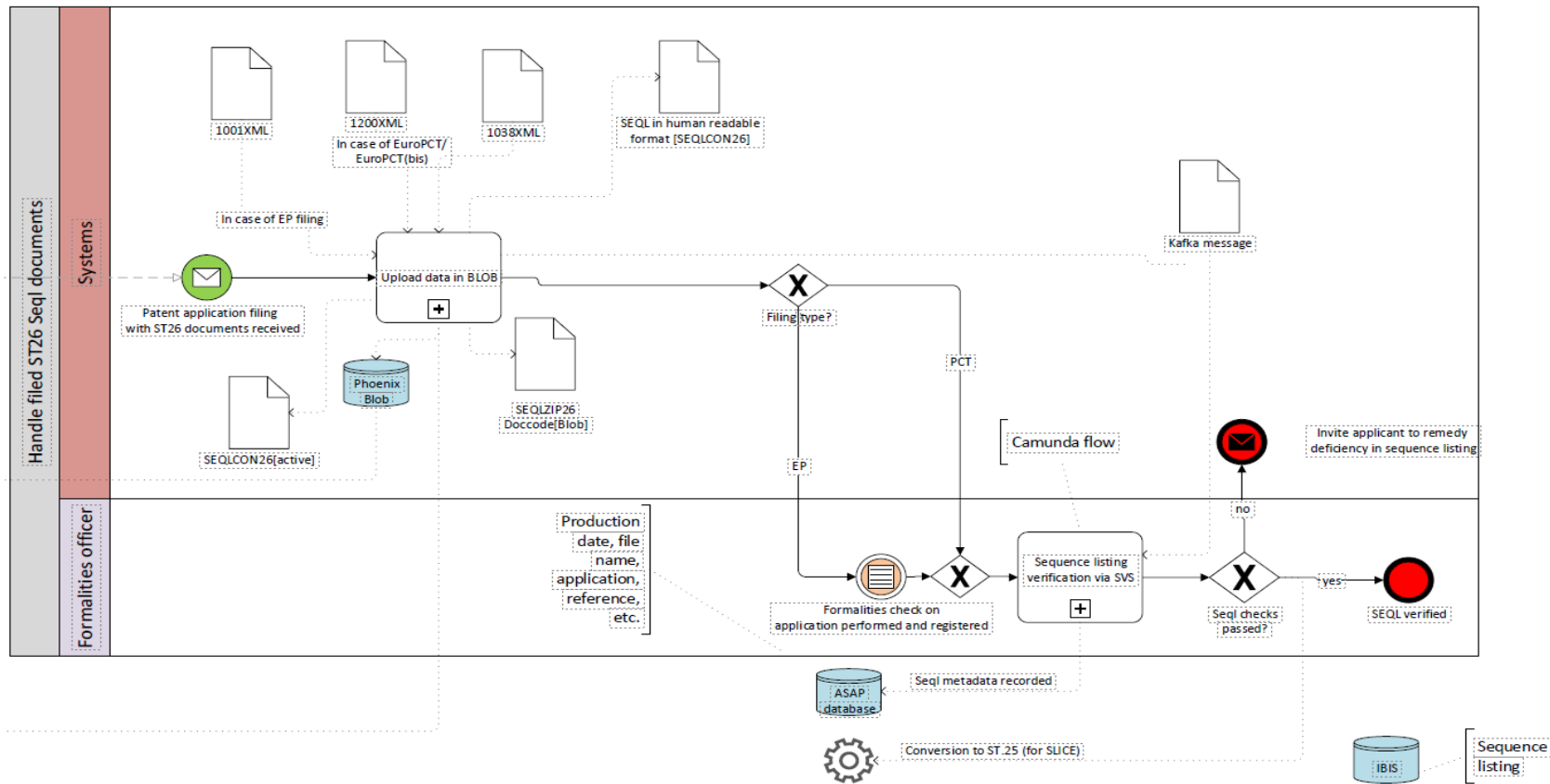 - compliance with INSDC requirements => more info available to the public and examiners

Continuous [Cloud-Native] Delivery Landscape

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SEQL issue, applicant decides to correct

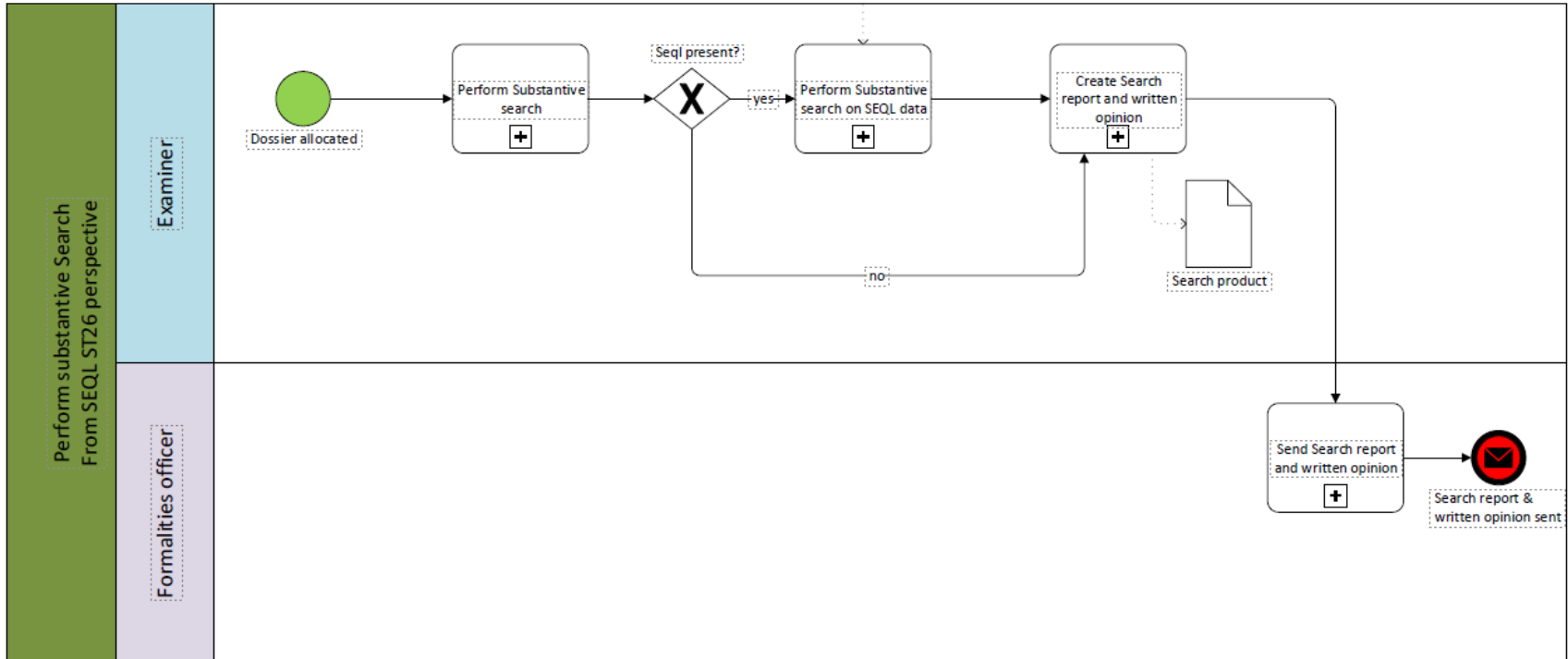SEQL issue, applicant decides to proceed

Filing Sequence listing online from a SEQL ST26 perspective (eOLF)

Applicant/representative

Draft online request

File format compliant?

No SEQL issue

Sign online request

Submit online request

SEQL Document

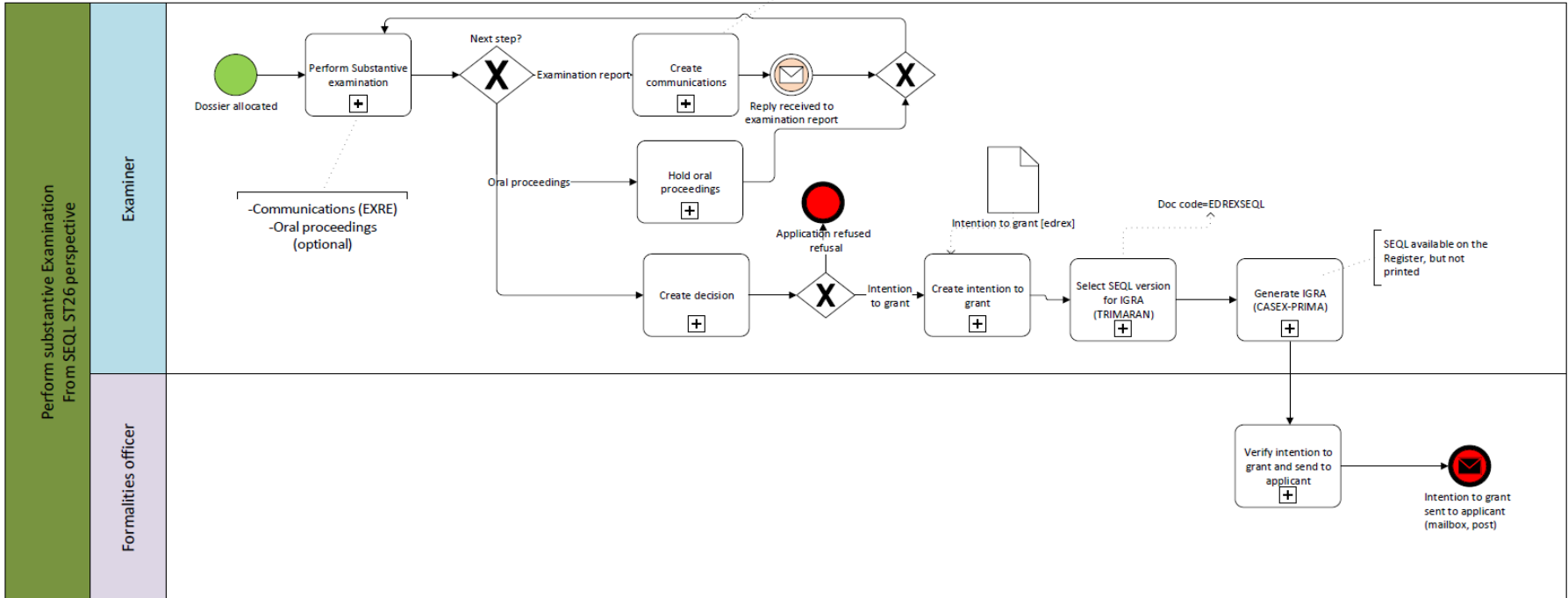eOLF filing with Sequence listing submitted

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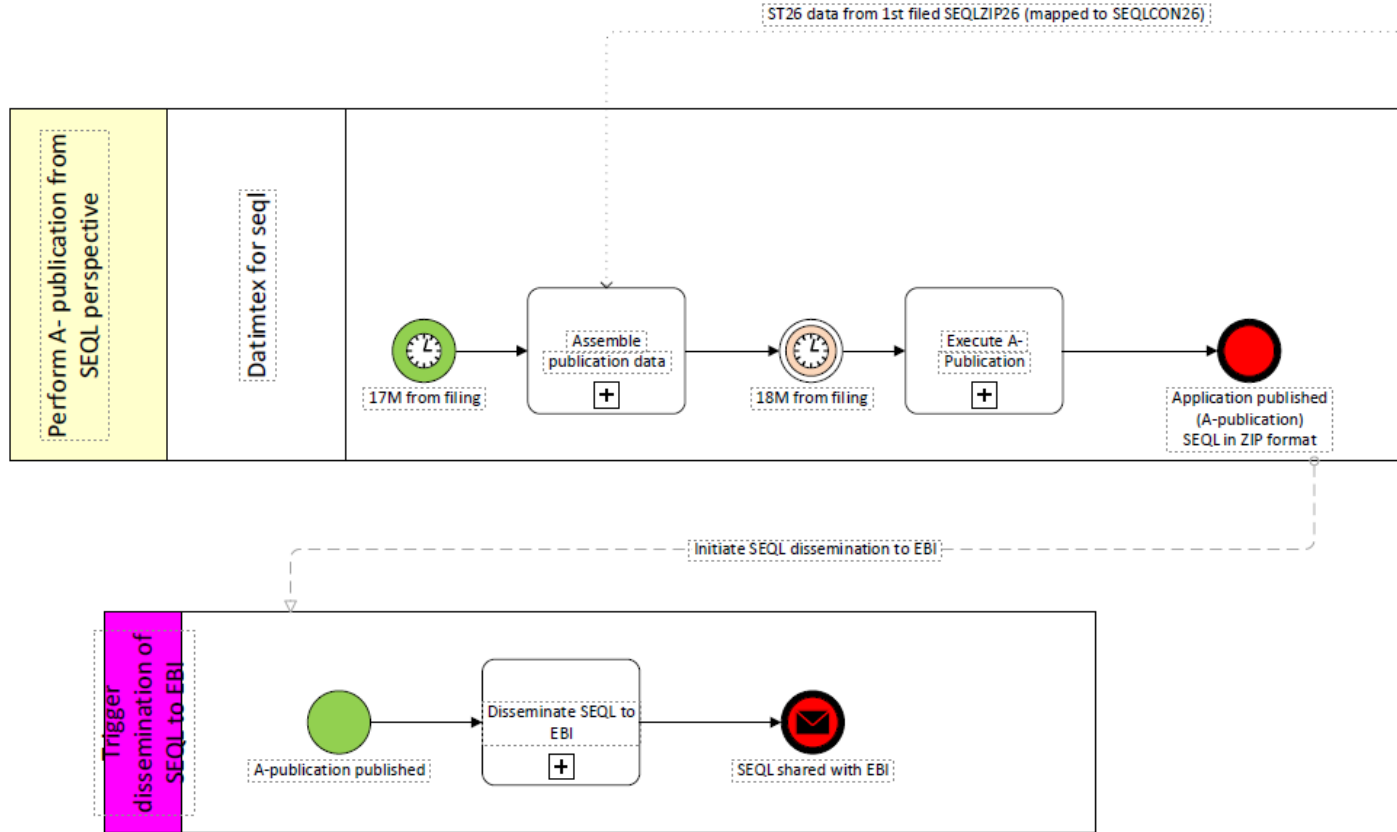
Note: Formalities officer is involved in sending out communications and submissions

Perform substantive Examination From SEQL ST26 perspective

Examiner

Dossier allocated

Perform Substantive examination

Next step?

Examination report

Create communications

Reply received to examination report

-Communications (EXRE)
-Oral proceedings
(optional)

Oral proceedings

Hold oral proceedings

Application refused refusal

Intention to grant [edrex]

Doc code=EDREXSEQL

SEQL available on the Register, but not printed

Create decision

Intention to grant

Create intention to grant

Select SEQL version for IGRA (TRIMARAN)

Generate IGRA (CASEX-PRIMA)

Formalities officer

Verify intention to grant and send to applicant

Intention to grant sent to applicant (mailbox, post)

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Perform B-publication from SEQL perspective

Intention to grant
Accepted by applicant

All criteria met

Assemble B-Publication

Execute B-Publication

Application published
(B-publication)
SEQL in ZIP format
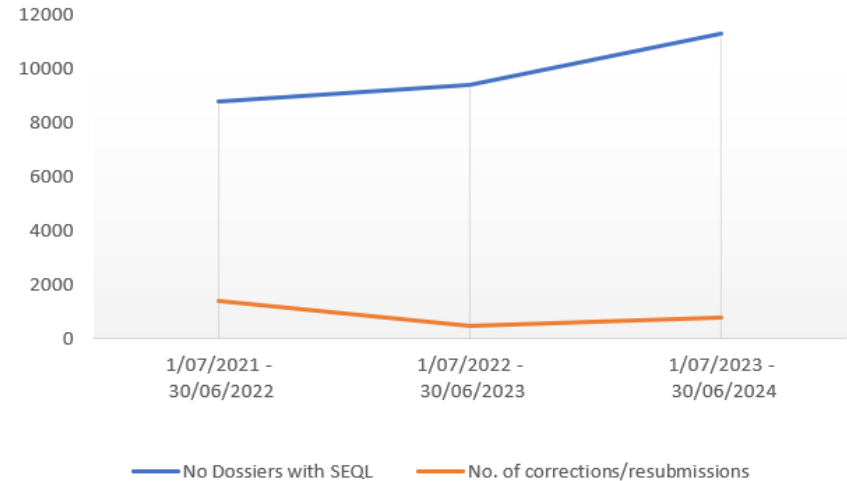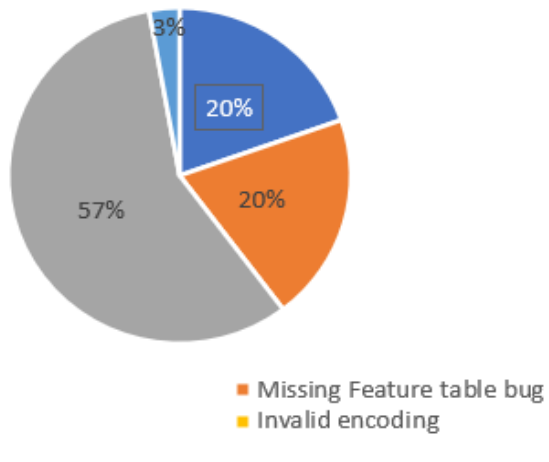
Claims
translations,
fees paid, etc.

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- 84% of all filed SEQL's were not deficient in the period 1/7/2021 - 30/06/2022

- 93% of all filed SEQL's were not deficient in the period 1/7/2023 - 30/06/2024

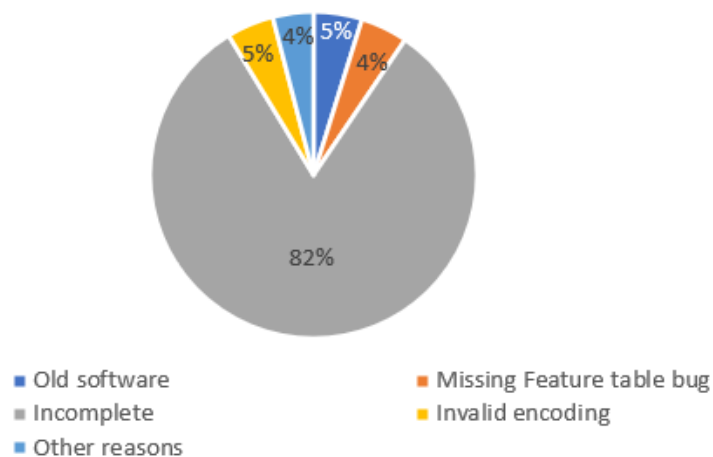- ST.26 clearly brought improvement to the patent grant process

No. filings with SEQL vs corrections/resubmissions

Distribution of the SEQL deficiencies found 1/07/2022 - 30/06/2023

- Old software
- Incomplete
- Other reasons
- Missing Feature table bug
- Invalid encoding

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THE ROOM FOR IMPROVEMENT

- The main reason for inviting applicants to resubmit a SEQL is its incompleteness:

  - There is no automatic way so far to detect whether all disclosed sequences are in the Sequence Listing upfront and some applicants do not have also preventive measures in place

- Another recurrent issue are nucleic acid sequences that are wrongly annotated as proteins (AA)

  - It may be overcome by implementing a warning in WIPO sequence tool

- Applicants are often unaware that some (short, non-specifically defined) sequences have been automatically replaced by skipped codes, leading to a unsolvable issue of loss of disclosure

  - It may be overcome by tolerating short sequences in the sequence listing