BIOVIA Biological Registration, BIOVIA Chemical Registration

BIOVIA Registration (Biological and Chemical Registration) contains an embedded copy of the BIOVIA Sequence Analysis Collection, which contains a component that is affected by the log4j vulnerability. To remediate this issue, please follow the instructions below. This does not have an impact on the functionality of neither BIOVIA Biological nor BIOVIA Chemical Registration.

1. BIOVIA Pipeline Pilot BiologyGPL Collection

- a) Our advice is to delete selected folders of this collection until a patch will be available. This allows customers to continue using other functionality in the collections and minimizes impact on other BIOVIA products.
- b) This collection is based on 3rd-party-components, which contain a vulnerable version of Apache Log4j. These are currently updated by their vendors. Once BIOVIA has received updated versions, a new version of this collection will be released.
- c) Please remove the following folder:<Install path>\apps\scitegic\seqanalgpl\bin\client\Artemis\
- d) The following component will not function after removing the Artemis folder: Components\Biology\Sequence Analysis\Viewers\Sequence Viewer (Artemis)

BIOVIA Pipeline Pilot

You **only** have an action to perform if you have deployed any of the following Pipeline Pilot packages or collections:

- 1. BIOVIA Hub package
- 2. BIOVIA Pipeline Pilot Next Generation Sequencing Collection
- 3. BIOVIA Pipeline Pilot BIOVIA BiologyGPL Collection

Please then follow the instruction below.

1. BIOVIA Hub package

- a) Our advice is to remove the scianalytics.war file and all the files associated with scianalytics.war from the BIOVIA Hub package.
- b) The only purpose of the scianalytics.war file is to provide control charts, i.e. for use with BIOVIA Discoverant. This war file is not related to any Hub functionality within e.g. BIOVIA OneLab.
- c) Please follow these steps in order to remove the scianalytics.war from the BIOVIA Hub package (also called the Scientific Analytics package) from a Pipeline Pilot Server.

On the Windows platform

1) Stop the Pipeline Pilot (PLP in the following) Windows services via the Services Windows application (Example Services shown for the Pipeline Pilot 21.x installation).

 Image: Signal State
 Image: Signal State<

PPS/21.2.0 Manages the lifetime of the BIOVIA Pipeline Pilo... Apache/2.4.41 (Win64) OpenSSL/1.1.1g authnz_ses_module... Jupyter Notebook Apache Tomcat

2) Open Windows Explorer and navigate to your PLP Server installation location:

Example location: C:\Program Files\BIOVIA\PPS\

In Windows Explorer, navigate to the *<Install Path>\apps\scitegic\hub\webapps* folder. Remove the two files below by deleting or moving to a backup location outside of the PLP Server Installation location:

- scianalytics.war
- scianalytics.xml
- 3) Navigate to the *<Install Path>\web\tomcat* folder. Remove the *scianalytics.xml* file by deleting it or moving it to a backup location outside of the PLP Server Installation location.
- 4) Navigate to the *<Install Path>\web\tomcat\webapps* folder. Remove the *scianalytics* sub-folder and its contents by deleting it or moving it to a backup location outside of the PLP Server Installation location.
- 5) Open a Command Prompt with Administrator privileges, and navigate to the *bin* directory of your PLP Server installation location: *<Install Path>\bin*

Execute the following command: *pkgutil -r scitegic/hub*

- 6) Wait for the command to complete. If it does not complete successfully, contact BIOVIA Support.
- 7) Start the PLP Windows Services via the Services Windows application (Example Services shown for the Pipeline Pilot 21.x installation).

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8) In Windows Explorer, navigate to the *<Install Path>\web\tomcat\webapps* folder. Verify that the *scianalytics* sub-folder still does not exist.

On the Linux platform

- 1) Open a Command Line from the user that owns the Pipeline Pilot (PLP in the following) installation, e.g. *biovia*
- 2) Navigate to the *linux_bin* directory of your PLP Server installation location:

Example location: /opt/BIOVIA/PPS/linux_bin

3) Shutdown the PLP service by running the *stopserver* script:

./stopserver

- 4) Navigate to the *<Install Path>/apps/scitegic/hub/webapps/* folder. Remove the two files below by deleting or moving to a backup location outside of the PLP Server Installation location:
 - scianalytics.war
 - scianalytics.xml

- 5) Navigate to the *<Install Path>/web/tomcat/* folder. Remove the *scianalytics.xml* file by deleting it or moving it to a backup location outside of the PLP Server Installation location
- 6) Navigate to the *<Install Path>/web/tomcat/webapps/* folder. Remove the *scianalytics* sub-folder and its contents by deleting it or moving it to a backup location outside of the PLP Server Installation location
- 7) Again, navigate to the *linux_bin* directory of your Pipeline Pilot Server installation location:

Example location: <Install Path>/PPS/linux_bin

Execute the following command:

pkgutil -r scitegic/hub

- 8) Wait for the command to complete. If it does not complete successfully, contact BIOVIA Support.
- 9) Start the PLP service by running the 'startserver' script: ./startserver
- 10) Navigate to the *<Install Path>/web/tomcat/webapps/* folder. Verify that the *scianalytics* sub-folder still does not exist.

2. BIOVIA Pipeline Pilot Next Generation Sequencing Collection

- a) Our advice is to delete selected folders of this collection until a patch will be available. This allows customers to continue using other functionality in the collections and minimizes impact on other BIOVIA products.
- b) This collection uses 3rd-party-components, which contain a vulnerable version of Apache Log4j. These are currently updated by their vendors. Once BIOVIA has received updated versions, a new version of this collection will be released.
- c) Please remove the following folders:
 <Install path>\apps\scitegic\nextgenseq\bin\client\IGV\
 <Install path>\apps\scitegic\nextgenseq\lang\java\
- d) This will impact IGV, GATK, Picard, and SnpEff functionality. In the Pipeline Pilot 2021 release, this includes the following components:

Components\Biology\Next Gen Sequencing\Viewers\Genome Viewers\Integrative Genomics Viewer (IGV)

Components\Biology\Next Gen Sequencing\Analysis\Variant Detection\Joint Variant Calling for Region (GATK)

Components\Biology\Next Gen Sequencing\Analysis\Mapping\Post-mapping Processing\Recalibrate Base Quality Score (GATK)

Components\Biology\Next Gen Sequencing\Analysis\Variant Detection\Post-detection Processing\Recalibrate Variant Quality Score (GATK)

Components\Biology\Next Gen Sequencing\Analysis\Variant Detection\Variant Calling for Region (GATK)

Components\Biology\Next Gen Sequencing\Utilities\Picard Utilities\Convert BAM to FASTQ (Picard)

Components\Biology\Next Gen Sequencing\Utilities\Picard Utilities\Create Sequence Dictionary (Picard)

Components\Biology\Next Gen Sequencing\Analysis\Mapping\Post-mapping Processing\Remove Duplicate Mapped Reads (Picard) Components\Biology\Next Gen Sequencing\Sequence Repository\Create and Modify\Add snpEff Database to Repository Components\Biology\Next Gen Sequencing\Utilities\snpEff Utilities\Download snpEff Database

Components\Biology\Next Gen Sequencing\Utilities\snpEff Utilities\List snpEff Databases Components\Biology\Next Gen Sequencing\Analysis\Variant Detection\Post-detection Processing\Predict Variant Effects (snpEff)

3. BIOVIA Pipeline Pilot BIOVIA BiologyGPL Collection

- e) Our advice is to delete selected folders of this collection until a patch will be available. This allows customers to continue using other functionality in the collections and minimizes impact on other BIOVIA products.
- f) This collection is based on 3rd-party-components, which contain a vulnerable version of Apache Log4j. These are currently updated by their vendors. Once BIOVIA has received updated versions, a new version of this collection will be released.
- g) Please remove the following folder:<Install path>\apps\scitegic\seqanalgpl\bin\client\Artemis\
- h) The following component will not function after removing the Artemis folder: Components\Biology\Sequence Analysis\Viewers\Sequence Viewer (Artemis)