Anomaly Analyses for Feature-Model Evolution

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Abstract

Software Product Lines (SPLs) are a common technique to capture families of software products in terms of commonalities and variabilities. On a conceptual level, functionality of an SPL is modeled in terms of features in Feature Models (FMs). As other software systems, SPLs and their FMs are subject to evolution that may lead to the introduction of anomalies (e.g., non-selectable features). To fix such anomalies, developers need to understand the cause for them. However, for large evolution histories and large SPLs, explanations may become very long and, as a consequence, hard to understand. In this paper, we present a method for anomaly detection and explanation that, by encoding the entire evolution history, identifies the evolution step of anomaly introduction and explains which of the performed evolution operations lead to it. In our evaluation, we show that our method significantly reduces the complexity of generated explanations.

CCS Concepts • **Software and its engineering → Software product lines**; **Software evolution**;

Keywords Software Product Line, Feature Model, Evolution, Anomalies, Explanation, Evolution Operation

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1 Introduction

A *Software Product Line (SPL)* is an approach to manage reuse for families of software products [39, 44]. Functionality of the products of an SPL is captured on a conceptual level using *features*. Commonly, features are organized in a *Feature Model (FM)*, expressing relations between features in a tree-like notation [16] and *cross-tree constraints* [17]. Moreover, features can be organized in groups. In *alternative* groups, exactly one feature has to be selected and in *or* groups, at least one feature has to be selected. A *configuration* is a set of selected features and it is valid if the feature selection satisfies all constraints posed by the FM and the cross-tree constraints. A valid configuration is used to derive *products* of an SPL using a variability realization mechanism [44].

To satisfy software requirement changes, SPLs need to evolve [25, 37]. As Passos et al. motivated, this evolution optimally starts with FM evolution [36]. When defining and changing FMs, anomalies may be introduced inadvertently, e.g., preventing the creation of valid configurations (void FM anomaly) or the selection of certain features [4]. Fixing anomalies is a complex task and, thus, entails significant costs. Understanding the cause for anomalies is a challenging but crucial activity to be able to fix them.

Numerous approaches exist to detect [15, 53] and explain [3, 10, 11, 18, 19, 21, 27, 42, 51, 52] FM anomalies in terms of violated constraints. For large FMs, some explanations have a significant size as a large percentage of features and cross-tree constraints contribute to the corresponding anomaly, making it hard to understand them. For instance, a recent bug in the tool FeatureIDE resulted in few group types of FMs to be changed.[1] For a large FM from industry (712 features and 1141 cross-tree constraints), this resulted in three changed group types making the FM *void* (i.e., no valid configuration exists). The explanation of this anomaly contained 91 constraints and 92 features were involved. Thus, developers had to inspect all these constraints and features despite the immediate cause being the change of the three group types.

[1] https://github.com/FeatureIDE/FeatureIDE/issues/662

Over the course of time, SPLs may have long evolution histories. As evolution yields additional complexity, the likelihood that developers inadvertently introduce anomalies during this evolution increases. Without proper methods for detection, the introduced anomalies remain undetected and harm the FM well-formedness. To fix these anomalies, developers need to identify all anomalies in the entire evolution history and pinpoint the FM version of the anomaly introduction. With current approaches, this requires significant manual effort as each evolution step needs to be analyzed on its own and all anomalies have to be traced manually throughout the entire history.

When planning future FM evolution, developers might draft several evolution steps [34], each possibly consisting of several evolution operations applied to the FM. Due to the complexity of anomaly detection and fixing, it is infeasible for developers to analyze the FM after each evolution operation. Instead, multiple evolution operations have been performed before searching for anomalies. Moreover, to fix anomalies, developers might need to perform multiple further operations which may introduce additional anomalies. If developers introduced anomalies in such planned evolution steps, it is hard to understand which of their operations lead to the anomaly. This is particularly important if few evolution operations result in large explanations. Existing approaches are not able to explain which of the operations performed by the developers lead to an anomaly.

We overcome these limitations by incorporating FM evolution information for anomaly detection and explanations. In particular, we make the following contributions:

- We propose a method enabling the detection of all anomalies in the evolution history and pinpointing the evolution step of anomaly introduction by analyzing the FM evolution in its entirety (as opposed to evolution steps individually).
- We introduce a novel concept for explaining anomalies by identifying causing evolution operations and, thus, reducing explanation complexity.
- We provide tool support for anomaly detection, explanation generation and their inspection.
- We evaluate our method by analyzing evolution histories of three real-world FMs, showing correctness, measuring performance and explanation reduction rates.

With these contributions, we are able to efficiently detect all anomalies in the past and future evolution of SPLs and, most importantly, explain them in a less complex way.

2 Background

A Feature Model (FM) is the most common representation of variability in an SPL on conceptual level [16, 44]. Features of an FM are structured in a tree-like notation. As an example, Figure 1 shows an FM of an in-car emergency call system. Two features representing different implementations of emergency call systems are available, i.e., `eCall` and `ERA/Glonass`. Moreover, two different language features are available, i.e., `English` and `Russian`. Each feature can only be selected if its parent is selected. A feature type can be either *mandatory* (e.g., feature `Languages`) and must be selected if its parent in the feature tree is selected, or *optional*. Additionally, optional features may be grouped: An *Or* group states that at least one of the group's features has to be selected if the parent feature is selected while an *Alternative* group states that exactly one of the group's features has to be selected if the parent feature is selected.

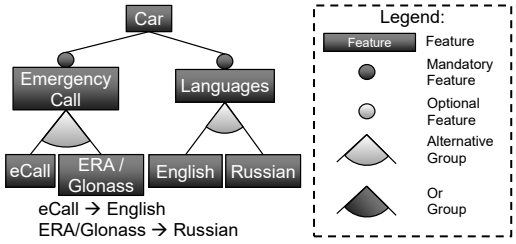


Figure 1. FM of an in-Car Emergency Call System

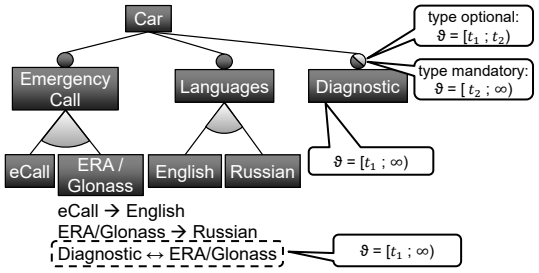


Figure 2. Evolution of the Running Example as TFM

To enable developers to model evolution of FMs, we introduced *temporal elements* in prior work [33]. Each temporal element has a *temporal validity* $\vartheta = [\vartheta_{since}; \vartheta_{until})$ – a right-open interval of dates stating the timespan in which the element is valid. With the right-open interval, seamless evolution can be modeled by setting ϑ_{until} of one element to the same value as ϑ_{since} of the succeeding element. Using temporal elements, it is not only possible to model past evolution history but also plan future evolution [34]. We applied this concept to FMs, resulting in *Temporal Feature Models (TFMs)* [33]. In TFMs, each element of the FM is modeled as temporal element. Thus, all features, names, and groups are modeled as temporal elements. As feature and group types need to evolve, they are modeled as temporal elements as well. To move features in the feature tree, the relations between features and their groups need to be modeled as temporal elements and, thus, as own entity.

The definition of the temporal validity enables to seamlessly change elements, such as a feature type, in the evolution history. As the temporal validity is a right-open interval,

a change of a feature type from $type_{old}$ to $type_{new}$ at point in time t can be realized by setting the end of the temporal validity of the old feature type to the beginning of the temporal validity of the new feature type: $\vartheta_{type_{old}} = [\infty; t)$, $\vartheta_{type_{new}} = [t; \infty)$ (whereas we denote validity since or until eternity as ∞). To keep relations between evolving elements, all evolving elements are stored in sets [33]. For instance, a feature is not only related to one name but to a set of names. Hence, we are able to model arbitrary FM evolution and capture its entire evolution history using a TFM. Each unique date contained in all temporal validities of a model represents one evolution step. As the dates of temporal validities are not limited to past dates but may also be in the future, TFMs also facilitate future planning of FM evolution [34].

Figure 2 shows the evolution of the running example modeled in a TFM. The temporal validities are illustrated as annotation at the model. In this TFM, two evolution steps are modeled resulting in three versions: t_0, t_1 and t_2. In this example, a new feature and a new cross-tree constraint are introduced at t_1. As the type of the new feature is *optional*, the type is added to the feature as well. Thus, the temporal validities of the new feature, its *optional* type, and the new cross-tree constraint are set to $\vartheta = [\vartheta_{since} = t_1; eternity)$. As the type of the new feature is changed at t_2 from *optional* to *mandatory*, a new respective *mandatory* feature type element is added. To replace the *optional* feature type, the temporal validity of the *optional* feature type is changed to $\vartheta = [\vartheta_{since} = t_1; \vartheta_{until} = t_2)$ and the temporal validity of the *mandatory* feature type is set to $\vartheta = [\vartheta_{since} = t_2; eternity)$. We implemented TFMs and respective editors in our tool suite DarwinSPL.[2] The DarwinSPL editors hide the complexity of TFMs by enabling developers to apply changes to the FM, as common in other editors, which are translated to temporal elements in the background [32].

Anomalies in FMs describe design flaws and mismodeling of FMs. Benavides et al. identified a set of relevant anomalies developers should avoid [4]. In particular, they introduced three main types of anomalies: i) *void FM* anomaly if no valid configuration of the FM exists; ii) *dead* feature anomaly if a feature cannot be selected in any valid configuration; iii) *false-optional* feature anomaly if an optional feature is part of each valid configuration. However, different notions of false-optional features exist. Schröter et al. define a *false-optional* feature as an optional feature that has to be selected in each configuration in which its parent feature is selected [45]. We consider the definition of Schröter et al. as more sensible but when we devised our concepts and implemented them, we were not aware of these differences. Thus, in the following, we consider the definitions of Benavides et al. [4]. For instance, in the running example, the feature `ERA/Glonass` is in an *alternative* group at t_2. However, as feature `Diagnostic` is a *mandatory* feature and the last constraint defines that `ERA/Glonass` and `Diagnostic` must always be selected together, `ERA/Glonass` became *false-optional*. As a consequence, the feature `eCall` became *dead* as it is in an *alternative* group with `ERA/Glonass`.

[2] https://gitlab.com/DarwinSPL/DarwinSPL

3 Evolution-Aware Anomaly Detection

Several approaches exist to detect [15, 53] and explain [3, 10, 11, 18, 19, 21, 27, 42, 51, 52] FM anomalies in terms of violated constraints. An anomaly explanation consists of the set of constraints that cannot be satisfied altogether and, thus, lead to the anomaly. To the best of our knowledge, none of the existing methods is considering evolution. Thus, when analyzing the FM evolution history, the entire analysis has to be performed for each evolution step on its own. Developers then have to search manually for the evolution step in which an anomaly has been introduced, what can be hard or unfeasible for large evolution histories. Even more important, when performing FM evolution, anomalies may be introduced by a small set of evolution operations but the explanation using current methods may become extremely large (cf. example in the Introduction with more than 90 involved constraints). Thus, the existing methods do not provide any information on which of the performed evolution operations caused an anomaly. As a consequence, fixing anomalies becomes complex both for existing and upcoming evolution steps. Because of this complexity, anomalies might not be fixed at all.

When searching for anomalies, existing approaches construct satisfiability problems and solve them by querying of-the-shelf solvers. In these satisfiability problems, all features are translated into variables that can be either *true* (i.e., selected) or *false* (i.e., deselected). The constraints imposed by the FM structure and the cross-tree constraints are translated into a formula. For instance, Listing 1 shows the propositional formula for the TFM of the running example and its cross-tree constraints at t_0. Many parts of this formula remain the same for each evolution step. For instance, for the running example, all parts of the formula of t_0 remain stable for the entire evolution history as only new parts are added. This results in redundancies in queries for solvers if multiple evolution steps are analyzed.

```
1  Car ∧
2  (Car → (EmergencyCall ∧ Languages)) ∧
3  ((EmergencyCall ∨ Languages) → Car) ∧
4  (EmergencyCall → (eCall ⊕ ERAGlonass)) ∧
5  ((eCall ∨ ERAGlonass) → EmergencyCall) ∧
6  (Languages → (English ⊕ Russian)) ∧
7  ((English ∨ Russian) → Languages) ∧
8  (eCall → English) ∧
9  (ERAGlonass → Russian)
```

Listing 1. Propositional Formula of the Running Example at t_0 ($\oplus$ stands for the exclusive or operator).

The idea of the evolution-aware anomaly detection is to incorporate FM evolution for anomaly detection and explanation by encoding the entire evolution history in one set of variables and one formula for a solver. This way, it is possible to i) reuse the solver for parts of the formula that remain stable over multiple evolution steps and the entire evolution history is analyzed automatically; ii) detect the evolution step at which an anomaly first arose; iii) derive evolution operations performed by developers to reduce explanation complexity. In particular, we consider three types of anomalies: *Void* FM, *false-optional* feature and *dead* feature (cf. Section 2).

3.1 Encoding the Evolution History

In this paper, we incorporate FM evolution for anomaly detection and explanation by utilizing TFMs. Instead of having individual states of an evolved FM, a TFM provides additional information about the evolution, i.e., model elements that changed and the corresponding evolution operations (cf. Section 2). To capitalize on this fact and, thereby, reduce the number of requests to the solver, we encode the notion of evolution into one single request. For this purpose, we *tag* evolving parts of the formula with the time spans for which they are valid. Parts that remain the same for the entire evolution history can be left as they are. These tags tell the solver for which point in time it needs to consider the tagged parts. To derive which parts need to be tagged, we make use of the *temporal elements* of TFMs (cf. Section 2). Each part of the formula is generated from a certain structure of the FM tree, such as group compositions or feature types, and these structures are modeled as temporal elements. As each temporal element has a temporal validity (i.e., the interval of dates $[\vartheta_{since}; \vartheta_{until})$ at which it is temporally valid), we generate the tags using this information.

To enable such an encoding and to be able to solve such a formula (e.g., using an SMT solver) we introduce a new *evolution variable* representing the evolution steps. As we may have multiple evolution steps, this variable has to have a larger domain than just *true* and *false*. Thus, we decided to use a formula in a first-order style notation which enables us to also use variables having an Integer domain. A tagged formula using the evolution variable looks as follows:

$$(\text{evolution} \geq t_i \wedge \text{evolution} < t_j) \rightarrow (\text{original formula})$$

As this variable represents all evolution steps, we need to identify all relevant steps and set the variable domain accordingly. For this purpose, we make again use of the temporal elements of TFMs. We can identify all relevant steps by inspecting the temporal validities of all temporal elements of a TFM. The domain of this variable is $[0; n]$, where n is the number of evolution steps identified in the TFM (e.g., $n = 2$ for the running example). The value 0 for the evolution variable represents the state before the first evolution step (e.g., the TFM at t_0 of the running example).

Listing 2 shows the formula with tagged parts for the entire evolution history of the running example. As can be seen, in this case, only three parts need to be tagged and the rest can be reused for each evolution step. This way, a solver only needs to evaluate the tagged part if the value of the evolution variable lies within the defined interval.

```
1  Car ∧
2  (Car → EmergencyCall ∧ Languages) ∧
3  (EmergencyCall ∨ Languages → Car) ∧
4  (EmergencyCall → eCall ⊕ ERAGlonass) ∧
5  (eCall ∨ ERA/Glonass → EmergencyCall) ∧
6  (Languages → English ⊕ Russian) ∧
7  (English ∨ Russian → Languages) ∧
8  (eCall → English) ∧
9  (ERAGlonass → Russian) ∧
10 ((evolution ≥ 0) → (Diagnostic → Car))
       ∧
11 ((evolution ≥ 0) → (Diagnostic ↔
       ERAGlonass)) ∧
12 ((evolution ≥ 1) → (Car → Diagnostic))
```

Listing 2. Formula of the Entire Evolution History of the Running Example

Note that our encoding enables the seamless analysis of three evolution types: past evolution history, currently performed evolution, and already pre-planned evolution steps. After this translation and tagging, the formula can be used as basis to detect anomalies using of-the-shelf solvers. In the following, we explain how we construct requests to search for anomalies in the entire evolution history.

3.2 Solving TFM Evolution Histories

Existing methods to solve queries for FM analyses are not aware of evolution and, thus, do not incorporate it. To overcome this limitation, we present a method to generate queries on TFM evolution for SMT solvers.

To understand how we detect anomalies in the evolution history, let us assume that, given a conjunction of constraints TFM_c that defines a TFM, we denote the set of all features as F and the evolution variable as e. To check whether a TFM is valid at a given time t_i, it is possible to check whether $SAT((e = t_i) \wedge TFM_c)$. If this formula is satisfiable, there exists a set of selected features in F that represents a valid configuration at point in time t_i. Conversely, if the formula is unsatisfiable, no set of selected features in F exists that satisfies all constraints, thus, implying that the TFM is void at t_i.

To check whether a feature $f \in F$ is a dead feature at time t_i, we check whether $SAT(f \wedge (e = t_i) \wedge TFM_{c)}$. If this formula is satisfiable, all constraints for point in time t_i are satisfied. Moreover, the feature f can be selected, thus, implying that f is not dead for the time t_i. Conversely, if the previous formula is unsatisfiable, no feature selection containing f exists satisfying all constraints, thus, proving that f is dead at t_i.

To determine whether a feature is false optional is very similar. While in the previous case we enforced the feature f to be selected, in this case we enforce the feature to be deselected by checking the formula $SAT(\neg f \wedge (e = t_i) \wedge TFM_c)$. Similar as for the dead feature check, if this formula is satisfied, there exists a valid configuration in which the feature f is deselected proving that f is not false optional at t_i.

To find all dead and false-optional features in the evolution history, we need to know which feature to check at which evolution step. For this purpose, we introduce a list `toCheck` that contains the list of features and values for the evolution variable that need to be analyzed. As mandatory features may not be false optional and a dead mandatory feature implies that its parent is dead too, we add all features to `toCheck` for all points in time at which they are optional. As feature types are modeled as temporal elements in TFMs, we iterate over all feature types of a feature and generate the list of values for the evolution variable by using the temporal validities of optional types.

For checking dead and false-optional features, we iteratively try to satisfy the previously mentioned formula for all optional features and time points in `toCheck`. Similarly, the validity check is performed for all the possible points in time. As the entire evolution history is encoded in one formula, the solver can reuse findings from already analyzed points in time to find dead or false-optional features or to prove voidness faster for other points in time. For this purpose, incremental solvers can be used that allow the addition and removal of constraints on-the-fly without restarting the search from scratch. In particular, for the dead feature analysis, we first check if TFM_c is satisfiable. Then we iterate over all the possible $\langle f_j, t_i \rangle \in$ `toCheck`. For every pair, we first add a formula setting the value of the evolution variable to t_i and add another formula setting the value of feature f_j to true. If this is unsatisfiable, f_j is dead at t_i. Then, we remove the previously added formulas and add the formulas for the next entry of `toCheck`. A similar check can be performed for false-optional features. Using this approach, we reuse the solver for all these checks and the solver can take advantage of things it learned from previous checks.

4 Evolution-Aware Anomaly Explanation

After being able to detect all anomalies in the evolution history and pinpoint their date of introduction, developers need to understand them in order to fix them. As help for developers to understand anomalies, several methods exist to explain anomalies in terms of parts of the formula that cannot be fulfilled [3, 10, 11, 15, 18, 19, 21, 27, 42, 51, 52]. However, for large FMs, anomaly explanation can have a significant size if many features and cross-tree constraints are involved. On top of that, when developers change FMs during evolution, they possibly apply many operations but a single evolution

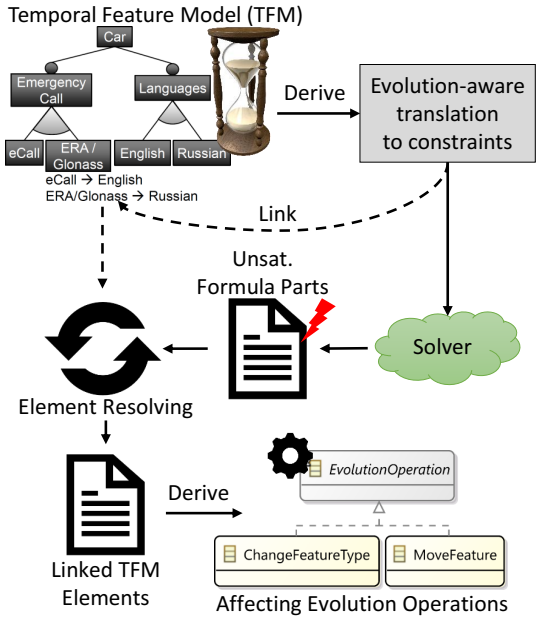


Figure 3. Evolution-Aware Explanation Workflow

operation, such as changing a group type, can cause an anomaly with a large explanation. When developers try to fix such anomalies using existing methods, in the worst case, they have to study the entire explanation to identify the cause of the anomaly. The existing methods do not incorporate information about evolution and, thus, are not able to identify evolution operations that caused a particular anomaly.

To overcome the previously mentioned limitations we explicitly incorporate information on the FM evolution in two ways. First, we explain anomalies for the point in time they were introduced taking over the task of searching for the point in time of anomaly introduction. Second, we identify performed evolution operations on the FM that caused an anomaly. With the identified evolution operations, we are able to narrow down the search for fixes for the respective anomaly. As a consequence, we reduce explanation length by reducing it to the performed evolution operations.

Existing approaches to compute anomaly explanations identify parts of formulas that cannot be satisfied and return them as explanation. Evolution operations that caused an anomaly contribute to the existence of these parts. Thus, to identify the anomaly-causing evolution operations, we need to identify the evolution operations that have contributed to parts of the formula of the explanation. Figure 3 shows the general workflow of the evolution-aware anomaly explanation. To compute an explanation for an anomaly in the evolution history and to identify evolution operations that caused them, we reuse results from our evolution-aware anomaly detection (cf. Section 3) which identifies the date of anomaly introduction. For the date of anomaly introduction, we derive the temporally valid formula of the TFM. At

the same time, we link the elements from which the parts of the formula have been computed and store them in a map. For instance, in the running example, if the formula part for the child feature of feature `Car` are computed for the evolution step t_2, the group and all of its sub features are linked to the translated formula part.

In the next step, we generate the explanation in terms of unsatisfiable formula parts using the same formula as before (cf. Section 3.1). After we generated an explanation, we need to identify the evolution operations that contributed to formula parts of that explanation. To this end, we resolve the TFM elements that we linked in the first step to the formula parts using the map in which we stored the translated formula parts to its related model elements. Then, to identify evolution operations that affected these elements, we reuse the information on evolution stored in the TFM. With TFMs, we have direct access to all elements and their temporal validity that have been changed during evolution. If an element changed during an evolution step, its temporal validity starts or ends at the date of the evolution step. Thus, we can derive the respective evolution operation. In particular, we are able to derive the following operations: adding and removing cross-tree constraints, adding and removing features, changing a feature type, moving a feature into another group, and changing a group type. More complex operations can be defined as well as the temporal validities are stored independently of the detected operations. As a result, we can present the performed evolution operations instead of the unsatisfiable formula parts.

In the running example, this would look like the following. For the false-optional feature anomaly at t_2 of the feature `ERAGlonass`, we retrieve the following formula parts as explanation from the solver:

```
1  Car
2  Car → EmergencyCall ∧ Languages
3  EmergencyCall → eCall ⊕ ERA/Glonass
4  Diagnostic ↔ ERA/Glonass
5  Car → Diagnostic
```

Listing 3. Unsatisfiable Formula Parts for the Dead Feature Anomaly of the Running Example

During the translation process for the SMT solver query, we link the formula parts to the respective TFM elements. For instance, the last part in Listing 3 results from the feature type of feature `Diagnostic` as it is *mandatory* at t_2 and, thus, we link the formula part to the feature `Diagnostic`. For each formula part, we analyze the TFM elements and check whether their temporal validity starts or ends at t_1. This is crucial to identify all evolution operations that contributed to the anomaly. In this case, we would identify that the type of feature `Diagnostic` has changed from *optional* to *mandatory* which is also the cause of this anomaly. Thus, we would reduce explanation complexity from five formula parts to one evolution operation.

5 Evaluation

We evaluate the anomaly analyses for past and future FM evolution by four means. First, we show its feasibility by providing tool support for the evolution-aware anomaly detection, the evolution operation derivation, and the inspection of anomalies including their explanations (cf. Section 5.1). Second, we qualitatively evaluate our method by verifying whether we correctly identify all evolution operations leading to an anomaly (cf. Section 5.2). Third, we quantitatively evaluate whether our method is applicable for the evolution of real-world large-scale FMs and verify whether we can improve performance due to reuse enabled by our evolution-aware encoding (cf. Section 5.3). Fourth, we evaluate to what extent we are able to reduce anomaly explanation complexity (cf. Section 5.4).

5.1 Implementation

In this section, we show feasibility of our method by providing an implementation by means of two open-source tools. The first tool, called HyVarRec[3], implements the solving part described in Section 3.2 and retrieval of explanation for unsatisfiable queries. In particular, we extended it to support the evolution-aware analyses and uses the Z3 SMT solver. The second tool, DarwinSPL, allows to translate the entire TFM evolution into a satisfiability problem for an SMT solver, following the method we described in Section 3.1. Moreover, we implemented the linking to TFM elements to formula parts for the retrieval of evolution operations as we described in Section 4. Finally, DarwinSPL provides views for anomaly and explanation inspection.

Figure 4 shows the TFM of the running example and the view of the detected anomalies. For each anomaly, the type, the affected feature and the timespan is shown. Additionally, for each anomaly, a button to start its explanation is visible. Using this button, the translation of the TFM is started again and the linking of the translated to TFM elements (cf. Section 4) is performed. Then, HyVarRec is contacted and queried for an explanation. HyVarRec provides the set of unsatisfiable formula parts for that respective anomaly. Since an anomaly may have multiple explanations, based on the internal search heuristics used for the SMT solver, we provide just one of them because at least one of the formula parts in the returned set must be changed or removed to fix the anomaly. Using a resolving mechanism, relevant TFM elements for that explanation are identified and evolution operations affecting these elements are derived. Afterwards, the explanation and the identified evolution operations are presented. Figure 5 shows the explanation and evolution operation for the running example. Currently, all unsatisfied

[3] https://github.com/HyVar/hyvar-rec

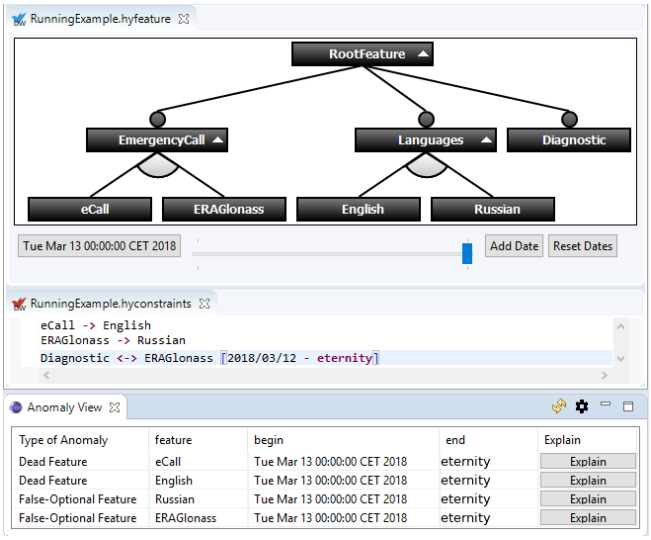


Figure 4. Screenshot of Detected Anomalies in DarwinSPL

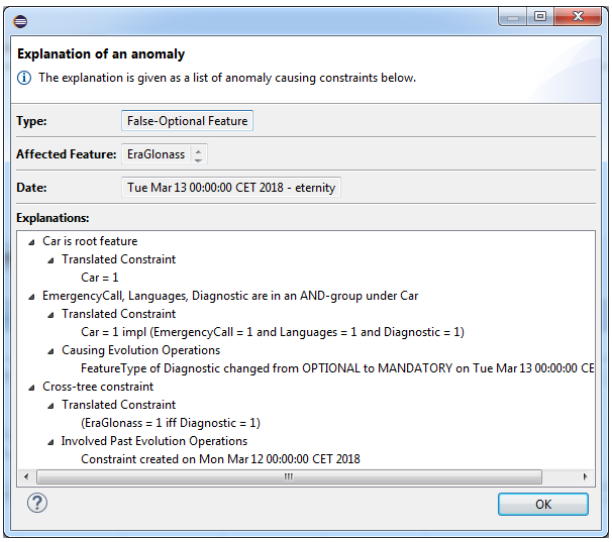


Figure 5. Anomaly Explanation from the Running Example

formula parts are still listed for evaluation purposes. The most relevant part is the identified evolution operation under "Causing Evolution Operations" as this is an operation leading to the analyzed anomaly. In a productive environment, all formula parts except the causing evolution operations could be hidden in the first place.

5.2 Qualitative Evaluation

In the qualitative evaluation, we investigate whether we are able to identify and explain anomalies and pose the following research questions:

RQ-1a: Do we identify all anomalies in FM evolution histories?

RQ-1b: Do we correctly identify evolution operations performed during FM evolution that lead to anomalies?

As a case study to answer these research questions, we use the real-world SPL *Body-Comfort System (BCS)*, originally presented by Oster et al. [35] and extended with evolution by Nahrendorf et al. [29]. The original version of the BCS contained 28 features [35]. Nahrendorf et al. introduced four evolution steps resulting in 49 features after the last evolution step [29]. To answer the research questions, we need a ground truth to know which anomalies indeed exist and what their causing operations are. As no cross-tree constraints exist in the original form of the case study, it does not contain any anomalies [21]. Thus, we manually seed anomalies by performing evolution operations. The fact that the FM has already an evolution history is important so that we can verify whether we can correctly find all anomalies and their date of introduction and to verify that explanation does not contain any incorrect evolution operations that have been performed in other evolution steps.

We create 12 different evolution scenarios of the BCS FM. In each of these scenarios, we manually introduce one anomaly. As some anomalies may entail other anomalies, we consider these additional anomalies as well. For instance, if a feature of an *alternative* group becomes false-optional, all of its sibling features become dead as a consequence. In particular, we create six dead feature anomalies and six false-optional feature anomalies. The explicitly introduced anomalies caused 11 further anomalies (e.g., a false-optional feature in an alternative group leads to other features of this group being dead). For each of the evolution scenarios, we document which evolution operations we performed in the DarwinSPL TFM editor in the description of the evolution scenario. All the data related to the evolution operation description, the corresponding requests for HyVarRec and the results can be found in our online repository.[4]

To answer **RQ-1a**, we investigate whether all of our seeded anomalies including their additionally entailed anomalies are found and the correct date of anomaly introduction is provided. For our case study, we are able to identify all anomalies, to classify them correctly, and to provide the correct date of anomaly introduction. The results of this evaluation can be investigated using our online repository.

Regarding **RQ-1b**, we need to verify whether the identified evolution operations in the explanation match those which we documented in the description for each evolution scenario for each anomaly. Moreover, the evolution operations of the explanations for the anomalies additionally entailed by the seeded anomalies should be the same as for the seeded anomalies themselves. In the considered evolution scenarios, all identified evolution operations in the anomaly explanations matched the evolution operations actually performed in the editor. Other irrelevant evolution operations

[4] https://gitlab.com/evolutionexplanation/evolutionexplanation

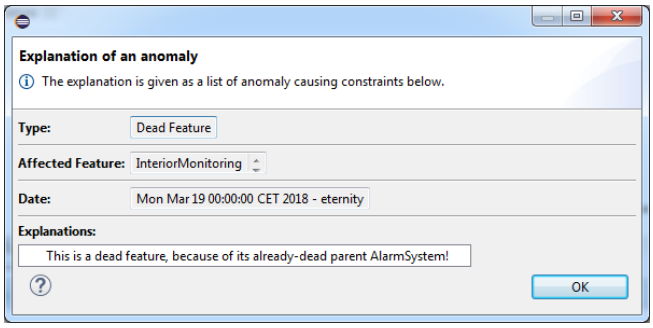


Figure 6. Relation Between two Anomalies of the Qualitative Evaluation

for the anomalies (i.e., those performed at a different evolution step or not related to that anomaly) are not listed.

Additionally, we are able to relate anomalies that imply other anomalies. For instance, if a certain feature is dead, all of its child features are dead as well. We detect this relation and make developers aware of it. Figure 6 shows how we present such a relation using two anomalies of one of our analyzed evolution scenarios. This explanation states that the feature `InteriorMonitoring` is dead because its parent `AlarmSystem` is dead, thus resulting in all its children being dead as well. The results indicate that we are able to identify all dead and false-optional feature anomalies in the entire evolution history of an FM and that we provide the correct evolution operations that lead to those anomalies.

5.3 Quantitative Evaluation

In the quantitative evaluation, we investigate whether our method is applicable for large-scale real-world FM evolution. As we are able to reuse the solver thanks to our evolution-aware encoding, we see potential for an improved performance. Thus, we analyze whether the incremental reuse of formula parts for the analyses increases the performance. To this end, we pose the following research questions:

RQ-2a: Is our method applicable to large-scale real-world FM evolution?

RQ-2b: Does the evolution-aware analysis (i.e., reuse of formula parts) for FM histories increase the performance?

As a case study to answer these research questions, we use the real-world FMs *Automotive02* and *FinancialServices1* with real-world evolution from the FeatureIDE example repository.[5] The evolution history of Automotive02 contains four versions. The Automotive02 FM contains between 14,010 (Version 1) and 18,616 (Version 4) features and between 666 (Version 1) and 1,369 (Version 4) cross-tree constraints. The evolution history of FinancialServices1 contains ten versions. The FinancialServices1 FM contains between 557 (Version 1) and 774 (Version 10) features and between 1,001 (Version 1) and 1,148 (Version 9) cross-tree constraints. We evaluated each evolution step on its own as well as the evolution-aware analyses of the TFM. To analyze the merged evolution history, we imported all single versions and integrated them into one TFM.

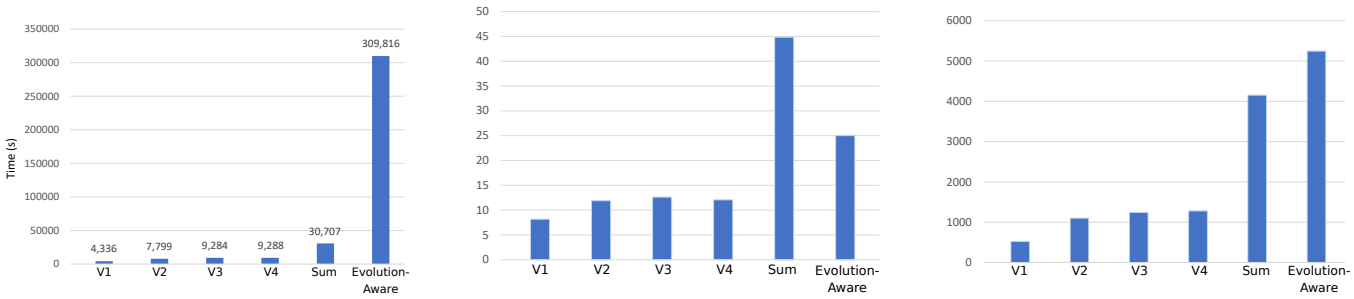
We deployed HyVarRec as Docker container on virtual machines provided by an OpenStack private cloud. Each virtual machine used Ubuntu 17.10, had four virtual cores and 8/16 GB RAM. We repeated each experiment five times and used the average values to cope with computation bias.

In the following, we only consider computation times of the HyVarRec backend. As HyVarRec is running as a cloud service, it has to parse the requests beforehand which took for Autmotive02 between ~ 30 seconds (average for single evolution steps) and ~ 79 seconds (average merged evolution history) and for FinancialServices1 between ~ 6 seconds (average for single evolution steps) and ~ 23 seconds (average merged evolution history). Figure 7 shows results using the Automotive02 and Figure 8 shows the results using the FinancialServices1. The first results in all diagrams (labeled as V1 – V4 in Figure 7 and V1 – 10 in Figure 8) show the computation times for analyzing each of the evolution steps (i.e., versions) of the case studies on their own. The second last result of each diagram (labeled as *Sum*) shows the aggregated computation time for analyzing all evolution steps on their own. The last result of each diagram (labeled as *Evolution-Aware*) shows the computation time for the evolution-aware analysis of the entire FM history. Additionally, as a benchmark, we compare our results to computation times of FeatureIDE as it is the most common feature modelling tool and also supports advanced explanation functionality. All data and results can be found in our online repository (cf. Footnote 4).

In the first version of HyVarRec and our experiments, we used an Integer encoding of the feature variables (i.e., features instead of being considered Boolean values considered to be integers in the $\{0, 1\}$ domain). Figure 7a shows the results of detecting feature anomalies using the Integer encoding. As can be seen, the computation times were extremely high. For the single evolution steps, finding all feature anomalies took in average more than 2 hours. For the merged model, it even took more than 86 hours. This might be the price to pay when analyzing cardinality-based FMs [8] where the Integer encoding may become necessary. As in our experiments, we are only dealing with FMs without cardinalities, we implemented the possibility to use a Boolean encoding for the feature variables.

Figure 7b shows the performance of detecting void FM anomalies for Automotive02 and using Boolean encoding. The average computation time for the void FM analyses for each evolution step is ~ 11 seconds. As can be seen, the sum of analyzing all individual evolution steps (~ 45 seconds) significantly exceeds the evolution-aware analysis (~ 25 seconds). Figure 7c shows the results for the false-optional and dead feature analyses for Automotive02 using Boolean

[5] https://github.com/FeatureIDE/FeatureIDE/tree/develop/plugins/de.ovgu.featureide.examples/featureide_examples/FeatureModels

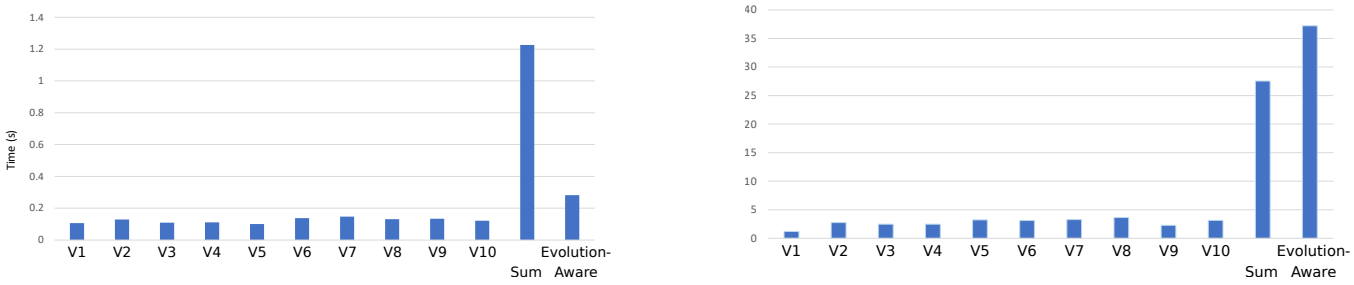


(a) Void Feature Model Analyses using Integer Encoding

(b) Void Feature Model Analyses using Boolean Encoding

(c) Feature-Anomaly Analyses using Boolean Encoding

Figure 7. Anomaly Analyses Computation Times for Automotive02



(a) Void Feature Model Analyses

(b) Feature-Anomaly Analyses

Figure 8. Anomaly Analyses Computation Times for FinancialServices1

encoding. For brevity, we refer to the false-optional and dead feature analyses as *feature-anomaly analyses* in the following. In this case, the average computation time for each evolution step is ~ 17.30 minutes. For this analysis, the sum analyzing all individual evolution steps (~ 69.22 minutes) is less than the evolution-aware analysis (~ 87.42 minutes).

Figure 8 shows the results of the void FM and feature-anomaly detection computation times for the FinancialServices1 case study. The average computation times for each individual evolution steps are ~ 0.12 seconds (void FM analysis) and ~ 2.80 seconds (feature-anomaly analyses). Similar to the Automotive02 case study, the sum of the individual computation times is significantly higher for the void FM analyses compared to the evolution-aware analyses but for the feature-anomaly detection, the evolution-aware analyses is slower.

To answer **RQ-2a**, we can conclude that our method is applicable for large-scale real-world FM evolution. Even if we have computation times around 87.42 minutes (cf. Figure 7c), it is an acceptable effort for analyzing the entire evolution history of such a large model. Compared to FeatureIDE, this still takes more time. In FeatureIDE, checking each evolution step of the Automotive02 for voidness takes a summed up computation time of ~ 0.53 seconds and searching for feature anomalies in each evolution step takes a summed up computation time of ~ 4.88 minutes. We performed the experiments with FeatureIDE on a Windows 10 machine with an Intel Core i7-5600U @ 2.60GHz and 12GB of RAM. We believe that this is due to the fact that FeatureIDE exploits the tree structure of the FM to perform many optimizations that unfortunately are not possible with HyVarRec that relies on a more general declarative specification of the FM. More importantly, FeatureIDE uses a different notion of false-optional features than the one proposed by Benavides et al. [4]. In particular, in FeatureIDE, a feature is false-optional if it must be selected if its parent is selected despite having the type *optional*. Despite this difference in performance and definition of anomalies, compared to FeatureIDE, we provide additional information such as the introduction date of an anomaly and the causing evolution operations. Thus, with our method, we significantly increase the support for developers in fixing anomalies in the evolution history.

Regarding **RQ-2b**, we do not have an unambiguous answer. As Figures 7b, 7c, 8a and 8b show, performing the evolution-aware analysis (i.e., for the merged model) is sometimes faster than performing the sum of all single step analyses. For the feature-anomaly analysis, the cumulative times taken by the single step analyses are faster. Unfortunately, since we are trying to solve NP-hard problems, we are not yet able to predict under which circumstances the evolution-aware analyses is faster. However, for the cases for which the evolution-aware analysis is slower, the factor is not that

high, but for the cases for which the evolution-aware analysis is faster, the difference is significant.

5.4 Explanation Reduction Evaluation

Explanations from existing methods can grow very large and during evolution, even single evolution operations can cause anomalies. Thus, understanding these explanations is a complex task. We argue that if the anomaly has been introduced during evolution, evolution operations causing the anomaly are easier to understand. Additionally, the number of evolution operations is fewer than formula parts of the explanation but operations are even more expressive. In this part of the evaluation, we evaluate whether our method is able to reduce anomaly explanation complexity. To this end, we pose the following research question:

RQ-3: Can evolution-aware anomaly explanation reduce anomaly explanation complexity?

As case studies, we use the FMs and their evolution histories of the qualitative (Body-Comfort System (BCS)) and quantitative evaluation (Automotive02 and FinancialServices1). In particular, we analyze the anomalies that have been introduced during evolution as for anomalies that have been there from the beginning, no evolution operations exist that have introduced these anomalies and, thus, no explanation complexity reduction is possible. For the BCS, we analyze 17 anomalies as we also consider anomalies that arised due to other anomalies (cf. Section 5.2). Most anomalies of the Automotive02 case study have already been there from the beginning and, thus, we cannot use them for this evaluation. As a consequence, we analyzed the explanations of six anomalies. During the evolution of the FinancialServices1 FM, nine anomalies were introduced. As a baseline, we use the number of unsatisfiable formula parts in explanations that other methods would provide. Between three to seven formula parts are unsatisfiable for the anomalies of the BCS, between four to 13 formula parts are unsatisfiable for Automotive02 and between eleven to 98 formula parts are unsatisfiable for FinancialServices1. The fact that the maximum number of unsatisfiable formula parts is larger for FinancialServices1 than for Automotive02 shows that even smaller FMs may have large explanations.

To analyze to what percentage we are able to reduce explanation length, we compare the number of unsatisfiable formula parts with the number of identified evolution operations causing the respective anomalies. Another approach for identifying the cause for anomalies could be to investigate the difference and, thus, the performed evolution operations between two FM versions [7]. However, this method would provide the set of all evolution operations between two FM versions. To compare our method with methods reasoning about FM differences, we measure the percentage of identified evolution operations causing an anomaly compared to the number of all evolution operations performed at the introduction date of the considered anomaly.

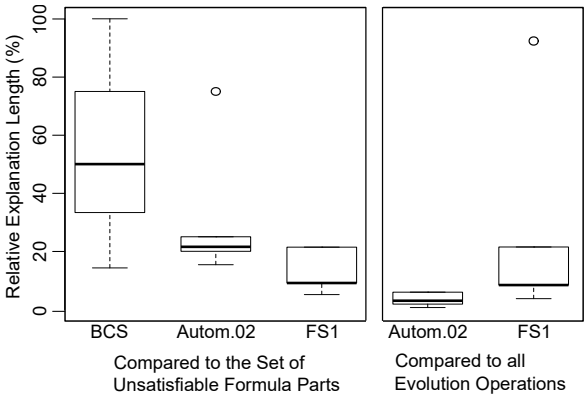


Figure 9. Anomaly explanation complexity reduction rates.

Figure 9 shows the relative explanation length of our method. Lower numbers are better as this indicates shorter explanations compared to the other methods. The first three plots compare the number of identified anomaly-causing evolution operations with the set of unsatisfiable formula parts. The last two plots compare the number of identified anomaly-causing evolution operations with the number of all evolution operations performed at the date of anomaly introduction. For the latter comparison, we did not include the BCS as we explicitly performed single evolution operations leading to anomalies (cf. Section 5.2) and, thus, it would always be 100% by design.

As can be seen, the relative explanation length compared with the number of unsatisfiable formula parts for the BCS are between $\sim$ 14% – 100%, for Automotive02 between $\sim$ 15% – $\sim$ 75%, and for FinancialServices1 between $\sim$ 5% – $\sim$ 21%. The longest explanation contained 98 unsatisfiable formula parts for FinancialServices1 and we identified five causing evolution operations. In two cases of the BCS, the number of identified evolution operations is equal to the number of formula parts in the original explanation and, thus, no reduction is achieved. However, in nine cases of the BCS and in three cases of the Automotive02 case study, we are able to reduce complexity by more than half.

For the comparison between causing evolution operations with all evolution operations, we achieve even more significant reduction rates. For Automotive02, the relative explanation length is between $\sim$ 0.6% – $\sim$ 6% and for FinancialServices1 it is between $\sim$ 4% – $\sim$ 92%. The reason for the low relative explanation length for Automotive02 are most likely as between the FM versions many operations were performed. The most significant reduction was achieved for the evolution step between Version 1 and Version 2 for which 169 evolution operations were performed and we identified 1 operation as cause for a dead feature anomaly. In contrast, one

anomaly in FinancialServices1 was caused by almost all performed evolution operations (12 out of 13). To answer **RQ-3**, we claim that the length of most of the explanations of the anomalies are significantly reduced by using our method.

5.5 Threats to Validity

The results of the evaluation are subject to threats to validity. In the qualitative evaluation, we manually seeded anomalies in the evolution history of an FM to verify whether all anomalies were found and the evolution operations of the explanations matched the actually performed ones. We used this setup as we had access only to SPLs with real-world evolution but without a meaningful number of anomalies that was still analyzable manually to find all existing anomalies. The internal validity might be biased as we probably did not know all introduced anomalies and evolution operations performed. To mitigate this threat, we used an FM with a moderate size so that a manual analysis was feasible and we documented all evolution operations we performed in the editor which we used as ground truth. Moreover, in the quantitative evaluation, we verified that we were able to detect the same anomalies using FeatureIDE.[6]

In the explanation reduction evaluation, we compare the number of formula parts of the original explanation with the number of identified evolution operations. Thus, we assume that understanding a formula part of the original explanation is as complex as understanding an evolution operation which is an internal threat to validity. However, our experiences with explanations has shown that understanding evolution operations is even easier for developers than understanding formula parts as the operations are common to developers.

The anomalies and evolution operations analyzed in the qualitative evaluation may not be representative for other evolution scenarios or SPLs. To mitigate this threat, we analyzed 12 different anomalies and evolution operations leading to these anomalies for a real-world FM with evolution.

The results of the quantitative evaluation may be subject to computation bias resulting in falsified results. To mitigate this threat, we performed each of these analyses multiple times and used the average values. The analyses we performed only once were those for which the results were clear, i.e., the experiments using the Integer encoding in Figure 7a.

The quantitative evaluation may not be representative as we analyzed the evolution history of only two FMs. We only used two FMs as we did not have access to other large-scale FMs with their evolution history. To mitigate this threat, we explicitly used two real-world FMs that are publicly available.

The explanation reduction evaluation may not be representative as we only analyzed 32 anomalies in total. To mitigate this threat, we used anomalies of the evolution of two real-world FM and their real-world evolution. Moreover, when discussing the results, we distinguished between the case studies to see which results stem from seeded anomalies and which stem from real-world anomalies. As the results of the real-world case studies are similar to the one from the qualitative evaluation, we are encouraged that our results are representative.

[6] In particular, we detect the same dead features but more false optional due to the different definition of false-optional features in FeatureIDE.

6 Related Work

Many approaches exist to analyze FMs with a high degree of optimization [3–5, 20, 28, 49]. Multiple approaches are able to detect anomalies but are not able to explain them [15, 53]. Other approaches are able to provide explanations for anomalies [3, 11, 18, 19, 21, 51, 52]. Some of these approaches focus on contradictions in the configuration process [3, 19]. Lesta et al. [21] are able to detect and explain dead features and false-optional features in attributed feature models. Trinidad et al. [51, 52] provide the tool suite FAMA which detects and explains dead and false-optional features as well. The method of Felferning et al. [11] to explain anomalies does not relate explanations to the FM structure, as we do. Finally, Kowal et al. [18] provide a method to detect and explain dead and false-optional features. Additionally, they also detect redundant constraints and highlight which parts of the explanations are more important than others. With the method of Ananieva et al. [2], it is possible to detect and explain implicit constraints in FMs. Using this method, it is possible to show only parts of an FM to engineers which are (implicitly) related to a constraint or an FM structure. Kowal et al. [18] and Ananieva et al. [2] also provide tool implementation in FeatureIDE. However, none of the previously mentioned methods incorporates evolution. Nonetheless, the integration of redundant constraint detection could be relevant for evolution-aware analyses. Additionally, we could improve our explanation presentation by only showing affected FM parts using the method of Ananieva et al. [2].

Multiple techniques were published dealing with the detection of range inconsistencies in cardinality-based FMs [40, 54]. In this paper, we consider special cases of cardinality-based FMs (i.e., each feature has a maximum cardinality of 1). Quinton et al. also define which evolution operations can lead to range inconsistencies and explain the found inconsistencies [40]. However, both approaches do not analyze the evolution history of an FM and do not incorporate evolution operations in their explanations. It could be interesting to combine these methods with ours to generalize our analyses for cardinality-based FMs in general.

To capture evolution of product lines, Schubanz et al. [46, 47], Pleuss et al. [38] and Botterweck et al. [6] introduce EvoFM and the EvoPL framework. With their method it is possible to model and plan FM evolution. They also provide techniques to check model and configuration consistency (i.e., void FM anomaly). They do not incorporate evolution in their analyses and do not detect feature anomalies.

Alves et al. present a theory for FM refactorings and a set of refactoring operations [1]. Similarly, Neves et al. propose a theory and a catalogue for safe evolution templates [30, 31]. However, the notion of refactorings of Alves et al. [1] and Neves et al. [30, 31] only allow changes that do not remove valid configurations from the FM but potentially add new ones. As a consequence, no new anomalies may arise but existing ones may be removed. Thüm et al. present a a more fine-grained categorization of FM changes [50]. They distinguish between refactorings (valid configurations remain the same), generalizations (valid configurations are added), specializations (valid configurations are removed) and arbitrary edits (valid configurations are removed but also new ones are added). Using the previously mentioned templates and categorizations, we could reduce the number of analyses based on the performed evolution operations as we know the potential effect on anomalies.

Sampaio et al. [43] relaxed the notion of safe evolution templates of Neves et al. [30] and present the concept of partially safe evolution templates. However, as these templates are only safe for a subset of configurations, they may introduce FM anomalies. Similarly, Seidl et al. present a method and templates for co-evolving FMs and their mapping to implementation artifacts [48]. It would be interesting to also analyze the potential of anomaly introduction for each of these templates. When applying such templates, we would only need to analyze the FM if the templates potentially introduce anomalies.

Guo et al. provide an approach to analyze the consistency (i.e., void FM anomalies) of an FM in the presence of evolution [12, 13]. They do not analyze the entire FM and its history again, but only focus on parts changed by evolution operations since the last check. However, this requires that the FM is valid before checking it again. Moreover, they do not find feature anomalies and do not provide any explanations for inconsistencies. Nevertheless, it might be sensible to investigate whether their method can be combined with ours.

Several techniques exist to reason about FM differences [7, 9, 50]. These differences can be assumed as changes between two evolution steps. To this end, Dintzner et al. provide a set of operations they identified in the Linux kernel variability model which they are capable to detect with their tool FMDiff [9]. However, this approach does only work for KConfig variability models. None of these techniques is capable of detecting FM anomalies. Nevertheless, the approaches may provide additional information about the evolution which can be used to analyze the FM history more efficiently. Tartler et al. analyzed the variability model of the Linux kernel and searched for anomalies [41]. The work has proven to be applicable to large-scale models. However, it is again specific for the Linux kernel variability model and does not incorporate evolution or provide anomaly explanations.

Lity et al. use the concept of higher-order deltas to capture the evolution of implementation artifacts in one 175% model [23, 24]. In the higher-order deltas, changes to existing deltas are modeled. As evolution of implementation artifacts may also have impact on FMs, analyses for the co-evolution of implementation artifacts and FMs could be interesting.

Guthmann et al. [14] and Liffiton et al. [22] provide methods to retrieve minimal explanations. For this purpose, Guthmann et al. [14] compute the minimal unsatisfiable core using an SMT solver and Liffiton et al. [22] provide algorithms to compute minimal unsatisfiable subsets of constraints. We use similar methods to compute the unsatisfiable formula parts.

7 Conclusion

We presented a method to analyze past and future evolution histories of FMs encoded in Temporal Feature Models (TFMs). We proposed a method to encode the entire TFM evolution history into one request for a solver by introducing evolution as a distinct variable. Using such requests, we identified FM anomalies, pinpointed their date of introduction, and identified the anomaly-causing evolution operations. Additionally, we integrated this method in our tools DarwinSPL and HyVarRec, allowing easy inspection of anomalies and their explanations. We performed three evaluations: First, we have shown that we are able to detect all anomalies in the evolution history of a real-world FM and provide the respective correct explanations. Second, we have shown that our method is applicable to real-world evolution of a large-scale FMs and measured performance of the analyses. In some cases, our evolution encoding resulted in a significantly higher performance but in other cases it was slightly slower. Third, we have shown that we are able to significantly reduce anomaly explanation length for real-world evolution of large-scale FMs by identifying evolution operations that caused the anomaly.

This work raises several further research opportunities. To investigate the increase of comprehensibility and the support for fixing anomalies in the evolution history, we want to perform a supervised experiment with two user groups. To support the anomaly detection for context-adaptive SPLs in presence of evolution, we plan to combine the results of this work with our previous work on context-aware analyses [26]. Additionally, we want to integrate the detection of more relations between anomalies (e.g., features that became dead because another feature became false-optional) or anomalies related to attributes (e.g., an attribute value that may never be selected). Finally, we want to investigate in which cases the evolution-aware analysis is faster.

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