Modelling the Probability of Contamination for Mars Missions

An ExoMars Rosalind Franklin Mission Case Study

Benjamin Andrews
ESTEC, Keplerlaan 1, Noordwijk, The Netherlands, benjamin.andrews@esa.int

- PDF version of the poster
- More info about the model
- Feedback form

Rationale for a Probabilistic Model of Mars Contamination

Forward contamination of Mars by terrestrial microorganisms is a key planetary protection concern. The risk of contamination is inherently probabilistic, as successful contamination requires a microorganism to survive and progress through multiple uncertain stages from launch to potential growth on Mars. A probabilistic modelling framework provides a structured way to quantify these uncertainties and identify the factors that contribute most strongly to contamination risk. Such an approach could support a transition from prescriptive, spore-based planetary protection requirements towards risk-informed decision-making.

Aim: To develop a probabilistic framework for Mars forward contamination risk assessment by integrating microbial abundance estimates with contamination pathway probabilities, using the ExoMars Rosalind Franklin mission as a case study.

Single-Cell Contamination Pathway

The event tree (Figure 1) represents the contamination pathway for a single microbial cell belonging to microbial class C at location on the spacecraft L. The probability of contamination is calculated as the product of the conditional probabilities associated with each event in the tree, where the probability of a given event is conditioned on the successful occurrence of all preceding events:

$$p_{C,L} = \prod_{i=1}^{n} P(E_i | E_1, \dots, E_{i-1})$$

$$E_i \in \{SL, SC, SEDL, SRSO, R, SR, T, ST, G\}$$

where $p_{C,L}$ is the probability that a single cell completes the contamination pathway leading to contamination, E_i represents an individual event in the tree, and n is the total number of events.

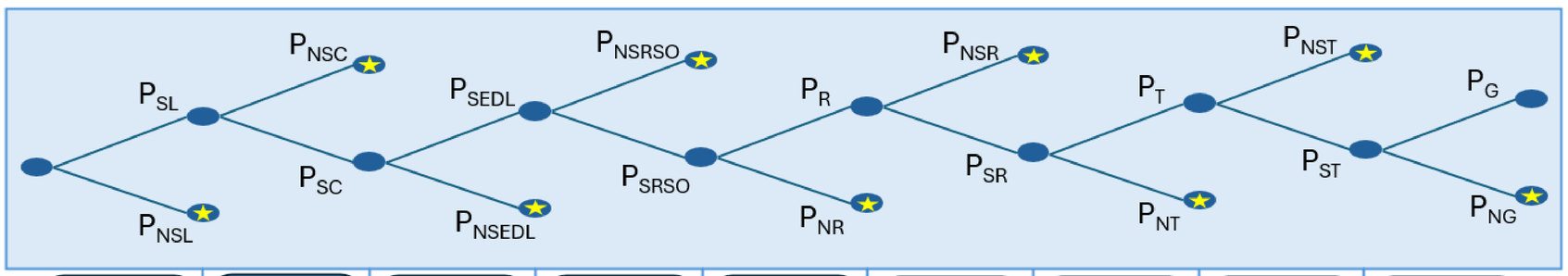


Figure 1. Single-cell contamination pathway for the ExoMars Rosalind Franklin mission. The single-cell probability of contamination is calculated as the product of the conditional probabilities associated with progression through each successive mission stage, from launch to potential growth in a Martian environment.

Expansion to Multiple Cells

For a microbial class-location group (C, L) containing $N_{C,L}$ cells, each cell is treated as an independent contamination opportunity. The probability of at least one contamination event from this (C, L) group is therefore:

$$P_{C,L} = 1 - \left(1 - p_{C,L}\right)^{N_{C,L}}$$

Expansion to Total Spacecraft Bioburden

Assuming independence between (C, L) groups, the probability of at least one contamination event arising from the total spacecraft bioburden is:

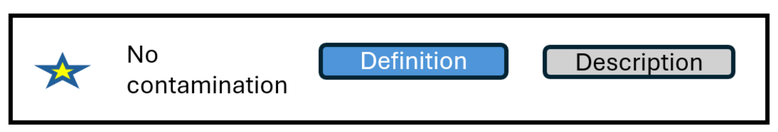
$$P_{cont} = 1 - \prod_{C,L} \left(1 - P_{C,L}\right)$$

This final equation combines the contamination probabilities of all microbial class-location (C, L) groups across the spacecraft, demonstrating that the overall contamination probability is determined by both the microbial abundance ($N_{C,L}$) and the single-cell contamination probability ($p_{C,L}$) of each group.

Assumptions

- Contamination pathway is represented as a sequential event tree.
- The probability of each event in the tree (stage in the pathway) is conditional on the successful occurrence of all preceding events.
- Individual cells within a microbial class-location group (C, L) are treated as independent contamination opportunities.
- Microbial class-location groups (C, L) are treated as independent.
- Both $p_{C,L}$ and $N_{C,L}$ may vary between (C, L) groups.

Key



Development of the Statistical Framework

The current model uses point estimates for contamination pathway probabilities and initial bioburden (microbial abundance) values. Therefore, parameter uncertainty is not yet explicitly represented. Future work will incorporate Bayesian statistical approaches to quantify uncertainty and update pathway probabilities as new data becomes available. Markov Chain Monte Carlo (MCMC) methods could also be used to propagate uncertainty through the contamination pathway and identify the dominant contributors to contamination risk through sensitivity analysis.

Example Estimation of Cruise-Phase Survival Probability (P_{SC})

The Cruise-Phase Microbial Survival Model (CPMS)[1] developed by Moores and Schuerger (2020) provides a first-order estimate of spacecraft bioburden reduction during cruise using experimentally derived inactivation kinetics for *Bacillus subtilis* endospores exposed to UV radiation and temperature-vacuum conditions. Figure 2 presents predicted bioburden reductions for the ExoMars Rosalind Franklin mission during a proposed Type-3 transfer trajectory (launch: 21 Sep 2028; arrival: 19 Dec 2030). Under the assumption that the spacecraft contains no pressurized compartments and all hardware is maintained above 250 K (-23°C), the model predicts a reduction of at least 10 orders of magnitude (≥10-log reduction) in the combined surface bioburden of *B. subtilis* endospores. These results can be used to estimate cruise-phase survival probabilities (P_{SC}) for microbial class-location (C, L) groups, including organisms on external surfaces (fully exposed), shallow internal surfaces (UV-shielded), and deep internal surfaces (shielded from both UV exposure and thermal fluctuations).

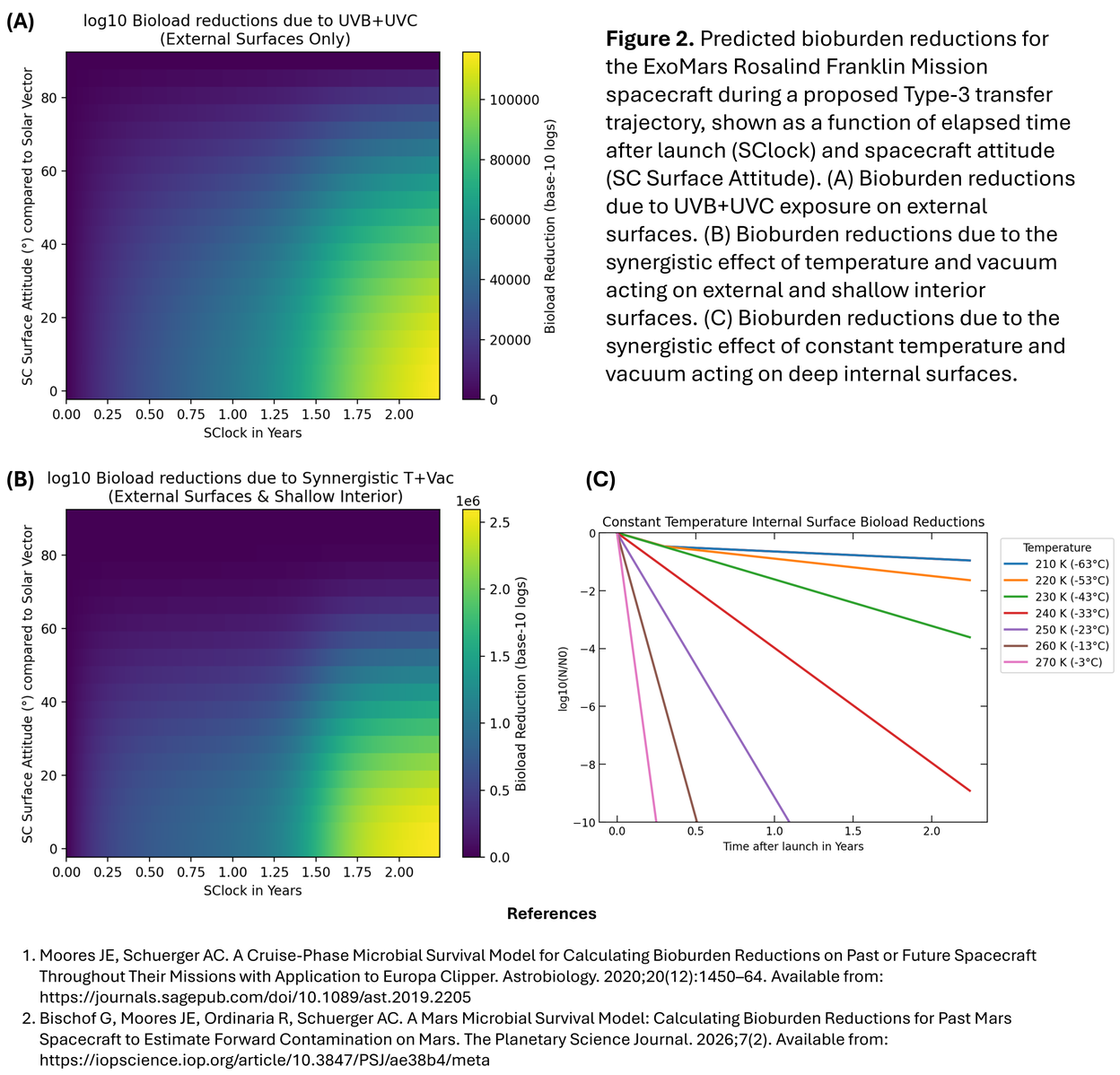


Figure 2. Predicted bioburden reductions for the ExoMars Rosalind Franklin Mission spacecraft during a proposed Type-3 transfer trajectory, shown as a function of elapsed time after launch (SClock) and spacecraft attitude (SC Surface Attitude). (A) Bioburden reductions due to UVB+UVC exposure on external surfaces. (B) Bioburden reductions due to the synergistic effect of temperature and vacuum acting on external and shallow interior surfaces. (C) Bioburden reductions due to the synergistic effect of constant temperature and vacuum acting on deep internal surfaces.

Determination of Initial Spacecraft Bioburden

Multiple complementary bioburden assessment approaches will be integrated to estimate $N_{C,L}$, the abundance of microorganisms belonging to microbial class C at location on the spacecraft L.

Table 1. Bioburden Assessment Approaches Supporting the Estimation of $N_{C,L}$

Objective	Methods
Cultivation and isolation	Standard cultivation, alternative cultivation
Taxonomic profiling	16s amplicon sequencing, metagenomics
Strain-level characterisation	Whole-genome sequencing of strains
Database development	Genome catalogue creation
Functional profiling	Phenotypic prediction software
Viability assessment	PMA-seq and related methods
Absolute quantification	ddPCR and related methods

Determination of Contamination Pathway Probabilities

Contamination pathway probabilities are informed by experimental studies, mission analyses, engineering models, environmental simulations, and expert elicitation. The dependence of these probabilities on microbial class C and location on spacecraft L varies between contamination pathway probabilities. Table 2 summarises a non-exhaustive selection of ongoing activities supporting their estimation. Although probabilities are conditional, shorthand notation is used for brevity.

Table 2. Ongoing Activities Supporting the Estimation of Contamination Pathway Probabilities

Activity	Primary probability term(s) informed
Literature review of space exposure experiments and ground-based microbial survival studies	P_{SC} , P_{SRSO}
Experimental assessment of TVAC- and UVC-induced inactivation kinetics across diverse microbial isolates and bioburden categories (surface, mated, and encapsulated)	P_{SC} , P_{SRSO}
Application of the Cruise-Phase Microbial Survival model[1] to EXM-RFM	P_{SC}
Application of the Mars Microbial Survival model[2] to EXM-RFM, including ray-casting UVC modelling and dust shielding simulations	P_{SRSO}
High-resolution mapping of Martian geological regions of interest, including potential Special Regions	P_T , P_G
Simulations of microbial transport on Mars, using large eddy simulations (LES), mesoscale models, and general circulation models (GCM)	P_T
Thermodynamic modelling of potential microbial growth in Martian environments, constrained by mineralogical simulant data	P_G
Experimental assessment of microbial growth under simulated Martian conditions	P_G

Conclusions

This work presents a simplified probabilistic contamination pathway framework for Mars missions that integrates microbial abundance estimates with contamination pathway probabilities, providing a structured approach for combining diverse datasets relevant to planetary protection. While no single model is expected to independently demonstrate mission compliance with planetary protection requirements, this approach can contribute to a broader assurance-case framework based on multiple lines of evidence. This model can help identify key data requirements and knowledge gaps, with future work focusing on uncertainty quantification and more advanced probabilistic approaches, including Bayesian and Markov-based methods.

References

1. Moores JE, Schuerger AC. A Cruise-Phase Microbial Survival Model for Calculating Bioburden Reductions on Past or Future Spacecraft Throughout Their Missions with Application to Europa Clipper. Astrobiology. 2020;20(12):1450–64. Available from: https://journals.sagepub.com/doi/10.1089/ast.2019.2205
2. Bischof G, Moores JE, Ordinaria R, Schuerger AC. A Mars Microbial Survival Model: Calculating Bioburden Reductions for Past Mars Spacecraft to Estimate Forward Contamination on Mars. The Planetary Science Journal. 2026;7(2). Available from: https://iopscience.iop.org/article/10.3847/PSJ/ae38b4/meta