




1 site-analysis: A Python package for crystallographic 2 site-projection analysis of molecular dynamics 3 trajectories

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DOI: [10.xxxxxx/draft](https://doi.org/10.xxxxxx/draft)

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Submitted: 01 January 1970

Published: unpublished

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8 Summary

9 Ionic transport in crystalline solids can often be considered to proceed via discrete “jumps”,
10 where mobile ions move between potential energy minima corresponding to specific crystal-
11 lographic sites. `site-analysis` is a Python package that transforms continuous molecular
12 dynamics trajectories into discrete site-occupation sequences, enabling quantitative analysis
13 of ionic diffusion mechanisms. It provides four site-definition methods—spherical, polyhe-
14 dral, Voronoi, and dynamic Voronoi—each offering different trade-offs between simplicity and
15 crystallographic fidelity. The package provides a reference-based workflow that automates
16 coordination-based site generation by identifying coordination environments in ideal structures
17 and mapping these to thermally distorted configurations. Integration with `pymatgen` provides
18 compatibility with existing computational materials science workflows.

Statement of need

19 Molecular dynamics simulations are widely used to study ionic transport in battery materials,
20 solid electrolytes, and ceramic ion conductors. While these simulations provide continuous
21 atomic trajectories, ionic diffusion in crystalline solids is more accurately described as a sequence
22 of discrete jumps between potential energy minima. These minima typically correspond to
23 specific arrangements of mobile ions within crystallographic sites. Analysing these simulations
24 requires methods that can spatially discretise the continuous trajectories onto sets of discrete
25 sites.

26
27 General-purpose trajectory analysis packages lack specialised functionality for crystallographic
28 site analysis in periodic systems. The most common approach uses spherical site defini-
29 tions, which have fundamental limitations: incomplete spatial coverage leading to unassigned
30 atoms during transitions, arbitrary radius parameters requiring manual optimisation, and poor
31 representation of anisotropic coordination environments.

32 More sophisticated coordination-based approaches—such as polyhedral sites defined by frame-
33 work atoms or dynamic Voronoi tessellations—provide better crystallographic representation
34 but typically require custom code for each material system. This creates a significant barrier
35 to adoption, limiting most analyses to simpler but less accurate spherical projections.

36 `site-analysis` addresses these challenges through a unified framework implementing multiple
37 site-definition paradigms. By projecting continuous coordinates onto discrete sites, it provides
38 two complementary perspectives: tracking which sites each atom visits over time, and monitor-
39 ing which atoms occupy each site. This enables calculation of time-averaged site-occupation

probabilities, analysis of sequential site visitation patterns, and quantification of temporal and spatial correlations between ion movements.

The package includes a reference-based workflow that automates the generation of coordination-based sites, eliminating the need for manual site specification. Users provide an ideal reference structure and specify coordination criteria; the software identifies all matching environments and automatically maps them to target structures, with sites adapting to thermal distortions while preserving chemical identity.

The package employs a builder pattern interface that provides method chaining for intuitive configuration while ensuring parameter validation. This enables researchers to apply sophisticated site definitions without developing custom analysis code for each system. The software supports standard molecular dynamics formats including VASP XDATCAR files and integrates with the pymatgen ecosystem, facilitating incorporation into existing computational workflows. Full documentation and tutorials are available at <https://site-analysis.readthedocs.io>.

The software has previously been used to analyse ion-transport mechanisms in lithium-ion and fluoride-ion solid electrolytes (Hu et al., 2025; Krenzer et al., 2023; Mercadier et al., 2023; Morgan, 2021). The package was initially written to reproduce the functionality of an earlier Fortran code that used dynamically defined coordination polyhedra, which was used to study ion-transport and defect distributions in a range of solid electrolyte materials (Burbano et al., 2016; Morgan & Madden, 2011, 2012, 2014a, 2014b). This code, in turn, was motivated by earlier studies that used projections onto tetrahedral sites (Castiglione et al., 1999; Castiglione & Madden, 2001; Marrocchelli et al., 2009).

Acknowledgements

B.J.M. acknowledges support from the Royal Society (UF130329 and URF/R/191006).

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