

Utilizing Tumor Growth Models to Estimate Rate of Growth and Decay with Lesion Size Measurements on Longitudinal Imaging

A Novel Methodology to Evaluate Treatment Efficacy in Cancer

mintmedical

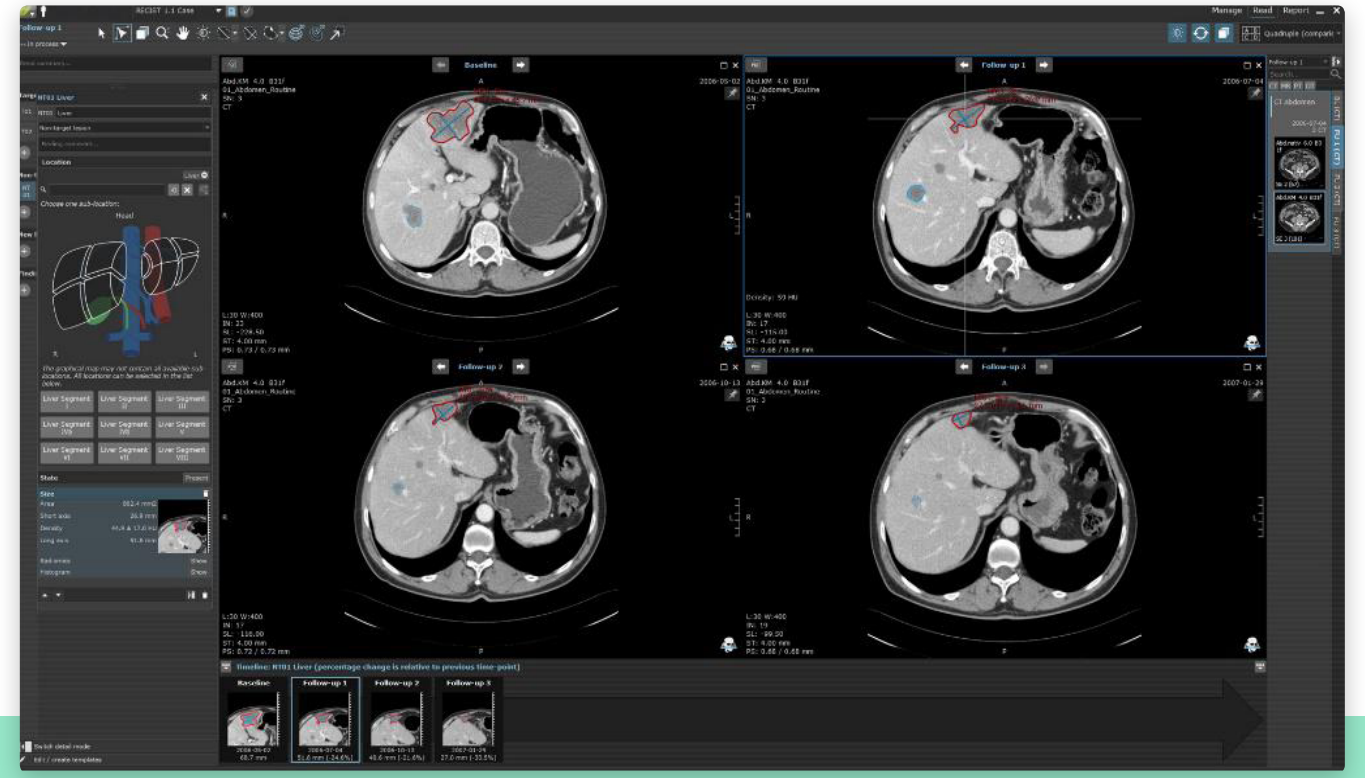
Quantifying Response to Treatment with Medical Imaging

Historically, clinical trials have relied on clinical outcomes to determine if a treatment is safe and effective. The reputed gold standard measure of efficacy is Overall Survival (OS) defined as time from randomization on the trial to time of death. OS, however, typically requires large datasets and extensive long-term follow up which can be both time and resource intensive. The addition of other therapies or interventions following the end of treatment for the therapy under investigation can further confound OS outcomes.

In time, as medical imaging (e.g., Computed Tomography (CT), Magnetic Resonance Imaging (MRI), Positron Emission Tomography (PET), etc.) improved, evidence grew that using tumor shrinkage as observed on imaging could provide objective evidence of efficacy. For nearly three decades, evidence of tumor shrinkage evaluated on medical imaging has supported the approval of new therapies in clinical trial evaluations using imaging as a surrogate endpoint. Compared to OS as primary endpoint, longitudinal evaluation of serially acquired scans in which response to therapy can be measured at time intervals (e.g., weeks) offers the advantage of predicting clinical benefit (e.g., efficacy evidence) in a shorter period of time while more directly evaluating the specific treatment under investigation. The objective of imaging-based endpoints is the possibility of bringing new effective therapies to patients in need faster.

To date, imaging evaluations in oncology clinical trials utilize response criteria guidelines as a standardized tool to evaluate the effect of therapy on a given disease indication. These published guidelines have specifications based on disease indication (e.g., solid tumors, primary brain metastases, lymphoma, etc.) with the “rules” of the criteria governed by the typical presentation of the disease type, industry standards, best practices for reproducibility, and quantitative statistical analysis of relevant datasets that inform the basis for such guidelines. Prominent response criteria examples are RECIST 1.1[1] for solid tumors, Lugano[2] for lymphoma as well as RANO[3] for primary brain tumors, amongst many others.

In these criteria, response is evaluated using radiological imaging acquired as repeated sequential imaging studies, referred to as timepoints. The assessment of tumor burden change (disease-specific lesions and pathological abnormalities related to cancer) across these longitudinal imaging timepoints determine a patient’s response to therapy. A hallmark of standardized response criteria are the provision of a common and transparent language to accompany clinical trials with image-based endpoints in communicating results of individual patients and across groups of patients as well as across comparative trials.



Limitations of Current Image-Based Response Evaluation Methods

Response criteria guidelines, such as RECIST 1.1, have been utilized and served their purpose across a litany of trials and thousands of patients in providing a standardized, reproducible means to evaluate anti-cancer treatment effects and allowing for comparison of these outcomes with historical trials and approved therapies. They come, however, with certain limitations that warrant consideration and necessitate the re-evaluation of how to objectively measure treatment efficacy. *(For further reading on the importance of RECIST and other response criteria as well as known limitations see Fojo et al.[7] and Sharma et al.[8])*

Standardized response criteria evaluations on imaging are based upon broad categorization and binning of response (e.g., Stable Disease captures both regression and increase in disease burden) which do not always account well for 'mixed response' or tumor heterogeneity. These categorical assessments are then converted to binary categories such as **Responders** (Complete Response (CR) and Partial Response (PR)) and **Non-responders** (Stable Disease (SD) and (Progressive Disease (PD)) or **Clinical Benefit** (CR + PR + SD vs PD) in endpoint trial cohort analysis. More recent response criteria have narrowed the response categories further (e.g., Major Response - between a PR and CR; Minor Response between a PR and SD) which may provide further refinement in correlating drug effect to benefit.

Response criteria rely on a snapshot evaluation of tumor size at predefined timepoints during the course of treatment. That is, imaging-based endpoints measuring time, such as Time to Progression and Duration of Response, are constrained by the rule that the frequency of imaging must be the same across all patients in a trial including the treatment arms (comparator and treatment under study). If the intervals are not the same, bias in the treatment effect is introduced. *(Refer to Delgado et.al.[4] for a comprehensive summary overview of endpoints in oncology clinical trials with their relative benefits and drawbacks).*

Many response criteria utilize diameter-based measurements, but lesions are not always spherical, and diameters might fail to capture changes of lesion size adequately (see figure 1). Furthermore, diameter measurements do not provide information on density, viable tumor, necrosis, or textural information which can provide important correlating information for understanding efficacy in therapeutic evaluations.



Figure 1: Longest Diameter measurements might fail to capture volumetric changes of lesions during anti-cancer treatment:

While the measurement of the longest diameter shows a substantial increase of size in the non-spherical shaped lesion on the left for the last two Timepoints, volumetric measurements indicate a further decrease in Timepoint 3 with only a slight increase in the last Timepoint. Diameter and volumetric measurements correlate better in spherical lesions as depicted in the right tiles.

While change in tumor size on imaging does provide a measure of therapy-effect with anti-cancer agents, very often early phase evaluations are extensively based on a smaller patient population who in many cases may be highly pretreated with multiple lines of prior therapy and may have developed treatment resistance. Early efficacy signals of warding off progression in early phase trials may be demonstrated with Stable Disease as a primary indication of success on balance with a smaller subset of short-term Partial Responders, and in exceptional cases, Complete Response. Sub-group analysis may be possible and reveal some further information on differences in responders vs. progressors such as with regard to mutation status. However, in the absence of an enhanced means to measure what these differences indicate for predicting later phase trial outcomes, findings may be limited. A decision to proceed to later phase trials may thus be based on inadequate information that is not entirely predictive of success in later stage study efficacy-focused endpoints that rely on more substantial and refined patient populations.

Clinical trial endpoints measuring Objective Response Rate (ORR) with evidence of a decrease in tumor burden and Progression Free Survival (PFS) with evidence of delay in disease progression, based on imaging-based evaluations, can be clinically meaningful to represent benefit to patients. A key aspect of response evaluation on imaging is that it is measuring just that – response and/or progression with the essential principle that the trajectory of cancer is to grow. In essence, the measurement of response and progression is providing evidence of therapy effect. As such, therapy effect is not a direct measure of extending survival or even quality of life in survival - it is a correlation through a surrogate method of how effectively cancer growth can be slowed or stopped. As example, a therapy that demonstrates a high ORR does not necessarily indicate that a therapy will have meaningful impact in extending survival. Rather, a high ORR may demonstrate that some cancer cells may be eliminated while others may be temporarily slowed in growth (e.g., treatment resistant fraction).

Yeh et al.[5] describes the crux of the current limitations in clinical trials with image-based endpoints by examining the background of the approval of Gemcitabine[6] as first-line therapy for standard of care for advanced pancreatic ductal adenocarcinoma in 1997 and the subsequent 20 years of research investigating how to further extend the median OS. That is, nearly 70 trials were conducted with over 16,000 patients in a span of 20 years to determine two treatment options with adding a second agent along with Gemcitabine to further improve median OS.

In a 2020 review of Clinical Trial Evidence Supporting US Food and Drug Administrative Approval of Novel Cancer Therapies Between 2000 and 2016[9], the authors report these novel therapies had considerable associated tumor response, but that median OS was extended by about two months. A 2023 report of The evidence base of US Food and Drug Administration approvals of novel cancer therapies from 2000 to 2020[10] details similar findings while indicating some further gain in median OS between 2016 to 2020 of 5.65 months with remarks of cautionary interpretation of this improvement. While there have been substantial novel cancer therapy approvals in the past two decades, surrogate endpoint measures have taken priority. OS benefits remain relatively slight.

Merino M, et al.[11] succinctly state the current dichotomy between efficacy endpoints measuring tumor-burden and the gold standard of OS in oncology drug approvals in the 2023 publication, Irreconcilable Differences: The Divorce Between Response Rates, Progression-Free Survival, and Overall Survival – *that ORR and PFS are not demonstrating evidence as surrogate endpoints for OS.*

A Refinement of Perspective



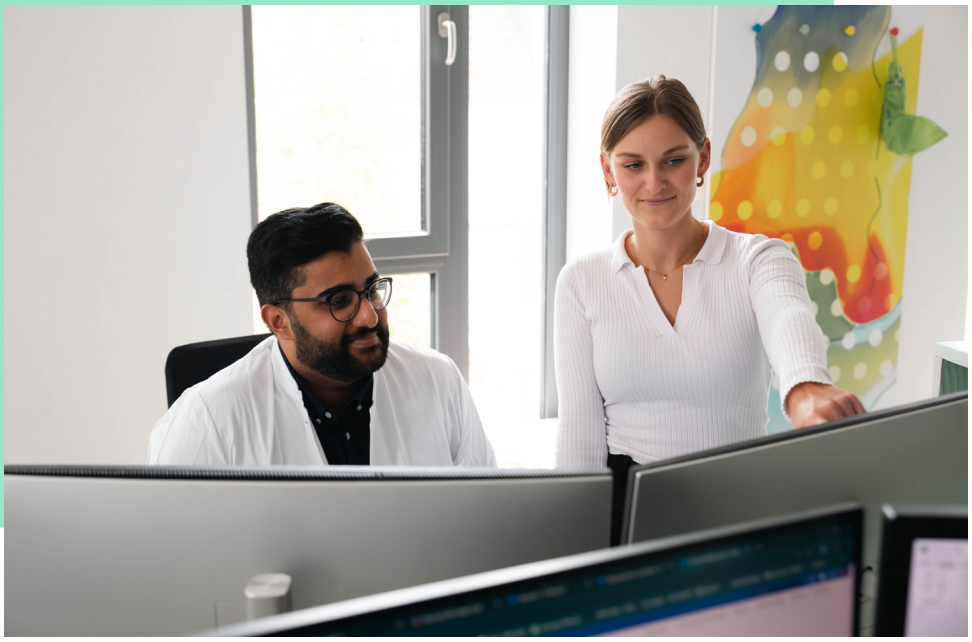
Quantitative measurement of drug-effect with medical imaging as a surrogate endpoint remains essential in evaluating treatment efficacy. The refinement to the perspective that may be needed is thinking differently - rather than only categorizing drug effect with response and progression cut-offs, measuring it in a way that leads to more insight on predicting the patient benefit with the same original time advantage gained with the introduction of medical imaging as a surrogate endpoint - *the ability to predict clinical benefit and improved OS in a shorter period of time.*

For someone facing a cancer diagnosis, recurrence, or treatment resistance, the priority need is evidence of which therapy, at which time, leads to survival as well as the ability to maintain a meaningful quality of life.

To address this need, we need to ask the following questions:

- Are the methods currently used to measure efficacy in anti-cancer treatment with measurement of tumor burden on medical imaging an optimal tool (e.g., Response criteria Guidelines, diameter-based measurements)?
- Are there impediments in the way we measure efficacy that are preventing innovative improvements in identifying and ensuring therapies are effective?
- Can earlier phase trials and smaller datasets be evaluated differently to provide better predictive means of efficacy prior to the conduct of larger, later phase studies (e.g., informing go/no go decisions earlier and with fewer patients)?
- As a therapy can bring exceptional benefit in a small percentage of patients but not all, are there improved ways to better predict which patients are likely to see benefit (e.g., there are exceptionally effective new drugs but the benefit is limited to a small fraction of the patient populations)?
- Can a different approach, providing more information, be done concurrently with the established standard of response criteria evaluations of longitudinal imaging (e.g., validating the approach while continuing to measure efficacy by the established means.)?
- If a different, “better” approach is taken, what certainty is there that it will not have similar limitations than those already employed in current efficacy evaluations?

Tumor Growth Rate Modeling Methodology



One alternative approach that follows a different way of thinking while utilizing the same standard of longitudinal evaluation of tumor burden on imaging may provide a refinement that enables earlier, more informative efficacy signals with smaller data sets – Tumor Growth Rate Modeling (TGRM).

The use of computational modeling[12, 13, 14, 15, 16, 17] to evaluate tumor quantity changes across timepoints is not an entirely new and different approach. However, these methodologies, while providing essential and valuable information, have not shown notable improvement over imaging-based endpoints with response criteria evaluations and have primarily focused on different single tumor growth models.

Stein et al.,[15, 18] however successfully demonstrated an approach with relatively simple computational modeling that can utilize measurement of tumor quantity on imaging with time as a variable. Wilkerson et al.[19] and Maitland et. al.[20] extended their approach by using a combination of four (4) tumor growth/decay models based on exponential functions, which is the referenced approach here.

While there is potential for this methodology to provide significant value in cancer therapeutic research, the use of this approach as a validated and accepted imaging biomarker in clinical trials is still required. That is, there remains extensive research and validation efforts to be done such that this methodology might supplement the established clinical trial endpoints currently employed with imaging.

The proposed Tumor Growth Rate Models utilize mathematical expressions to measure changes in tumor burden as measured on imaging evaluations during a given treatment providing two key values:

the rate of growth/regrowth **g** and the rate of regression/decay **d**

This approach is based on the concept that the tumor burden changes over the course of treatment are based on two independent processes that occur concurrently: Firstly, decay of tumor cells sensitive to treatment and secondly, growth of cancer cells that show treatment resistance. Depending on the fraction of the tumor cells (in)sensitive to treatment, one of three growth patterns can be observed in longitudinal imaging: Steady increase of tumor size, steady decrease of tumor size, or a decrease followed by an increase. For both decay and increase, an exponential growth pattern is assumed, leading to the four equations described in detail in the table below (there are two different equations for the decay-regrowth pattern).

As tumor growth patterns may vary across individual patients, and in particular with certain therapeutic mechanisms of action (e.g., immunotherapy induced pseudo-progression), not all patients in a clinical trial evaluation will have a fit. However, the models referenced here demonstrate a majority of patients with a fit using this approach, suggesting this framework is a feasible method in clinical trial cohorts to evaluate efficacy effect (e.g., approximately 10 % of subjects with adequate imaging evaluations and measurements had no fit[20]).

Importantly, time is a factor in these equations, and this removes the constraint of imaging intervals at fixed timepoints (e.g., the limitation of response evaluation where the time between evaluations must be the same across treatment arms) and thereby also provides precedence for use with real-world data.

References of Note on the TGRM Methodology

In their 2008 publication, Stein et al.[18] demonstrated a method to utilize tumor measurement data in clinical trials to predict survival with a biexponential model estimating the simultaneous rates of tumor growth (rate constant **g**) and regression (rate constant **d**). Modeling against serial levels of prostate-specific antigen (PSA), they demonstrated that survival was strongly correlated with the growth rate (**g**) whereas the rate of regression (**d**) did not predict survival. The growth rate constant **g**, as validated surrogate for survival with applicability in other tumor types, was postulated during drug development to evaluate therapy effectiveness in extending survival.

In 2017, Wilkerson[19] et al. used existing clinical data from patients with metastatic castration-resistant prostate cancer of eight randomized clinical trials and applied mathematical models in order to estimate rates of growth and regression of the tumor burden (PSA level) over time. With a trial simulation using the **g** value as primary endpoint to compare two different treatments, they found small sample sizes sufficient to achieve median **g** values statistically identical to the original data set. These findings indicate that growth rate modelling could help to reduce the number of patients that need to be enrolled in clinical trials.

In 2020, Maitland et al.[20] presented data of almost 1000 colorectal cancer patients from two phase III trials: All metastatic lesions in this cohort were measured on CT retrospectively, and in parallel, tumor regression (**d**) and growth (**g**) rates were estimated for each patient with uni-dimensional and volumetric measurements. This analysis established that a combination of volume measurement and TGRM data holds the potential to improve the evaluation of a treatment of colorectal cancer that would not have been obtained with uni-dimensional measurements.

Yeh et al.[5] in 2023 retrospectively applied a tumor growth model in over 3000 patients with stage III and IV pancreatic ductal adenocarcinoma to evaluate the rate of growth based on serial imaging measurements and CA-19-9 values. These data sets were obtained from patients enrolled in six Randomized Control trials, two single arm trials and two real world data sets. This rich data set demonstrated that **g** is inversely associated with Overall Survival and importantly, can distinguish between therapies within the same trial as well as across different trials. They also demonstrated that the differences in the growth rate of different metastatic lesion sites can be characterized by **g**. Examples of how **g** can be used to benchmark phase II and III clinical data with virtual control reference arms are provided as well as further pathways to expedite approval of new effective therapies.

Implementation of TGRM in mint Lesion

The equations

Generally, the behavior of a tumor can be described as an interplay of tumor growth and tumor decay. mint Lesion provides four possible fit models (mathematical expressions) that can be used alone or in combination: GD, GX, DX and GDϕ. (Of note, there are other mathematical models in tumor dynamics[21]). The estimates values g (rate of tumor growth) and d (rate of tumor decay) are determined based on curve fitting according to the four equations. Which equation fits the data best is determined based on further values which evaluate the goodness of the fit.

The timepoints

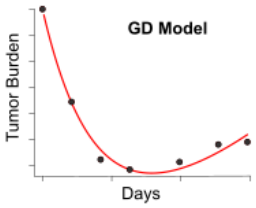
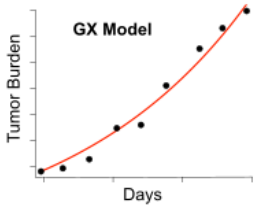
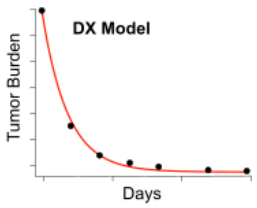
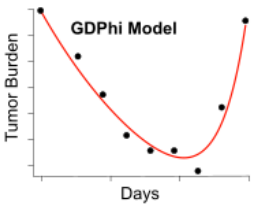
A given patient case may have a fit to a certain model determined at a point in time (e.g., based on the number of timepoints). It is suggested to use a minimum number of three (3) timepoints for each case - baseline plus two (2) follow-up timepoints. One fit model, GDϕ, is only applicable for four (4) total timepoints and, in addition to the **g** and **d** estimates, a third parameter, **ϕ**, the fraction of tumor showing regression, is calculated.

Radiological Evaluations

The same methodologies currently utilized in serial assessment of longitudinally acquired patient images can be applied to tumor growth rate models. That is, the quantitative measurement of tumor burden at baseline as performed with response evaluations such as RECIST 1.1 and measurement of the same baseline tumor burden at follow-up imaging. The model can be used with uni-dimensional, bi-dimensional, and volumetric measurements, with volumetrics providing some additional benefit with regard to sample size, for example.[20]

The dataset

In a clinical trial, a best fit is evaluated for each patient according to one of these four models. The best fit determines which **g** and **d** values (e.g., the estimates) are considered for that patient, and the median **g** and **d** values represent the patient cohort. Not all patients will have a fit according to these four models and therefore some patients will be excluded from the analysis. This may include data sets with fewer than the minimum number of timepoints (e.g., at least three (3) for most models), cases with lesions evaluated as Not Evaluable (NE), or tumor growth behavior which cannot be fitted by any of the four models (e.g., regression following a progression). While a Best Response and/or Timepoint of Progression can still be derived based on response criteria evaluations of the same dataset, modeling with **g/d** values is approached differently, and rules must be defined for either excluding lesions that become NE (excluding entirely from the data set) and basing on the remaining measured values, or excluding the patient as a non-fit. This approach also provides an opportunity to utilize historical control arms or pre-treatment **g/d** values as a comparator to on-study outcomes, and further substantiate treatment efficacy.

Fit Model	GD	GX	DX	GDϕ
Description	Biexponential growth and regression model. 	Exponential growth or re-growth where the tumor burden is only increasing. d in this model is removed. 	Exponential decay or regression where the tumor burden is only decreasing. g in this model is removed. 	Tumor growth and decay but with an additional value ϕ that estimates the fraction of tumor that undergoes cell death due to treatment. 
Equation	$f(t) = e^{gt} + e^{-dt} - 1$ $g > 0, d > 0$	$f(t) = e^{gt}$ $g > 0$	$f(t) = e^{-dt}$ $d > 0$	$f(t) = (1 - \phi)e^{gt} + \phi e^{-dt}$ $g > 0, d > 0, \phi > 0$
Values reported	g and d	g only (d = 0)	d only (g = 0)	g, d, and ϕ
Minimum Imaging Evaluation requirements	Three (3) Evaluations (e.g., baseline plus two (2) follow-ups)	Three (3) [a] Evaluations (e.g., baseline plus two (2) follow-ups)	Three (3) Evaluations (e.g., baseline plus two (2) follow-ups)	Four (4) Evaluations (e.g., baseline plus three (3) follow-ups)
Where	f(t) – Tumor quantity at time t in days relative to initial tumor quantity t – time in days after treatment start d – rate of tumor regression (decay) g – rate of tumor growth (or regrowth) ϕ – fraction of tumor showing regression (only for GDϕ model)			

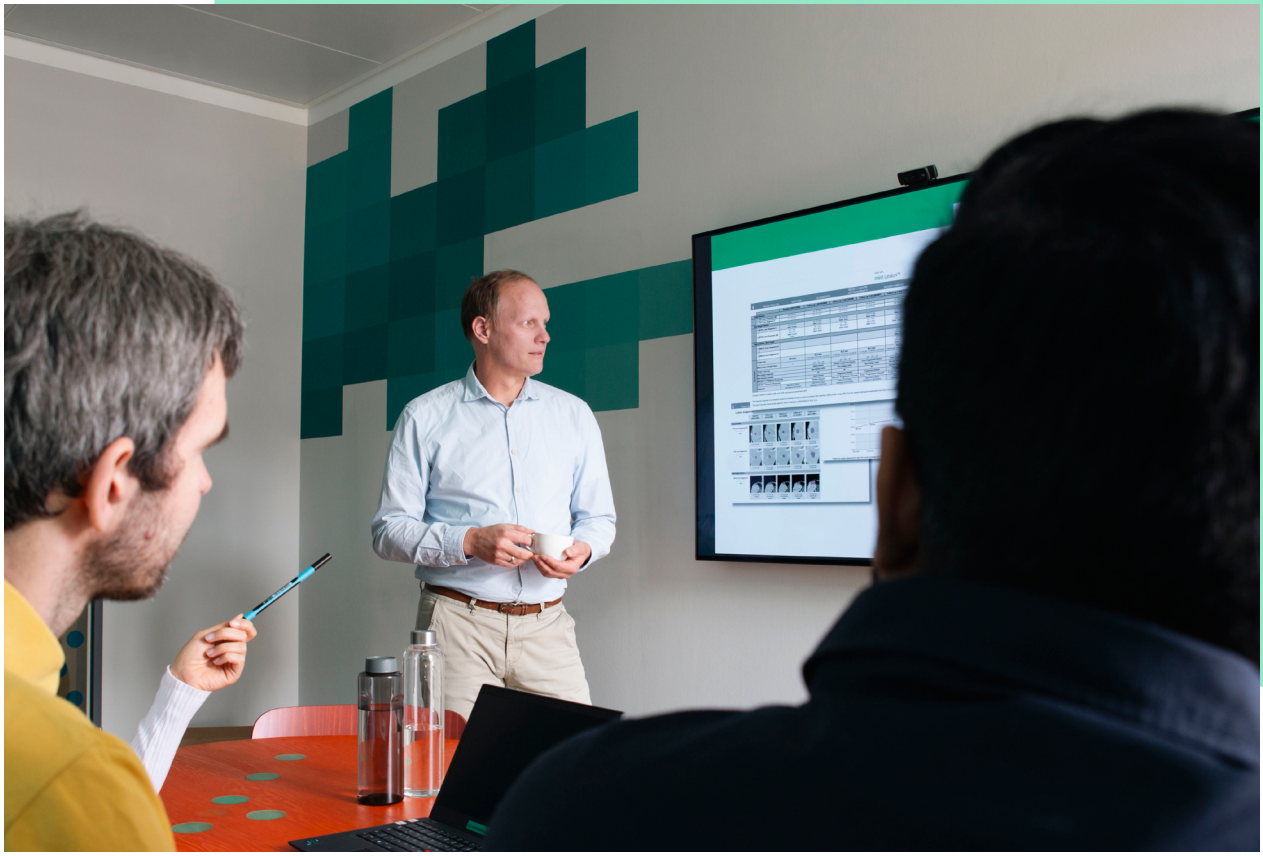
[a]Baseline plus one follow-up timepoint may be considered for inclusion in certain evaluations where the first follow-up is also consistent with progression by established response criteria. However, generally patients with less than three evaluable timepoints are excluded from TGRM.

Further remarks on fit model selection:

- In reference publications[19, 20] with TGRM, a p-value threshold is pre-defined to determine if a fit is considered as good enough for further consideration. *(For the fitting parameters, the p-value gives the probability of how good the value of the fitted parameter is compared to a null hypothesis. Convention is that p-values below 0.1 or 0.05 indicate a good fit.)*
- The dataset is evaluated and considered as relevant if all estimates of **g**, **d** and **ϕ** have a p-value < 0.1 (or the defined p-value threshold).
- More than one fit model may be selected based on the p-values. In such cases, the fit model with the lowest Akaike Information Criterion (AIC) value is considered as the best fitted model. AIC estimates the quality of each model, relative to each of the other models. *(AIC is used to compare the goodness of the fit between different models - the fit model with lower AIC is considered to fit better.)*
  - A dataset will have “No Fit” when no model predicts tumor burden, so no model shows a fit good enough implying that the p-values of the estimates fulfill the p-value threshold.
  - When the sample size is small, there is the probability that the AIC will tend to select models with many parameters (e.g., preference for GDϕ). Corrected AIC (AICc) can be used as a correction for a small sample size (as the number of imaging evaluations (timepoints in this case) goes towards infinity, AICc converges to AIC.)
- ***See also:*** tumgr - Tumor Growth Rate Analysis[22]

Potential Benefits of using this TGRM Methodology

One significant advantage of the TGRM methodology is that time is a variable. This characteristic addresses a current challenge in clinical trial study design, namely the constraint of fixed imaging intervals. By allowing flexibility to utilize diameter or volumetric measurements, TGRM enables comparison to historical trial data in which volumetric measurements may not have been available. Importantly, TGRM can be conducted concurrently with the conventional response criteria evaluations as utilized in the current clinical trial methodology while this approach is further validated.



Other potential benefits include:

- Providing a refinement to response assessment with a cost effective, surrogate endpoint that takes a different approach and with the potential for smaller patient sample sizes and earlier detection of efficacy that correlates with OS and PFS.
- Informing decision making on all phases of oncology drug development with particular opportunity in early phase for efficacy signals for go/no go decisions
- Informing dose-optimization based on refined information related to the rate of growth and regression over time.
- Evaluating tumor growth rate for pre-treatment imaging compared to therapeutic intervention, which may provide additional efficacy signals.
- Single-arm trial-benchmarking with historical control arms in clinical trials exploring a new therapy.

Mint Medical Provision of this TGRM Methodology in mint Lesion



Mint Medical's software mint Lesion is the leading medical imaging evaluation in oncology software used in clinical trial evaluations today. Trusted worldwide by the leading healthcare institutions, contract research organizations (CROs), and pharmaceutical/biotech companies, mint Lesion brings the highest quality radiology evaluations for clinical research. With the tenet that no data should be left behind on the image, Mint Medical facilitates research investigations in using this novel TGRM methodology to support continued innovation in the face of tradition in bringing new efficacious therapies to patients in need faster.

Accessible TGRM Data extracted from any image evaluation

The implementation of this TGRM methodology in mint Lesion enables the reporting of clinical trial response assessments **concurrently** with a highly configurable data export for estimates of growth rates, **g** and decay rates, **d**.

- TGRM can be implemented **with** or **without** response assessment, and data can be extracted concurrently. Furthermore, previously conducted trials in mint Lesion can export TGRM at a subsequent time even after the trial has concluded.
- On-going validation of this methodology is facilitated as TGRM is an export of data and does not interfere with the endpoint analysis of the on-going clinical trial.
- Response assessment evaluations can be conducted with any measurement parameter such as diameter-based evaluations or volumetrics. Volumetric lesion evaluation will derive the correct diameter-based Sum of Diameters, for Target, Non-Target, and New Lesion compartment responses as well as Overall Response according to published guidelines for all published read template response criteria in mint Lesion.
- The export can be configured in many ways, e.g., to include:
  - Only Target Lesions **or** including Non-Target and New Lesions (if measured)
  - Only specified lesion locations (e.g., lung lesions, or liver and lymph nodes only)
  - Using a Long-axis diameter for all lesions **or** using Long-axis for non-nodal and short axis for nodal sites (for diameter-based evaluations using TGRM).
  - Only patient cases with three (3) or more timepoints (or another defined minimum)
  - Only certain fit models such as:
    - Including GD, GX, DX and excluding GDϕ
    - Including GD, GX, DX and GDϕ
- Further export configurations, such as definition of p-value threshold, choice of AIC or AICc as well as other variable configurations (such as Too Small to Measure values and handling of NE lesions), can be defined.
- Multiple exports can be generated for primary analysis evaluation as well as additional sub-analysis with variable inclusion/exclusion parameter configurations applied.

Standardized Response Criteria Read Templates

With over 25 read templates based on published guidelines, mint Lesion can be utilized across oncology therapeutic programs. Although response criteria templates are standardized according to the related publication guideline, they are modifiable with mint Lesion to support modified criteria based on therapy mechanism of action, indication, or protocol design.

Response criteria available in mint Lesion

Solid Tumors	Immunotherapy	Neuro-Oncology	Lymphoma and CLL
RECIST 1.1	iRECIST	RANO HGG	Lugano
PERCIST	irRECIST	RANO LGG	Cheson
WHO	imRECIST	RANO-BM	LYRIC
Choi	irRC	RAPNO-pLGG	iwCLL
mRECIST HCC		RAPNO-pHGG	RECIL
PCWG3		RAPNO-pDIPG	
mRECIST-Mesothelioma			

Data liquidity – All Data in All Formats

Data Liquidity is vital in the context of clinical trials and ensures the continuous forward momentum of therapeutic discovery and development, research, and delivery of new effective treatments to patients. mint Lesion assures the uniformity of data by generating reliable, high-quality data – reported in a consistent, compliant, and structured format. mint Lesion data is **Connected, Mobile, Comprehensive, and Minable** - enabling real-time data analytics, in-depth investigation, AI, and Machine learning.

Subjects/Patient Level Exports	Images/Measurement Annotations	Trial and Cohort Level Exports	Presentation Formats
• PDF Report • Case XML • Case CSV • Textblocks	• NRRD / NIFTI • DICOM-SC • DICOM-RTSTRUCT • DICOM-SEGSURFACE • DICOM-SEG	• Trial XML • Trial CSV (including CDISC) • Radiomic Feature Export • g/d Tumor Growth Rate Export	• Image Snapshots • Lesion Overview Charts • Graphs • Textblocks

mint to mint Data Exchange

As Mint Medical strives to support the goal of data interoperability and data liquidity in healthcare, mint Lesion data can be directly exchanged between mint Lesion instances. Imaging evaluations in a clinical trial conducted in one mint Lesion instance can be exported and imported into another mint Lesion instance.

The comprehensive **Export Clone** includes the evaluated data, annotated images, and trial specific criteria enabling imaging CROs, for example, to directly export completed trials with all images and annotations de-identified of personnel/reader assignees directly to the Sponsor for import into another mint Lesion Instance. The imported trial data can be further modeled and interrogated.

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