

IMAGE INFORMATICS APPROACHES TO ADVANCE CANCER DRUG DISCOVERY

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DECLARATION

This thesis presents my own work, and has not been submitted for any other degree or professional qualification. Wherever results were obtained in collaboration with others, I have clearly stated it in the text. Any information derived from the published work of others has been cited in the text, and a complete list of references can be found in the bibliography. Published papers arising from the work described in this thesis can be found in the appendices.

– Scott Warchal, 2018

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ABSTRACT

High content image-based screening assays utilise cell based models to extract and quantify morphological phenotypes induced by small molecules. The rich datasets produced can be used to identify lead compounds in drug discovery efforts, infer compound mechanism of action, or aid biological understanding with the use of tool compounds. Here I present my work developing and applying high-content image based screens of small molecules across a panel of eight genetically and morphologically distinct breast cancer cell lines.

I implemented machine learning models to predict compound mechanism of action from morphological data and assessed how well these models transfer to unseen cell lines, comparing the use of numeric morphological features extracted using computer vision techniques against more modern convolutional neural networks acting on raw image data.

The application of cell line panels have been widely used in pharmacogenomics in order to compare the sensitivity between genetically distinct cell lines to drug treatments and identify molecular biomarkers that predict response. I applied dimensional reduction techniques and distance metrics to develop a measure of differential morphological response between cell lines to small molecule treatment, which controls for the inherent morphological differences between untreated cell lines.

These methods were then applied to a screen of 13,000 lead-like small molecules across the eight cell lines to identify compounds which produced distinct phenotypic responses between cell lines. Putative hits were then validated in a three-dimensional tumour spheroid assay to determine the functional effect of these compounds in more complex models, as well as proteomics to determine the responsible pathways.

Using data generated from the compound screen, I carried out work towards integrating knowledge of chemical structures with morphological data to infer mechanistic information of the unannotated compounds, and assess structure activity relationships from cell-based imaging data.

LAY SUMMARY

Drugs act by altering the behaviour of cells, usually by disrupting the internal cellular machinery necessary for normal function, or in the case of diseases, by trying to reverse dysfunctional cellular processes responsible for disease initiation and progression back towards a normal state. Subtle changes in cellular functions can be detected visually through microscopy and fluorescent labels which bind to subcellular components such as DNA. Using automated image analysis methods it is possible to analyse these microscope images of cells and create a detailed description of each individual cell, represented as a series of measurements describing various attributes such as the cell's size, location and concentration of various biomolecules, this can be thought of as the cell's "fingerprint". Using these cellular fingerprints it is possible to test drugs in an effort to find those that convert a disease-like fingerprint into a healthy looking one, or to compare the fingerprints produced by unknown drugs to ones produced by molecules whose function is already known.

My work focuses on how to generate and exploit compound fingerprints across a number of different cells which represent different types of breast cancer. A significant challenge in studying distinct cancer cell types is that each cell has its own unique fingerprint regardless of drug treatment, which makes comparisons between cells more difficult. In addition, I investigate how more advanced computational tools alongside this varied dataset can aid predicting how novel compounds work.

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LIST OF ACRONYMS

2D Two-dimensional

3D Three-dimensional

ABL Abelson murine leukemia viral oncogene homologue

BCR Breakpoint Cluster Region

ANN Artificial Neural Network

BSA Bovine Serum Albumin

CCLE Cancer Cell Line Encyclopedia

CCM Cerebral Cavernous Malformation

CNN Convolutional Neural Network

DMEM Dulbecco's Modified Eagle Medium

DMSO Dimethyl sulfoxide

EMA European Medicines Agency

FDA U.S Food and Drug Administration

GDSC Genomics of Drug Sensitivity in Cancer

GPU Graphics processing Unit

HCS High Content Screening

HTS High Throughput Screening

MCL Markov Clustering Algorithm

MoA Mechanism of Action

MOI Multiplicity Of Infection

mRMR Minimum-Redundancy-Maximum-Relevancy

PBS Phosphate Buffered Saline

PCA Principal Component Analysis

PDD Phenotypic Drug Discovery

QED Quantitative Estimate of Drug-likeness

RGB Red Green Blue

SAR Structure Activity Relationship

STS Staurosporine

TCCS Theta Comparative Cell Scoring

1 | INTRODUCTION

1.1 Eroom's Law: The increasing cost of drug discovery

Throughout the last 70 years the cost of developing a new drug has steadily increased, a study by Scannel *et al.* noted the cost has approximately doubled every 9 years,¹ this observation has been dubbed “Eroom’s law” in a homage to Moore’s law.ⁱ The cost of bringing a new drug to market is now approaching £1 billion, taking 10 years from initial concept through to regulatory approval, the reasons behind this ever-increasing cost are still under debate although it is clear the issue is multi-faceted. One explanation may be that the low-hanging fruits of drug discovery have already been taken; for example the most effective traditional remedies have been studied and their active ingredients commercialised, natural products screened to identify the most potent bioactive molecules, many single gene disorders and eminently druggable oncogene-driven homogeneous tumours have been cured, leaving us to tackle the more complex diseases and pharmacological targets. This pessimism has led to the ever present idea that drug discovery is undergoing a productivity crisis,² and that the investments made in early stage research do not translate into actionable pharmacology which can be used to develop effective therapies for patients, and has led to a renewed interest in alternative drug discovery paradigms.

1.2 The drug discovery process

1.2.1 Target-based screening

Over the past 30 years the majority of drug discovery programmes have seized upon technological advances in robotics and automation to screen ever expansive compound libraries against pre-defined protein targets. It would be difficult to argue that this target-based high-throughput screening (HTS) approach has not been fruitful, yielding many successful therapeutics across a range of disease areas, largely attributed to an increased understanding of the genomic basis of many diseases. However, despite numerous clinical and commercial success stories, HTS is not a panacea, with a high attrition rate of lead compounds once they enter clinical trials.³ A large majority of these clinical trial failures are not due to toxicity, but rather a lack of efficacy which can often be traced back to limited validation of the hypothesised target in the face of complex disease aetiology.⁴

ⁱThe well-known observation that the number of transistors in microprocessors approximately doubles every 2 years.

1.2.2 Phenotypic screening

Phenotypic screening differs from target-based screening in that it does not rely on prior knowledge of a specific target, but instead interrogates a biologically relevant assay to identify compounds which alter the phenotype in a biologically desirable way. This target-agnostic approach can prove useful in diseases with poorly understood mechanisms or those with no obvious druggable protein targets. Phenotypic screening is not a new approach in small molecule drug discovery, it was the primary method for many decades before the genomics revolution made target hypothesis more tractable.⁵

Many concerns related to phenotypic screening are centred on the lack of mechanistic information for a given lead compound. Whilst the lack of a known target presents challenges and may cause concerns within a commercial drug discovery programme, regulatory bodies such as the Food and Drug Adminstration validation of the hypothesised target Agency (EMA) do not require a known target for drug approval, only that the drug is safe and efficacious. Metformin is a first-line therapy for type 2 diabetes and is on the World Health Organisation's list of essential medicines, it decreases liver glucose production and has an insulin sensitising effect on many tissues. Despite approval since 1957 and widespread clinical use, the molecular mechanism of metformin remained unknown for 43 years.⁶ Although knowledge of the molecular target is not necessary to get a drug into the clinic, target deconvolution is still an important part of most phenotypic drug discovery programmes, without knowing the protein or proteins a compound is binding to lead optimisation via structure activity relationship (SAR) studies becomes extremely difficult. In addition, knowledge of the molecular target of a lead compound generated by a phenotypic screen can be used as a basis for instigating a conventional high-throughput hypothesis-driven screen on a novel target, this is why many view phenotypic screening as a complimentary method to target based screening rather than a competing approach or proposed replacement.⁷

1.3 High content imaging

High content imaging is a technique utilising high-throughput microscopes and automated image analysis, commonly used in phenotypic screening as a method for gathering multivariate datasets from images of biological specimens and has proven useful in a wide variety of phenotypic assays, ranging from 2D mammalian cells,^{8,9} *in vivo* studies in zebrafish¹⁰ and even plants and crops.¹¹

High content screens – screening studies carried out with high content imaging – are particularly useful in phenotypic drug discovery for several reasons. High content imaging provides spatial resolution enabling the use of more complex assays including co-culture and 3D models, which might better represent the biological complexity of disease relative to 2D reductionist models. However, these complex assays often have phenotypes which are more difficult to quantify, which a single univariate readout may fail to accurately recapitulate, therefore the multivariate datasets produced by high content screening enables a more in-depth view into the endpoints which should be measured in a complex assay. A second benefit is the multivariate data generated by high content screening offers a more unbiased method for detecting hits in a phenotypic assay, as predicting which variable to measure beforehand may lead to missed biologically interesting phenotypes. With the advent

of more complex datasets generated from high-content imaging, the process of image-analysis and computational methods for data processing has given rise to the term “high-content analysis”.

1.3.1 Image analysis

Image analysis is the process in which raw image data from a high-content screen is transformed into measurements which can be used to describe the observed morphology of the biological specimen exposed to a perturbagen. Here I will focus on cell-based assays for small-molecule screening, though the same methods apply for most other assays (spheroids/organoids etc) and perturbagens (siRNA, CRISPR etc).

The standard approach to extracting numerical features from cell morphologies is through segmenting cells and sub-cellular structures into “objects”, and then computing image-based measurements on those objects. Typically each cell within an image is identified by first segmenting nuclei from the background. A number of well-established image thresholding algorithms can be used for segmenting nuclei from background, most automatically calculate an intensity threshold to binarise an image based on histograms of pixel intensities.^{12,13} The segmented nuclei can then be used as seeds to detect cell boundaries, either through edge detection in a channel containing a cytoplasmic marker, or more crudely by expanding a number of pixels from the nuclei centre to approximate cell size. There are also less commonly used methods which utilise machine learning based on trained parameters to segment cells,¹⁴ or forgo segmentation entirely to measure morphological features from the raw images.^{15,16}

After cells and sub-subcellular objects have been segmented morphological characteristics are measured for each object, these measurements can cover a wide variety of morphologies depending on the aims of the assay, although can be grouped into 4 main classes:

Shape. Calculated on the properties of the object masks, e.g. area, perimeter, eccentricity. Shape features are commonly used as they are interpretable, robust, and quick to calculate.

Intensity. These features are based on the pixel intensity values within the object boundaries. They can be calculated for multiple channels and include measurements such as average intensity, integrated intensity, and radial distribution of intensity values. Great care has to be taken when using intensity values as they are susceptible to batch effects and microscope artefacts such as vignetting.¹⁷

Texture. Measures of patterns of intensities within objects, typically derived from grey level co-occurrence matrices.¹⁸ This can be used to quantify morphologies such as small speckles or stripes within an image. Texture measurements are often computationally expensive and difficult to interpret although can be useful for measuring subtle morphological changes.

Spatial context. These are typically relationships between objects, such as the number of neighbouring cells or nuclei, percentage of a cell boundary in contact with neighbouring cells. This class can also include the simple measure of cell or nuclei count within a field of view.

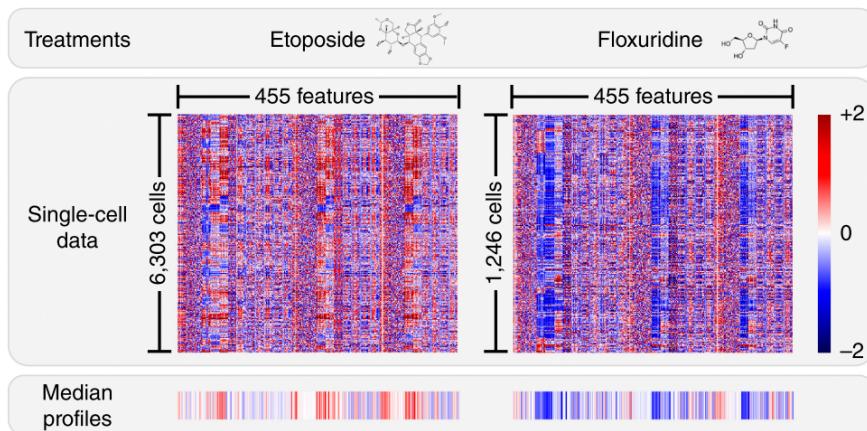


Figure 1.1: Single cell data aggregation to a median profile. Two matrices representing single cell morphology data for a treatment, with columns displaying multiple measured morphological features for each cell represented as a row. (*Figure re-used from Caicedo et al. Nat Methods, 2017*)

1.3.2 Data analysis

Measuring morphological features produces an $m \times n$ dataset per object class, where m is the number of objects and n is the number of morphological features measure for that object. Commonly single object level data is aggregated to population level, where the population can be a field of view, microtitre-well, or treatment level (see figure 1.1); with the most popular aggregation method being a simple median average.¹⁹ Once the object-level data has been aggregated to a common population level such as per well data, the features from each object class can be combined into a dataset represented by a single $p \times q$ matrix, where p is the number of wells (or other level of aggregation), and q is the total number of combined features from all object classes. It is then useful to view each row of this matrix as a feature vector, or morphological profile which summarises the morphology induced by a treatment.

There are a number of fairly standard data pre-processing steps involved in high content analysis, consisting of: quality-control checks and outlier removal, batch correction, normalisation, standardising feature values, and dimensional reduction or feature selection.¹⁹

Quality control. Errors are usually introduced at the imaging or segmentation phase of high-content assays, either through poor image quality caused by out-of-focus wells or debris, or poorly chosen segmentation parameters causing artefacts with otherwise acceptable images and subsequent outlier morphological features. As assays often generate thousands if not millions of images, it is not practical to manually check each image and segmentation mask for quality, therefore a number of automated methods have been developed to flag potential image artefacts and extreme feature values.

Image artefacts can be detected through measures of image intensity, as out-of-focus images tend to have shallow intensity gradients across the image and lose high-frequency intensity changes,²⁰ whereas images containing debris such as dust and fibres contain a large percentage of saturated

pixels. Segmentation errors usually create extreme values for most feature measurements which can be highlighted using typical outlier detection methods such as Hampel filtering²¹ and local outlier factor.²²

Batch correction. Batch effects are accumulations of multiple sources of technical variation such as equipment, liquid-handling error, reagents and environmental conditions which can influence measurements and mislead researchers, and are particularly prevalent in high-throughput experiments. They are normally identified by visually through boxplots of features, with plates or weeks on the x-axis, or through comparing correlations, within plates, between plates of the same batch and across batches. If batch effects are apparent they can be corrected, the simplest method is to standardise each batch separately, other methods include 2-way ANOVA²³ or canonical correlation analysis.²⁴

Standardisation. When many morphological features are measured from an image, they are unlikely to share the same scale/units or have similar variance – e.g. cell-area measured in pixels which may range from zero to several thousand and cell-eccentricity which is constrained between zero and one. It is therefore useful to standardise all feature values to be mean centred and have comparable variance. This aids in many downstream data analysis methods which assume standardised feature values.

Dimensional reduction and feature selection. As with any high-dimensional data a large number of features can cause issues with analysis and interpretation, this is commonly known as the “curse of dimensionality”.²⁵ Another issue is that many of the measured features may not contribute information, either as they have little or no variation between samples, or are redundant due to high correlation with existing features. Dimensional reduction and feature selection methods are both commonly used in other biological fields such as genomics and proteomics, and are now routinely used in high-content imaging analysis. A widely used technique is principal component analysis (PCA), which is an unsupervised approach to maximise variation through a linear combination of orthogonal features. PCA can be used to reduce the number of features by selecting a subset of principal components which explain a specified proportion of variance in the data. Loss of interpretability can be an issue when using PCA, and is why some researchers favour feature selection methods which aim to retain original feature labels whilst still reducing dimensionality by removing uninformative features. Many of the feature selection methods are supervised, which may not fit in with unbiased analyses, although Peng *et al.* developed an unsupervised minimum-redundancy-maximum-relevancy (mRMR) feature selection method which has found use in high-content analyses.²⁶

Following data pre-processing, downstream analysis is typically focused on one of two tasks: identifying hit compounds in a screen, or comparing the similarity of morphology profiles created by treatments – both of which use distance as a metric, either comparing hits against a negative control, or treatments against one another respectively.

1.3.3 Image based screening

Phenotypic and image-based screens can be used in traditional drug discovery roles whereby a compound library is screened in a biologically relevant cell-based assay in order to identify compounds which produce a favourable phenotype and hits or lead compounds identified from a high throughput biochemical assay are evaluated in a more complex image-based cell assay to determine their quality. These assays typically rely on either a positive control compound which is known to elicit the phenotype of interest in order to optimise and validate the assay has appropriate signal-to-noise attributes for testing multiple compounds. Or alternatively, a carefully designed assay in which a disease model utilising abnormal patient-derived or genetically engineered cells is used to identify compounds which revert the disease associated phenotype towards a healthy or wild-type phenotype. An example of this is demonstrated by Gibson *et al.*,²⁷ whereby they modelled cerebral cavernous malformation (CCM) using siRNA knockdown of the *CCM2* gene in human primary cells, and screened small molecules to identify candidates which rescued the siRNA induced phenotype using fluorescent markers of the nucleus, actin filaments, and VE-cadherin cell-cell junctions. Candidate compounds were then validated in an *in vivo* mouse model, which lead to the ongoing pre-clinical development of 4-Hydroxy-TEMPO as a novel therapeutic for CCM. This is an elegant demonstration that combining good disease models with target agnostic phenotypic screens can effectively yield promising therapeutic candidates without complex bioinformatics techniques.

1.3.4 Image based profiling

In contrast to screening studies which are mainly interested in looking for a defined phenotype, profiling is used to create phenotypic “fingerprints” of perturbagens analogous to transcriptional profiles, which can be used for clustering, inference and prediction. One of the main uses of phenotypic profiling is to compare the similarity of morphological profiles allowing clustering and machine learning methods to build rules in order to classify new or blinded treatments according to similar annotated neighbouring treatments.

One of the landmark papers of high-content profiling was published in 2004 when Perlman *et al.*²⁸ first demonstrated that morphological profiles between drugs could be clustered according to compound mechanism-of-action using a custom similarity metric and hierarchical clustering. Most studies utilising morphological profiling use unsupervised hierarchical clustering in order to group treatments into bins which produce similar cellular phenotypes,^{29,30} although other clustering algorithms such as graph-based Markov clustering algorithm (MCL),^{31,32} and spanning trees³³ are sometimes used.

1.4 Phenotypic screening in cancer drug discovery

Cancer drug discovery programmes of past decades seized upon uncontrolled proliferation as a clinically relevant phenotype to use in screening studies, giving rise to a number of anti-proliferative and cytotoxic compounds, which are still used in the clinic but often renowned for their severe side-effects. Many modern day oncology drug discovery programmes still retain anti-proliferation

as a key predictor for pre-clinical success, although increased understanding of cancer's molecular underpinnings has driven many oncology programmes towards a more target-directed approach. The prototypical success story of target-driven drug discovery in oncology is imatinib, a tyrosine kinase inhibitor targeting the BCR-ABL fusion protein in chronic myeloid leukemia. However, despite imatinib's exceptional success, unfortunately in most cases targeting a single driver in a complex signalling network results in compensatory signalling, activation of redundant pathways and unpredicted feedback mechanisms, all of which diminish efficacy *in vivo*.

In a review of 48 small molecule drugs approved for use in oncology between 1999 and 2013, 31/48 were discovered through target based screens, whereas 17/48 were based on leads from target-agnostic phenotypic screens,⁷ of those compounds discovered through target directed screening programmes the vast majority (75%) were kinase inhibitors. However, phenotypically derived compounds did not live up to the hypothesis that target-agnostic screening should be more likely to identify compounds with novel MoAs,³⁴ with only 5/17 being first in class molecules. An explanation for this sparsity of novel mechanisms is that phenotypic assays which use cytotoxicity readouts are likely to find low-hanging fruit such as targeting microtubule stabilisation and DNA replication dynamics.⁷ One option to combat this narrow attention on a select few targets – caused by either hypothesis-driven or simplistic phenotypic screens – is to utilise the more detailed mechanistic information offered by high-content imaging to explore novel biological mechanism and this broader areas of therapeutic target space rather than relying on cellular death as catch-all phenotypic readout.

In addition to high-content imaging screens with cells grown in 2D monolayers, more complex phenotypic models such as 3D tumour spheroids are being increasingly adopted in pre-clinical oncology. 3D tumour spheroids are multi-cellular aggregates thought to better recapitulate environment and biology of real tumours compared to cells grown in 2D monolayers on tissue culture plastic. There is mounting evidence that spheroids offer a more predictive model of *in vivo* compound efficacy than their 2D counterparts,^{35,36,37} this is thought to be caused by the hypoxic environment in the centre of the spheroid, increased cell-cell contact and greater presence of extracellular matrix components which better represents conditions found *in vivo*. Three-dimensional spheroid models lend themselves well to phenotypic and image-based screening projects, with compound efficacy determined through use of fluorescent markers of cell-viability,³⁷ cell-cycle dynamics,³⁸ or by analysis of spheroid morphology which can also incorporate 3D volumetric measurements.³⁹

1.4.1 Cancer cell line panels

Panels of multiple cancer cell lines such as the NCI-60, Cancer Cell Line Encyclopedia (CCLE)⁴⁰ and Genomics of Drug Sensitivity in Cancer (GDSC)⁴¹ have been widely used to facilitate high-throughput screening and increase certainty in hit selection / disease-specificity,^{42,43} and as a research tool to study pharmacogenomics.^{44,45,46} The use of cancer cell line panels can also benefit phenotypic screens by mirroring the heterogeneity found in patient populations, as well as heterogeneous cell populations found in tumours.⁴⁷ Throughout this body of work I have used a panel of eight breast cancer cell lines (table 1.1), these cell lines were chosen based on a number of criteria:

Cell line	Molecular subclass	Mutational status	
		PTEN	PI3K
MCF7	ER	WT	E545K
T47D	ER	WT	H1047R
MDA-MB-231	TN	WT	WT
MDA-MB-157	TN	WT	WT
HCC1569	HER2	WT	WT
SKBR3	HER2	WT	WT
HCC1954	HER2	*	H1047R
KPL4	HER2	*	H1047R

Table 1.1: Panel of breast cancer cell lines chosen for study. PI3K:Phosphoinositide-3-kinase, PTEN:Phosphatase and tensin homolog, ER:Estrogen receptor, TN:triple-negative, HER2:human epidermal growth factor, WT:wild-type, *:lack of consensus regarding the mutational status.

1. Relatively fast growth to allow compound screening to be performed in weekly batches.
2. Adherent to tissue culture plastic to enable 2D imaging.
3. Form a monolayer when grown in 2D – overlapping cells cause difficulties for most image segmentation methods.
4. Amenable for morphometric imaging – larger and/or flatter cells allow for better discrimination of sub-cellular features.
5. Distinct morphologies to evaluate the robustness of morphological profiling methods.
6. A collection which represents a range of molecular sub-classes of breast cancer.

1.4.2 Breast cancer

The cell lines used in this work are all immortalised human cancer cell lines originating from breast cancer patients. Breast cancer cell lines were chosen as the disease has been the focus of many years of research resulting in many well characterised cell lines with freely available genomic, proteomic and imaging datasets. Breast cancer is sub-divided into several subclasses defined by the molecular components which drive disease progression. The three main drivers of breast cancer are oestrogen receptor (ER), progesterone receptor (PR), and human epidermal growth factor receptor 2 (HER2). Aberrant signalling in one of more of these pathways is responsible for approximately 80-85% cases of breast cancer. The remaining 15-20% of cases are classified as triple negative (TN). Molecular subclasses are used clinically to stratify patients based on immunohistochemically stained tumour sections examined by pathologists to inform therapeutic and surgical options. In addition to these simple subtypes, there are alternative and more complex methods of stratifying patients based histopathological phenotype, response to endocrine and (neo)adjuvant therapy, and copy number alterations.⁴⁸

1.5 Thesis structure

The following chapters focus on selected topics from my PhD, some of which has been published (see appendix). Chapter 2 contains general methods which are used throughout and apply to multiple chapters. Chapter 3 is an analysis of machine learning methods to classify compound MoA from high content imaging data, with a focus on how well classifiers transfer across to new data from morphologically distinct cell lines. Chapter 4 describes the development and application of a novel analytical method to detect and quantify differential phenotypic responses between morphologically distinct cell lines when treated with small molecules. Chapter 5 describes a high content screen of 13,000 small molecules in order to identify compounds which produced distinct phenotypic responses between cell lines, functional assays to validate hits and proteomics to investigate potential pathways responsible. Chapter 6 describes work towards developing methods which combine cheminformatics of compound chemical structure with high content morphological data in order to infer MoA of unannotated compounds, as well as assess the correlation of chemical similarity and phenotypic similarity. Chapter 7 presents general conclusions from the my PhD and future directions.

2 | GENERAL METHODS

These methods are used throughout the work in this thesis and are listed here to reduce repetition. Each subsequent chapter will have a separate methods section which refers to methods unique to that particular chapter, or how they differ from the general methods described here.

2.1 Cell culture

The cell-lines were all grown in DMEM (# CATNO MANUFACTURER) and supplemented with 10% foetal bovine serum and 2 mM L-glutamine, incubated at 37°C, humidified and 5% CO₂.

2.2 Generation of GFP labelled cell lines

Stable GFP expressing cell lines were created from the eight breast cancer cell lines in order to aid with spheroid image segmentation. Cells were seeded at approximately 35,000 cells per well of a 6-well plate in 3 mL of DMEM and incubated for 24 hours (37°C) to achieve 20% confluence. After 24 hours of incubation, 35 µL of IncyCyte NucLight Green Lentivirus (#4624 Essen) was added to each well at an MOI of 1 with 1.5 µL of polybrene (1:2000). Plates were then incubated for an additional 24 hours followed by a media change, and another 24 hour incubation. Media was then changed for selection media consisting of 1 µg/mL puromycin and complete DMEM, followed by another 24 hour incubation. Following selection of puromycin resistant cells, cells were trypsinised and placed in a T75 tissue culture flask for further growth. GFP labelled cells and parental cell-lines were compared to ensure growth characteristics remained the same. This was achieved by measuring confluence in 6 well plates seeded with 10,000 cells per well and confluence measured with the Incucyte ZOOM. Following successfull transduction, GFP labelled cells were maintained in 0.5 µg/mL puromycin complete DMEM.

2.2.1 Culturing cells in 96-well plates

2.2.2 Culturing cells in 384-well plates

2.3 Compound handling

2.3.1 24 compound validation set

Compounds (table 2.1) were diluted in DMSO at a stock concentration of 10 mM. Compounds plates were made in v-bottomed 96-well plates (#CATNO MANUFACTURER), at 1000-fold

Compound	MoA class	Supplier	Catalog no.
Paclitaxel	Microtubule disrupting	Sigma	T7402
Epothilone B	Microtubule disrupting	Selleckchem	S1364
Colchicine	Microtubule disrupting	Sigma	C9754
Nocodazole	Microtubule disrupting	Sigma	M1404
Monastrol	Microtubule disrupting	Sigma	M1404
ARQ621	Microtubule disrupting	Selleckchem	S7355
Barasertib	Aurora B inhibitor	Selleckchem	S1147
ZM447439	Aurora B inhibitor	Selleckchem	S1103
Cytochalasin D	Actin disrupting	Sigma	C8273
Cytochalasin B	Actin disrupting	Sigma	C6762
Jaskplakinolide	Actin disrupting	Tocris	2792
Latrunculin B	Actin disrupting	Sigma	L5288
MG132	Protein degradation	Selleckchem	S2619
Lactacystin	Protein degradation	Tocris	2267
ALLN	Protein degradation	Sigma	A6165
ALLM	Protein degradation	Sigma	A6060
Emetine	Protein synthesis	Sigma	E2375
Cycloheximide	Protein synthesis	Sigma	1810
Dasatinib	Kinase inhibitor	Selleckchem	S1021
Saracatinib	Kinase inhibitor	Selleckchem	S1006
Lovastatin	Statin	Sigma	PHR1285
Simvastatin	Statin	Sigma	PHR1438
Camptothecin	DNA damaging agent	Selleckchem	S1288
SN38	DNA damaging agent	Selleckchem	S4908

Table 2.1: Annotated compounds and their associated mechanism-of-action label used in the classification tasks.

concentration in 100% DMSO by serial dilutions ranging from 10 mM to 0.3 μ M in semi-log concentrations. Compounds were added to assay plates containing cells after 24 hours of incubation by first making a 1:50 dilution in media to create an intermediate plate, followed by a 1:20 dilution from intermediate plate to the assay plate, with an overall dilution of 1:1000 from the stock compound plate to the assay plate.

2.4 Cell painting staining protocol

In order to capture a broad view of morphological changes within a cell using fluorescent microscopy, a choice has to be made which cellular structures to label. This choice is limited by the availability of the fluorescent filter sets fitted to the microscope, reagent costs, and the scalability of the protocol when used in a large screen. Fortunately, this problem was already addressed by another group who published a protocol – named “cell painting” – for labelling 7 cellular structures, using 6 non-antibody stains imaged in the same 5 fluorescent channels available with our microscopy setup.^{29,49}

The cell-painting protocol was initially optimised by Gustafsdottir *et al.* for use in the U2OS osteosarcoma cell line, and briefly tested in a few other commonly used cell-lines. However, when tested on the panel of 8 breast cancer cell lines, the staining protocol was observed to induce morphological changes on certain cell lines, in the absence of compounds. It was found that changing the media, and adding the MitoTracker DeepRed stain to live MDA-MB-231 cells produced a

Stain	Labeled Structure	Wavelength (ex/em [nm])	Concentration	Catalog no.; Supplier
Hoechst 33342	Nuclei	387/447 ±20	2 µg/mL	#H1399; Mol. Probes
SYTO14	Nucleoli	531/593 ±20	3 µM	#S7576; Invitrogen
Phalloidin 594	F-actin	562/624 ±20	0.85 U/mL	#A12381; Invitrogen
Wheat germ agglutinin 594	Golgi and plasma membrane	562/624 ±20	8 µg/mL	#W11262; Invitrogen
Concanavalin A 488	Endoplasmic reticulum	462/520 ±20	11 µM	#C11252; Invitrogen
MitoTracker DeepRed	Mitochondria	628/692 ±20	0.6 µM	#M22426; Invitrogen

Table 2.2: Reagents used in the cell painting protocol and the excitation/emission wavelengths of the filters used in imaging, ex: excitation, em: emission

rounded morphology, which was not observed in the other cell lines. As any morphological changes introduced by the staining protocol would mask those caused by small-molecules, the protocol was adapted by removing the media change step, and moving the addition of wheat germ agglutinin and MitoTracker DeepRed until after fixation. As the cells were now fixed immediately in their existing media this prevented any alterations to the morphology and improved the wheat germ agglutinin staining, although as the MitoTracker stain relies on membrane potential of the mitochondria, the selectivity of the MitoTracker stain was reduced when used on fixed cells, though it still produced selective enough labelling to capture large changes in mitochondrial morphology.

To stain cells in a 96 or 384 well plates, the cells are first fixed by adding an equal volume of 8% paraformaldehyde (#CATNO MANUFACTURER) to the existing media resulting in a final paraformaldehyde concentration of 4%, and left to incubate for 30 minutes at room temperature. The plates are then washed with PBS (100 µL for a 96 well plate, 50 µL for a 384 well plate) and permeabilised with (50 µL 96-well, 30 µL 384-well) 0.1% Triton-X100 solution for 20 minutes at room temperature. A solution of cell painting reagents was made up in 1% bovine serum albumin (BSA) solution (see table 2.2). Cell painting solution was added to plates (30 µL 96-well, 20 µL 384-well) and left to incubate for 30 minutes at room temperature in a dark place. Plates were then washed with PBS (100 µL 96-well, 50 µL 384) three times, before the final aspiration plates were sealed with a transparent plate seal (#CATNO MANUFACTURER).

2.5 Imaging

2.5.1 ImageXpress

Imaging was carried out on an ImageXpress micro XL (Molecular Devices, USA) a multi-wavelength wide-field fluorescent microscope equipped with a robotic plate loader (Scara4, PAA, UK).

2.5.2 Cell painting image capture

Images were captured in 5 fluorescent channels at 20x magnification, exposure times were kept constant between plates and batches as to not influence intensity values.

2.6 Image analysis

2.6.1 Cellprofiler

Images were analysed using Cellprofiler v2.1.1 to extract morphological features. Briefly, cell nuclei were segmented in the Hoechst stained image based on intensity, clumped nuclei were separated based on shape. Nuclei objects were used as seeds to detect and segment cell-bodies in the cytoplasmic stains of the additional channels. Subcellular structures such as nucleoli and Golgi apparatus were segmented and assigned to parent objects (cells). Using these masks marking the boundary of cellular objects, morphological features are measured for multiple image channels returning per object measurements.

2.7 Data analysis

2.7.1 Preprocessing

Out of focus and low-quality images were detected through saturation and focus measurements and removed from the dataset. Image averages of single object (cell) measurements were aggregated by taking the median of each measured feature per image. Features were standardised on a plate-by-plate basis by dividing each feature by the median DMSO response for that feature and scaled by a z-score (z) to a zero mean and unit variance by

$$z = \frac{x - \mu}{\sigma} \quad (2.1)$$

where μ is the mean and σ is the standard deviation.

Feature selection was performed by calculating pair-wise correlations of features and removing one of a pair of features that have correlation greater than 0.9, and removing features with very low or zero variance.

3

CELL MORPHOLOGY CAN BE USED TO PREDICT COMPOUND MECHANISM-OF-ACTION

3.1 Introduction

Cellular morphology is influenced by multiple intrinsic and extrinsic factors acting on a cell, and striking changes in morphology are observed when cells are exposed to biologically active small molecules. This compound-induced alteration in morphology is a manifestation of various perturbed cellular processes, and we can hypothesise that compounds with similar MoA which act upon the same signalling pathways will produce comparable phenotypes, and that cell morphology can, in turn, be used to predict compound MoA.

In 2010 Caie *et al.* generated, as part of a larger study, an image dataset consisting of MCF7 breast cancer cells treated with 113 small molecules grouped into 12 mechanistic classes, these cells were then fixed, labelled and imaged in three fluorescent channels⁴⁷. This dataset (also known as BBBC021) has become widely used as a benchmark in the field for MoA classification tasks, with multiple publications using the images to compare machine learning and data pre-processing approaches.^{50,51,52,53} Whilst this is important work, it has led to the situation whereby the vast majority of studies in this field have based their work on a single dataset generated with a one cell-line.

One of the issues associated with phenotypic screening when used in a drug discovery setting is target deconvolution. Once a compound has been identified which results in a desirable phenotype in a disease-relevant assay it is common to want to know which molecular pathways the hit compound is acting upon. While target deconvolution is a complex and difficult task, image-based morphological profiling represents one option similar to transcriptional profiling that can match an unknown compound to the nearest similar annotated compound in a dataset, while at the same time being far cheaper than the transcriptional methods such as LINCS1000⁵⁴.

3.1.1 Machine learning methods to classify compound MoA

Predicting compound MoA from phenotypic data is a classification task. This type of machine learning problem is well researched, and there are several models appropriate for our labelled data. As the raw data is in the form of images, it can be approached as an image classification task, a problem in the field receiving lots of attention due to recent theoretical and technological breakthroughs. Whereas a more classical approach would be to extract morphological information from the images, generating a multivariate dataset from the images, and training a classifier on these morphological

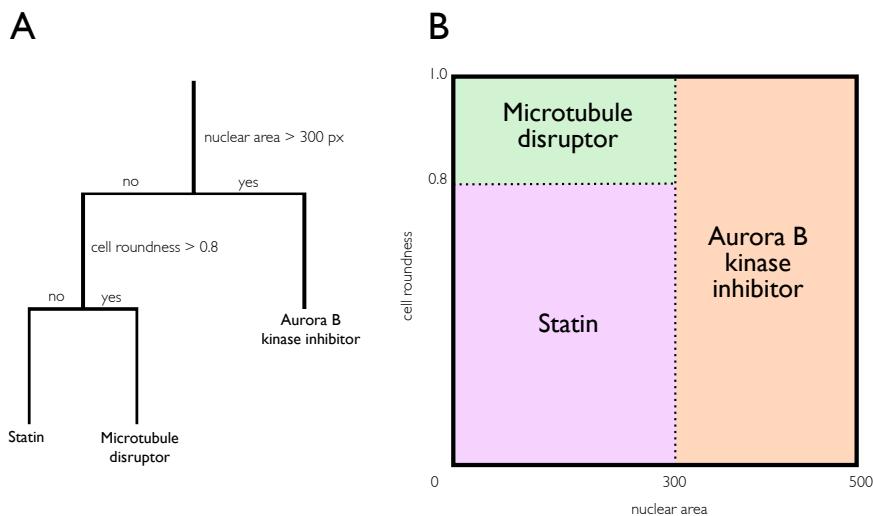


Figure 3.1: (A) An example of a simple mock decision tree to classify compound mechanism of action based on morphological features. (B) Depiction of decision space as divided by the decision tree model. Shaded areas show how new input data will be classified based on the decision rules (dotted lines).

features.

To develop and validate a machine learning model the dataset has to be split into training, validation and test sets. This is because overfitting is a common problem in machine learning, whereby the model is trained and accurately predicts labels on one dataset, but performs poorly when applied to new data on which it was not trained. Most classification models will overfit to some degree, typically performing better on the training dataset than any other subsequent examples, but the challenge is to limit this overfitting, and also to ensure that the data used to report accuracy measures has not been used in any way to train or validate the model.

3.1.2 Ensemble of decision trees trained on extracted morphological features

A decision tree is a very simple method that can be used for both regression and classification. The method works by repeatedly dividing the decision space using binary rules on the feature values until a terminal node containing a classification label is reached (figure 3.1). Simple decision trees like those shown in figure 3.1 perform relatively poorly on all but the simplest of classification problems. However, by aggregating many decision trees and their predictions we can create more accurate and robust models in a practice known as ensemble learning.⁵⁵ Bagging⁵⁶ and Boosting⁵⁷ are two popular methods for constructing ensembles of decision trees. As combining the output of several decision trees is useful only if there is a disagreement among them, these two methods both attempt to solve the same problem of generating a set of correct decision trees, that still disagree with one another as much as possible on incorrect predictions.

Decision tree methods work best with multivariate tabular data, with well defined features describing each observation, this is in contrast to image data which consists of 2D arrays of pixel intensities. Therefore, in order to train such a model, cellular morphology needs to be quantified by measuring cellular features. This is a common task with multiple software packages available, which follow two main steps: (1) Segment objects from the background. Objects may be

sub-cellular structures or whole-cell masks (2) Measure various attributes from the object, this is typically based on size, shape and intensity. Cellprofiler⁵⁸ was chosen primarily due to the high configurability and the permissive license enabling large-scale distributed processing on compute clusters in order to reduce the image analysis time. The images captured on the ImageXpress were analysed using Cellprofiler, quantifying approximately 400 morphological features. The datasets produced by the Cellprofiler analysis contained morphological measurements on an individual cell level. Although we can train a model on single cell data we are not interesting in classifying morphologies of single cells, but rather classifying an image or a collection of images that represent a compound treatment, this therefore allows several approaches to structuring the training data:

1. Train and test on median profiles.
2. Train on single cell data, test on image or well median profiles.
3. Train on single cell data, test on single cell data and classify the parent image as the most commonly predicted class of cell in that image.
4. Train on median profiles of bootstrapped single cell samples within an image, and test on median profiles.

3.1.3 Convolutional neural networks trained on pixel data

Artificial neural networks (ANNs) are becoming increasingly common in a wide range of machine learning tasks. Although many of the theories underpinning ANNs are decades old,⁵⁹ they have only recently achieved widespread practical use due to improved methods for training⁶⁰ and the availability of more computing power allowing the use of more complex models. ANNs are (very) loosely inspired by the structure of biological brains, with interconnected neurons passing signals through layers onto subsequent neurons forming a chain with the output of one neuron becoming the input for the next neuron. In between neurons, the signals can be altered by multiplying the value by a weight (W), it is through adjusting these individual weights that ANNs optimise their performance for a particular task, similar to how long-term potentiation is used to strengthen synaptic connections in biological brains. When a signal reaches a neuron, it is combined via a weighted sum with all the other inputs from other connected neurons and passed through an activation function. This activation function – similar to an action potential in neurons – determines the output of the neuron for the given aggregated input, which is then passed as new inputs onto subsequent neurons and so on, however, in contrast to an all-or-nothing output of an action potential there are several types of activation functions used in ANNs, most of which have a graded output (figure 3.2B).

The neurons in an ANN are typically arranged in several layers: an input layer; one or more hidden layers; and a final output layer (figure 3.3). With each layer, the network transforms the data into a new representation, through training the network these representations make the data easier to classify. In the final layer, the data is ultimately represented in a way which makes a single output neuron activate more strongly than the other neurons in that layer, and so the data

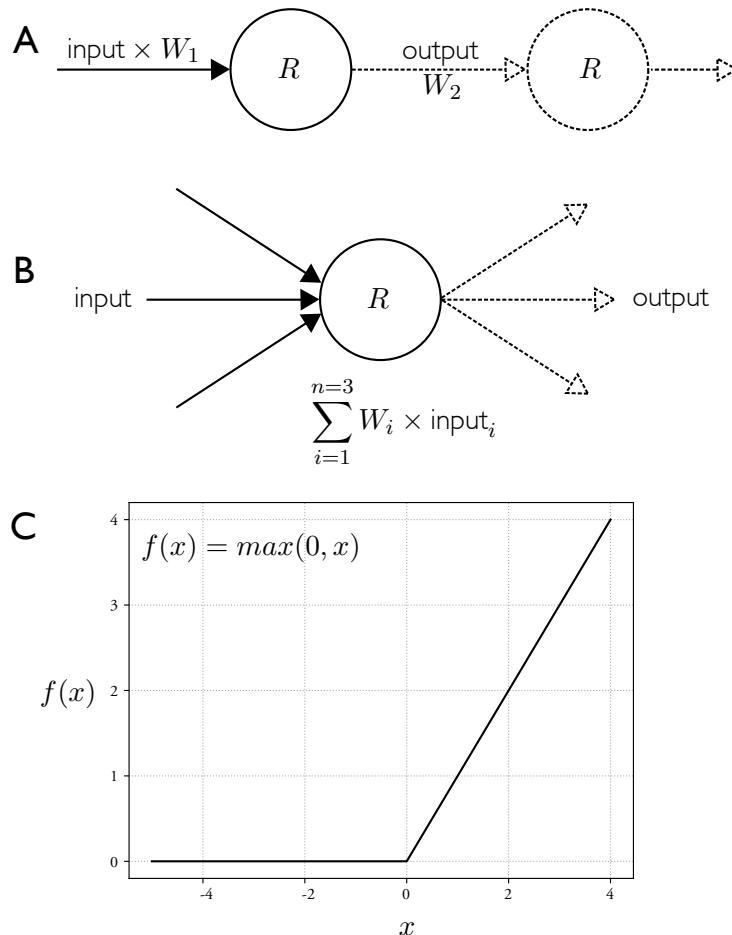
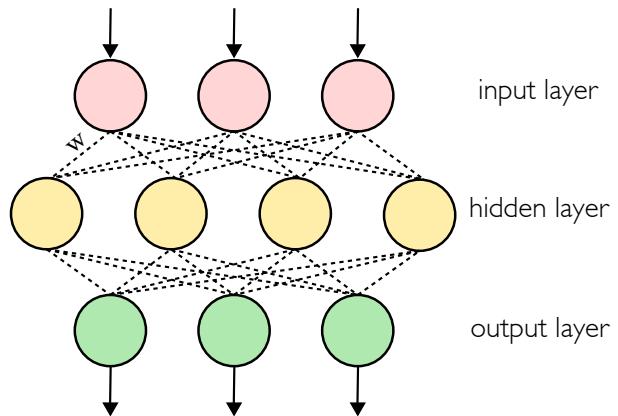


Figure 3.2: (A) A representation of a single connected neuron in an ANN, the input value to the neuron is multiplied by the weight (W_1), before being passed through the activation function R , the output of which is then multiplied by W_2 , and passed as the input to the next neuron. (B) A neuron with multiple inputs and outputs, typical of those in a hidden layer. The activation function acts on the weighted sum of all inputs, and returns a single output value which is then directed to all connected neurons in the next layer. Where W_i is the weight of input_i . (C) A common activation function also known as a rectifier, in this example a rectified linear unit (ReLU), in the inputs (x) is transformed and passed as output. So $f(x)$ can be viewed as the output for a given value of x .

Figure 3.3 Representation of a simple 3-layer ANN with a single fully connected hidden layer, three input neurons and three output neurons. W denotes a weighted connection between an input neuron and a hidden-layer neuron, with all connections between neurons having an associated adjustable weight. A network such as this would take a vector of three numbers as input, and would be capable of predicting three classes from the output layer of three neurons depending on the activation strengths of the neurons in the final output layer.



is ultimately transformed into a single value – the index of the active neuron which corresponds to a particular class. A new ANN is initialised with random weights, to train a neural network these weights are adjusted by feeding in labelled data and adjusting weights in order to minimise classification errors through a process known as backpropagation.⁶⁰

The convolution aspect of convolutional neural networks plays an important role when working with image data. Two-dimensional convolutions are widely used in image processing – blurring, sharpening and edge detection are all common operations which use this operation. They work by mapping a kernel – a smaller matrix of values – across a larger matrix, thereby using information from a small region of pixels in their transformation of each individual pixel. This lends itself well to ANNs, as a pixel value in isolation is less informative than a pixel value in the context of the neighbouring values. Depending on the size and the values within the kernel, the transformations highlight different features within an image. Two dimensional convolutions are used in ANNs by starting with many randomly initialised kernels, and updating the kernel values through training in order to best highlight features which prove useful for accurately predicting classes. Using a single convolutional layer highlights simple features in an image such as edges and speckles, by combining several convolutional layers more complex features are highlighted through combinations of these simple features. These convolved images are then flattened into a one-dimensional vector which is used as an input in a fully connected ANN such as that depicted in figure 3.3.

TODO: need some intro into the tasks, the mechanistic classes.

TODO: aims of the chapter

3.2 Results

3.2.1 CNN predictions are improved using sub-images

The images generated by the ImageXpress microscope with zero binning are 2160×2160 pixel tiff files, with a bit-depth of 16, whilst these image properties are common in microscopy, they are extreme for current CNN implementations. Most image classification tasks involving CNN's use 8-bit images in the region of 300 by 300 pixels, relatively small images are used as the convolutional layers of deep CNN's generate many thousands of matrices, and using smaller input images drastically reduces the computing resources and time required to train such classifiers.

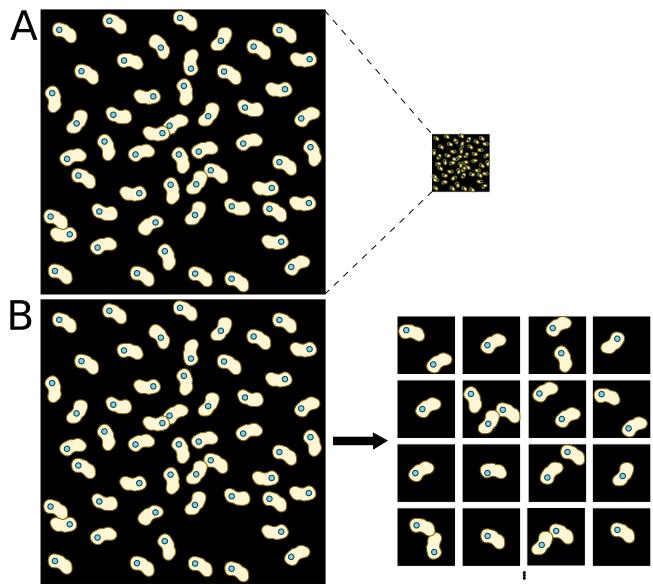


Figure 3.4: Two options for adapting large microscope images to work with the smaller input size of typical CNNs. **(A)** Full-sized images are downsized to the desired dimensions via bilinear or bicubic interpolation. **(B)** Images are chopped into smaller sub-images, cell detection can be carried out beforehand to ensure images contain at least one cell.

This presents the issue of how to reduce the 2160×2160 images into small images, one option is to downscale the entire image using bi-linear or bi-cubic interpolation, while a second option is to chop the original image up into smaller sub-images (figure 3.4). Downsizing the original image by simple scaling has a few potential problems which make it unsuitable for this particular task: many of the finer-grained cell morphologies such as mitochondria and endoplasmic reticulum distribution will be lost due to the reduction in image resolution; in addition, it was found that whole well images are susceptible to over-fitting as the classifier learned biologically irrelevant features such as the locations of cells within an image, which although should be random might have some spurious association with particular class labels. When chopping images into sub-images the most simple and commonly used method is to chop each image into an evenly spaced grid, whilst this is unbiased and easy to implement, it has the downside of potentially returning many images that do not contain any cells. A more nuanced approach is to first detect the x,y co-ordinates of each cell in the image, and creating a 300×300 bounding-box around the centre of each cell. This method returns an image per cell, negating the issue of empty images; it does however require detecting cell locations and handling cells located next to the image border.

To compare the performance of using either downsized whole images or cropped sub-images, a pair of ResNet18 models were trained using either one of the datasets. It was evident during training that using sub-images resulted in a higher final validation accuracy (0.847) compared to whole-images (0.778), as well as converging much faster than the whole-image-trained model (figure 3.5). Although it should be noted that whole images performed surprisingly well given their low resolution of cellular features.

It should be noted that the validation accuracy reported from the sub-image trained model is for

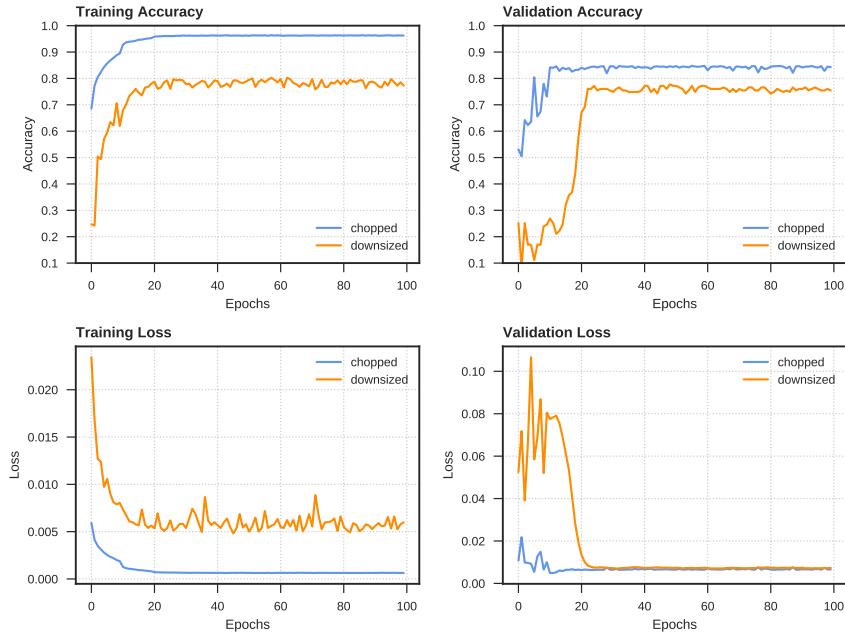


Figure 3.5: Comparison of training ResNet18 model on chopped sub-images vs down-sized images from the MDA-MB-231 cell line. Chopped images were 300×300 crops centered on nuclei. Whole images were 2160×2160 images downsized to 300×300 pixels.

classifying individual sub-images. One way to better use these individual sub-image classifications is to predict the parent image class based on a consensus of the predicted classes of the child sub-images. Using this consensus prediction, the sub-image validation classification accuracy increased from 0.847 to 0.912. Looking at confusion matrices calculated for both sub-image and whole images revealed that neither approach had difficulties at predicting a particular MoA class (figure 3.6).

Following these results the rest of the work involving CNNs used sub-images during training and prediction. Whilst sub-images improved model training and classification accuracy, it also introduces more complexity as images have to pre-processed to indentify cells and crop to a bounding box. It also introduces another parameter in terms of image size which has to be considered and optimised. While here I chose 300×300 pixel images corresponding to $97.5 \mu\text{m}^2$, this was chosen pragmatically to fully capture a single cell and a portion of any adjacent cells. This value could be optimised by running several models with differently sized cropped images, although this value is largely dependent on cell line characteristics, magnification and image binning.

3.2.2 More complex CNN architectures outperform simpler AlexNet

As CNNs can be constructed with a wide variety of architectures, and the field is still rapidly developing, I remained closed to well established architectures in the literature. However, as most images are digitally represented in three colour channels (red, green, blue (RGB)), the vast majority of CNN models are constructed in a way that input is restricted to three colour channels, therefore it is necessary to adapt these architectures to work with the differently shaped inputs and additional

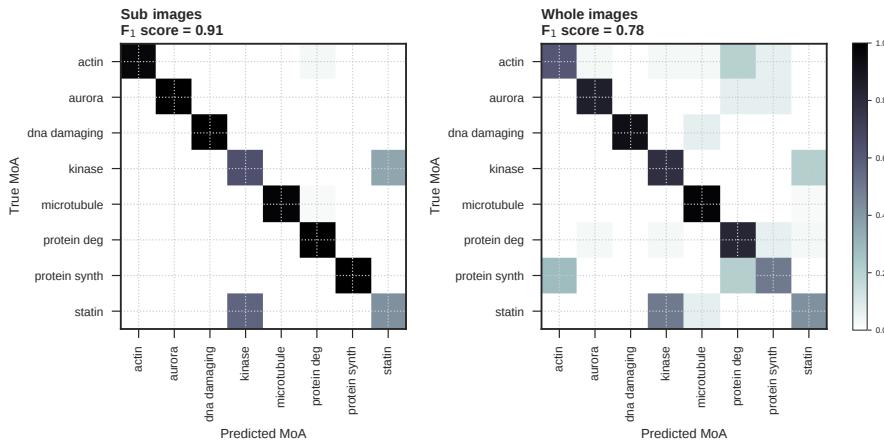


Figure 3.6: Confusion matrices comparing sub-image and whole image classification accuracy on 8 mechanistic classes of compounds.

parameters generated by the 5 channel images generated with the ImageXpress.

The two different CNN architectures were tested based on the hypothesis that a deeper, more complex architecture (ResNet18⁶¹) will be capable of learning more subtle features, although more complex models with greater numbers of internal parameters are more prone to overfitting when training data is limited. On the other hand, a more simple model such as AlexNet⁶² which contains fewer convolutional layers will be less able to perform complex transformations of the data, and therefore theoretically limit the subtle features which can be extracted and learned from an image. While this might theoretically reduce accuracy, in the absence of large amount of training data it may reduce overfitting due to the fewer number of parameters.

In an effort to reduce over-fitting, both models were evaluated with and without dropout in their dense layers during training. Dropout is a form of regularisation and works by randomly ignoring a fixed proportion of neurons during the training phase, with the theory that this prevents the model becoming too dependent on the output of particular neuron and leads to more robust features used for classification.

Four models in total were trained on sub-images of all eight cell-lines pooled into a single dataset. The models were ResNet18, ResNet18 with dropout, AlexNet and AlexNet with dropout. During training the two ResNet18 models outperformed the AlexNets in both training and validation accuracy (figure (3.7)). AlexNet with dropout layers did outperform the other three approaches when it came to validation loss, as loss did not increase even after many epochs this model demonstrated it is less liable to overfit data. However, the ResNet18 models showed a substantial increase in classification accuracy, and if training is limited to fewer than 10 epochs they do not show worse over-fitting compared to the AlexNet models. Additional dropout layers does not seem to reduce ResNet18's liability to overfit beyond 10 epochs, this is not too surprising as principle behind ResNet18's residual architecture is to limit overfitting, and adding additional dropout to the final fully-connected layers is a crude approach.

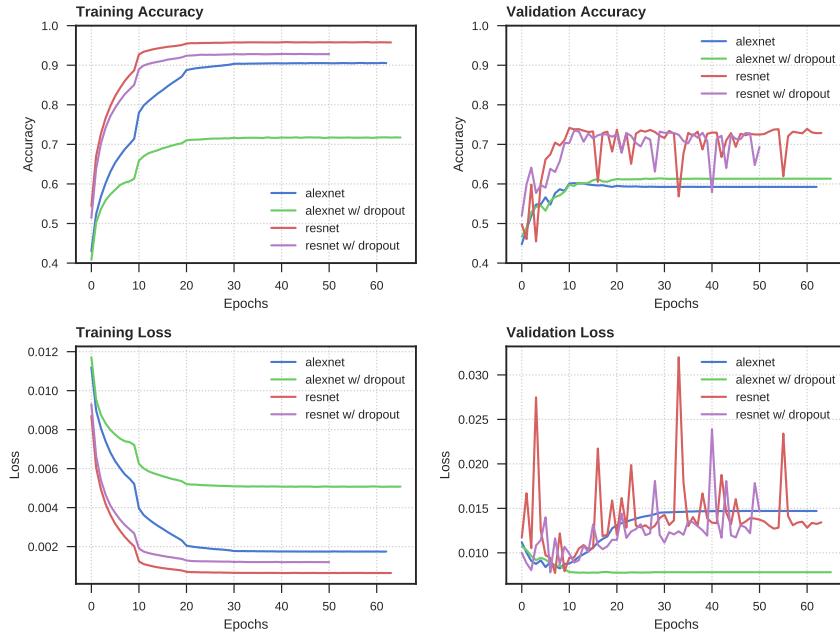


Figure 3.7: Comparison of CNN architectures. A comparison of AlexNet and ResNet18 architectures with and without dropout training and predicting on 5 channel 244×244 pixel 5 channel images of all eight cell lines. Loss was calculated using cross entropy on 8 mechanistic classes of compounds.

3.2.3 Standardising image intensity does not improve CNN model convergence

When training CNN models it is common practice to standardise image intensities. This pre-processing step consists of subtracting the mean of the image (or image batch) from each pixel and dividing the result by the standard deviation. The theory is this reduces training time and helps CNN models converge faster by ensuring the weights calculated during training are all on a similar scale which in turn restrains the gradients used in backpropagation. This pre-processing makes sense in the classical and traditional academic use of CNNs which are often trained on images or photographs from many different sources with inconsistent lighting and colours. However, the images used in this high-content screening dataset are all from a single microscope with a carefully controlled light source, in addition the intensities of the different channels carry a biological information relating to the abundance of different proteins or cellular structures. Therefore I wanted to assess if standardising image intensities per image channel improved model convergence and classification accuracy compared to un-normalised intensity valuesⁱ.

Two models based on the ResNet18 architecture were trained on chopped 300×300 pixel images of a pooled dataset of all eight cell lines, one of the models was fed images standardised per channel, the other raw image intensities. After 48 hours of training (54 and 64 epochs for unnormalised and normalised models respectivelyⁱⁱ) both models demonstrated identical training curves for training

ⁱAlthough un-normalised, intensity values were converted from 16 bit unsigned integers (65536 grayscale values) to 8 bit unsigned integers (256 grayscale values). This reduces training time and storage size at the expense of intensity accuracy.

ⁱⁱThe number of epochs per 48 hours does not indicate how fast a model converges, but rather the affect of availability of compute resources used for image loading.

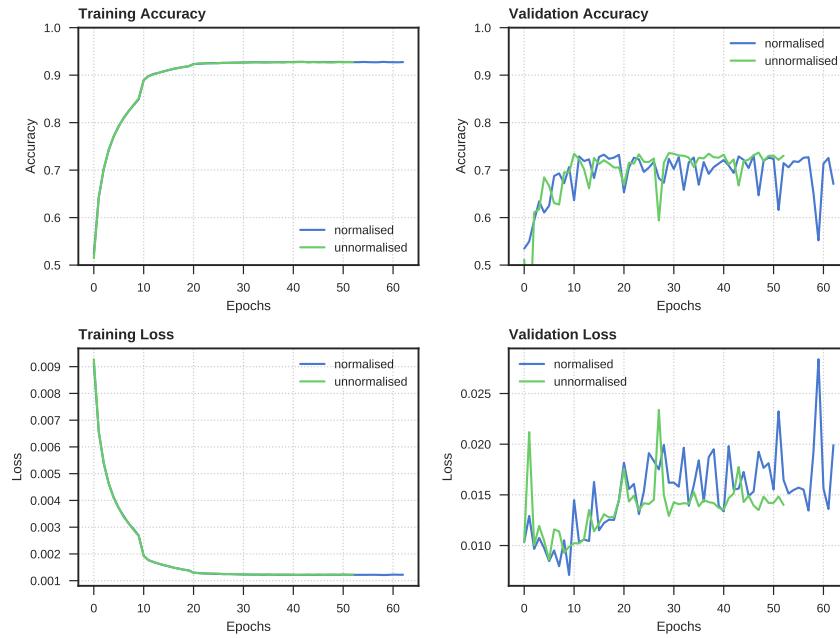


Figure 3.8: Effect of image intensity normalisation on CNN training. ResNet18 models training and predicting on eight pooled cell-lines with and without standardising image intensities per image per channel.

accuracy and loss, while validation accuracy and loss curves showed no striking difference in the performance between the two methods, although the normalisation pre-processing step appears to cause sudden drops in model performance indicated by decreased accuracy and increased loss (figure 3.8).

There is the possibility that training a model on disparate imaging datasets – from either different microscopes with different illumination settings, or different concentrations of reagents – then image standardisation may play a more important role. However, as intensity standardisation did not improve model performance in this case I chose to continue CNN work using un-standardised images, as there is an argument that standardisation may remove biologically relevant information for no benefit.

3.2.4 Single cell/Image aggregates improve classification accuracies with decision trees.

TODO, delete as appropriate when results come in.

3.2.5 Principal component analysis does (not) improve classification accuracy with decision trees.

TODO, delete as appropriate when results come in.

3.2.6 RF/CNN outperforms CNN/RF when using a single cell-line

TODO, delete as appropriate when results come in.

3.2.7 Data from additional cell lines does (not) improve model performance

TODO, delete as appropriate when results come in.

3.2.8 On the transferrability of models to new unseen cell lines

TODO

3.3 Discussion

TODO.

3.4 Methods

3.4.1 Accuracy

Validation accuracy during training was measured using the Jaccard similarity score of the i th samples with true label set y_i and predicted label set \hat{y}_i :

$$J(y_i, \hat{y}_i) = \frac{|y_i \cap \hat{y}_i|}{|y_i \cup \hat{y}_i|} \quad (3.1)$$

The F_1 score was used post training to determine classification accuracy. The F_1 score is the harmonic mean of both the precision and recall. So given true positives (tp), false positives (fp) and false negatives (fn):

$$\text{precision} = \frac{\text{tp}}{\text{tp} + \text{fp}} \quad (3.2)$$

$$\text{recall} = \frac{\text{tp}}{\text{tp} + \text{fn}} \quad (3.3)$$

the F_1 score can be calculated as:

$$F_1 = 2 \times \frac{\text{precision} \times \text{recall}}{\text{precision} + \text{recall}}. \quad (3.4)$$

3.4.2 Ensemble of decision trees

Models were created using scikit-learn version 0.19 in python 3.6.2.

3.4.3 Convolutional neural networks

All code related to neural networks was written in pytorch v0.3 for python 3.5, and all ANN models were trained on nvidia K80 GPUs.

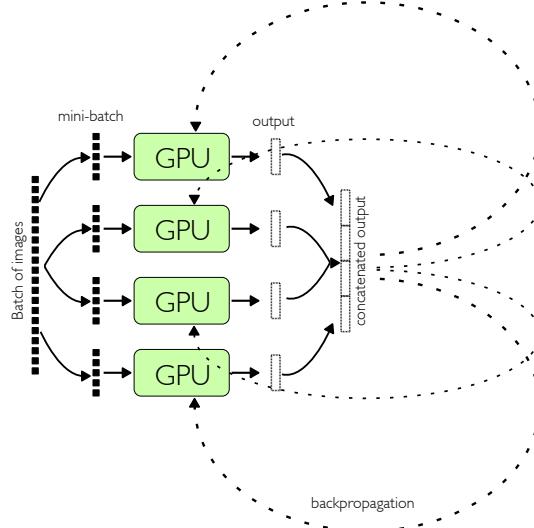


Figure 3.9: Increased training speed by data parallelism. Models are replicated across an array of GPUs, the input batch is split evenly among the devices, with each device processing a portion in parallel. During backpropagation the updated weights for all replicas are averaged and models weights are updated synchronously.

Data parallelism

As training CNNs is computationally expensive and time consuming, data parallelism was used to share batches of images across multiple GPUs trained in parallel. This technique replicates the CNN model on each device, which processes a portion of the input data, the updated weights for all devices are then averaged and model replicates are updated synchronously after each batch (figure 3.9). This speeds up model training approximately linearly with the number of GPUs and allows use of larger batch sizes.

Architecture

Training parameters

Image intensities were standardised on an individual image and channel basis by taking each image in the form of a [width \times height \times channel] array and subtracting the mean of each channel from each pixel value in that channel, and dividing the pixel value by the standard deviation of the original channel.

Batch sizes during training were kept at 64 images. In the case of using GPU arrays then this was multiplied by the number of GPUs. Learning rate was set to $1e^{-3}$ decreasing 10-fold every 10 epochs (figure 3.10). Decay was used to aid gradient descent and model convergence. Models were trained for 100 epochs or 48 hours, whichever was reached first, with model checkpoints every epoch there was an increase maximum validation accuracy. The optimiser used was ADAM⁶³ with the categorical cross entropy loss function.

Image preparation

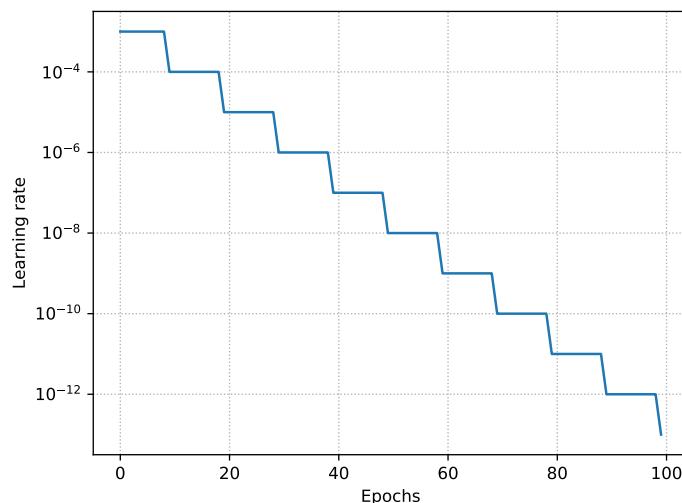


Figure 3.10: Learning rate and decay for training CNN models, initialised at $1e^{-3}$ and reduced 10-fold every 10 epochs.

4

MEASURING DISTINCT PHENOTYPIC RESPONSE

Note: this chapter is based on previously published work: "Development of the Theta Comparative Cell Scoring Method to Quantify Diverse Phenotypic Responses Between Distinct Cell Types", S Warchal, J Dawson, N.O Carragher. *ASSAY and Drug Development Technologies*, pages 395-406, 7:14, 2016. and "High-Dimensional Profiling: The Theta Comparative Cell Scoring Method", *Phenotypic Screening. Methods in Molecular Biology* 1787, 171-181.

4.1 Introduction

4.1.1 Comparing response to small molecules across a panel of cell lines

Comparative analysis of cell line panels treated with compounds are routinely used in pharmacogenomic studies and drug sensitivity profiling. These studies often use large numbers of cell lines and simple measures of compound response such as growth inhibition or cell death, allowing researchers to interrogate sensitivity of various small molecule therapies in a number of genomic backgrounds representing different diseases, disease-subtypes or patient populations.

Using high-content imaging methods with cell line panels enables more complex cellular readouts than cell death resulting in a more detailed characterisation of compound effect. However, in order to apply multiparametric high-content data to pharmacogenomic studies, there needs to be a robust – and ideally univariate – measure of compound response to correlate drug sensitivity with genomic or proteomic datasets.

4.1.2 Quantifying compound response in high content screens

A simple but effective method to quantify the magnitude of compound response from multiparametric data is to calculate the distance from the negative control to the compound induced phenotype in feature space. This idea was first demonstrated by Tanaka *et al.* using PCA to reduce the dimensionality of a high content screening dataset to 3 principal components, and taking the distance from the centroid of the negative control replicates to the compound co-ordinates.⁶⁴ The distance from the negative control in PCA space is an effective metric for detecting phenotypically active compounds. In addition, distance measurements can be repeated for multiple concentrations of a compound to produce a concentration – phenotypic-distance response curve (see figure 4.1) and EC₅₀ values. However, one issue in calculating the distance-from-negative-control metric of compound activity is that it disregards much of the information relating to the position in feature space, as depicted in figure 4.1, two compounds may have similar distances yet those distances may be produced by very different morphological changes. In order to discern between two such compounds there needs to be a measure of directionality.

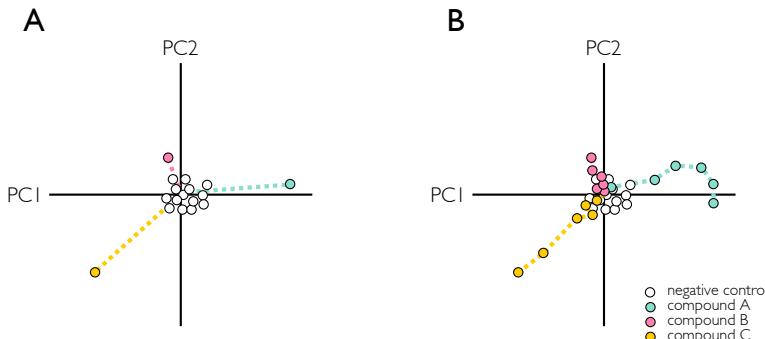


Figure 4.1: Diagram illustrating measuring magnitude of compound response by distance from the negative control centroid in principal component space. **(A)** Phenotypic distance to three different compounds. Compound A and B show phenotypic activity as they are distanced from the negative control cluster, whereas compound B shows little activity. Note that compound A and compound C have similar distances from the negative control centroid, yet have very different values in principal component space. **(B)** A titration series for each of the three compounds, showing how increasing concentrations of compounds A and C show increasing distance from the negative control, whereas weakly active compound C does not increase in distance.

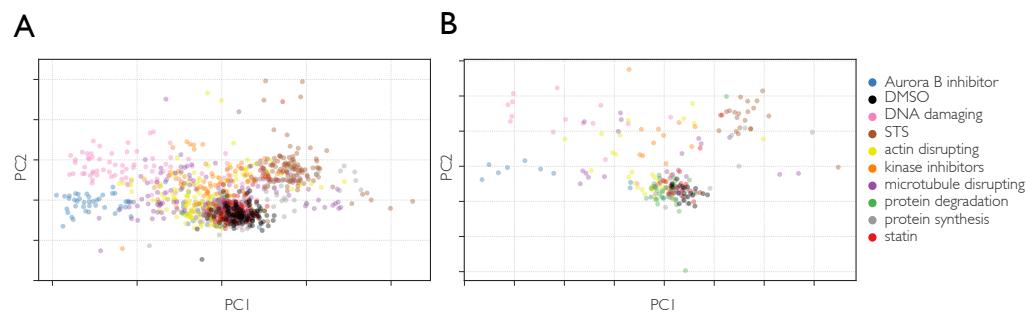


Figure 4.2: MoA clustering of compounds based on PCA of their morphological features. Principal components calculated from morphological features of 24 compounds grouped into 8 mechanistic classes. **(A)** Principal components calculated from an image average of individual cell measurements. **(B)** Each point represents a well average from individual cell measurements as each well contains 9 image sites. STS: staurosporine.

4.2 Results

4.2.1 Compound titrations produce a phenotypic ‘direction’

Visualising high-content imaging data from compound screens in principal component space reveals a number of patterns and produces a representation of the overall structure of the data. Performing PCA on morphological feature data from 24 compounds representing 9 mechanistic classes and plotting the first 2 principal components reveals compounds with the same MoA tend to cluster with one another in PCA space (figure 4.2).

When taking concentrations of compounds into account, is it possible to visualise the effect of increasing concentrations of a compound and how the distance from the negative control and inactive compounds increases. Figure 4.3 shows two highlighted compounds from the same data as in figure 4.2, we can see as compound concentration increases morphologies become increasingly distant

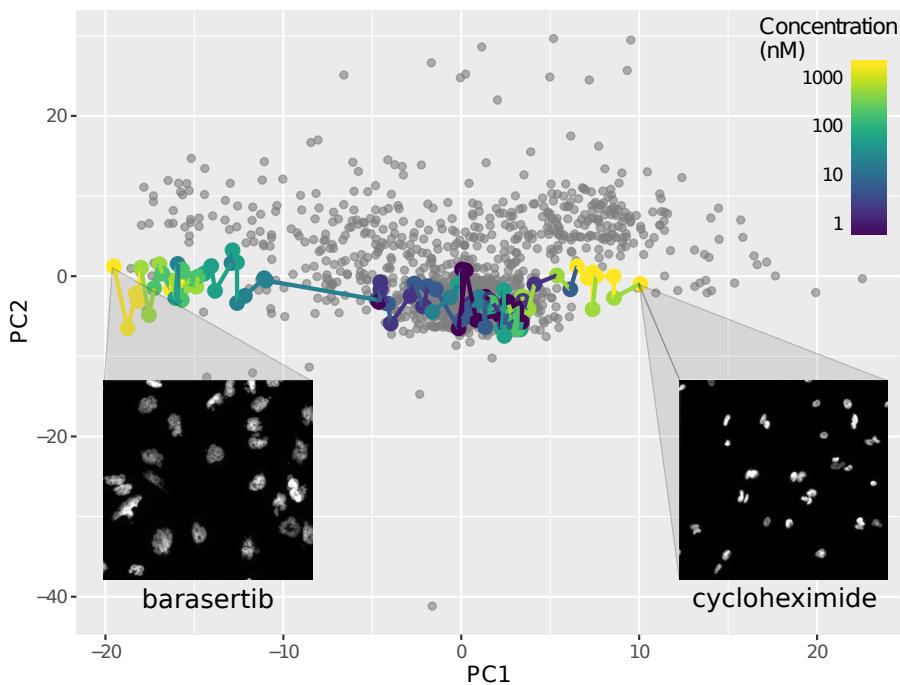


Figure 4.3: Principal components of Cellprofiler features calculated from a 24 compound high content screen in MDA-MB-231 cells. Barasertib (left) and cycloheximide (right) titrations are highlighted to show two active compounds with distinct phenotypes heading in different directions in phenotypic space with increasing concentration. Images shown next to points are from the Hoechst stain labelling nuclei morphology produced by $1 \mu\text{M}$ of each compound.

from the untreated negative control cluster positioned centrally, with the two different compounds producing opposite directions. Mirroring the differences in direction, the morphologies produced by barasertib and cycloheximide are also very different from one another, with barasertib – an Aurora B kinase – inhibitor producing large irregular nuclei, and cycloheximide creating small bright nuclei. This direction in PCA space can be thought of as a phenotypic direction, which can be measured and quantified independent from potencyⁱ.

4.2.2 Difference in phenotypic direction can be used to quantify distinct phenotypes

Using direction in addition to distance it is now possible to distinguish between equally phenotypically potent compounds with distinct morphological effects. By calculating an angle (θ) between phenotypic directions as a function of cosine dissimilarity, a univariate value can be used to quantify phenotypic distance between either different compounds, or cell-lines treated with the same compound to detect distinct phenotypic response. By calculating θ against a fixed reference vector, the difference in θ ($\Delta\theta$) between two treatments can be quantified and visualised in polar co-ordinates as histograms or rose plots (figure 4.4). Compounds with the same phenotypic direction will have a small $\Delta\theta$ and compounds with dissimilar phenotypes having a large $\Delta\theta$, when expressed in degrees the values are constrained between 0° and 180° .

Although the data in figures 4.3 & 4.2 show the negative control points clustered near the origin

ⁱas measured by distance from the negative control cluster centroid

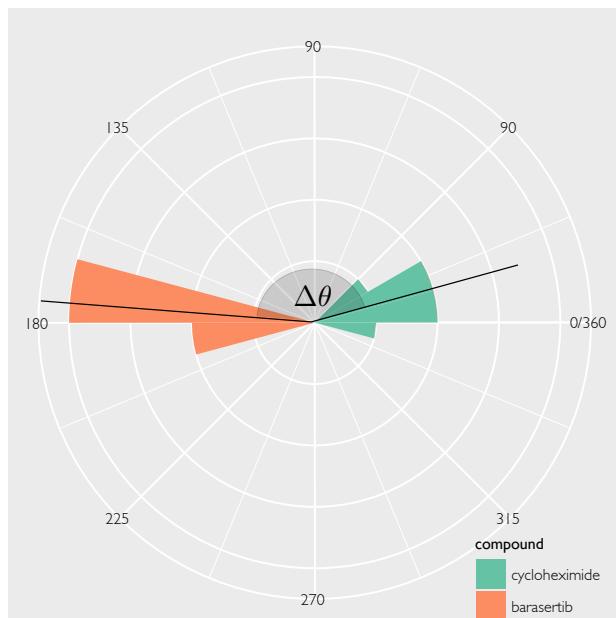


Figure 4.4: Visualisation of $\Delta\theta$ to quantify the difference in phenotypic direction between two compounds. Histograms in polar co-ordinates show the θ values of treatments against a fixed reference vector, with $\Delta\theta$ calculated as the difference between the average θ (black lines) of each compound.

(0, 0) in principal component co-ordinates this is not guaranteed and should not be relied upon, so it is necessary to translate the principal components co-ordinates so that the negative control centroid is positioned over the median. In addition, inactive compounds will be positioned in proximity to the negative control points and calculated θ values will be misleading, therefore removing inactive compounds based on distance from the negative control is an important pre-processing step.

4.2.3 SN38 elicits a distinct phenotypic response between cell lines

Instead of calculating $\Delta\theta$ between compounds it is also possible to calculate $\Delta\theta$ between cell lines per compound. To identify and quantify differential phenotypic responses, $\Delta\theta$ was calculated between pairs of 8 breast cancer cell lines treated with 24 small molecules at the three highest concentrations (0.1 μ M, 0.3 μ M, 1 μ M). 21 out of the 24 compounds were found to be sufficiently active across the 8 cell lines to proceed, and the difference in phenotypic direction was calculated for all pairs of cell lines for each compound. Figure 4.6 shows a heatmap of the calculated $\Delta\theta$ values. Some compounds such as the Aurora B inhibitors ZM447439 and barasertib showed very little difference in phenotypic response between the breast cancer cell lines, whereas compounds such as the topoisomerase I inhibitor SN38 demonstrated a single cell-line (KPL4) having a distinct response compared to the 7 others. Particularly striking is the difference between the MCF7 and KPL4 cell lines with a $\Delta\theta$ of 179°, indicated near opposite phenotypic responses between the pair of cell lines to the topoisomerase I inhibitor.

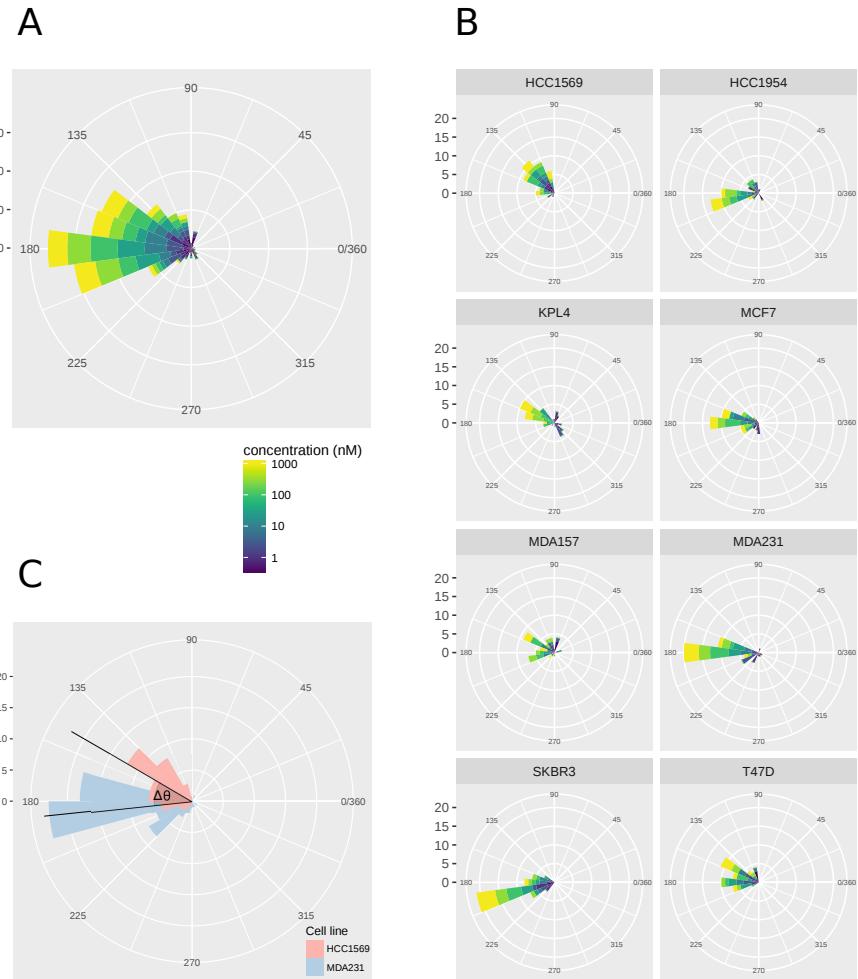


Figure 4.5: Visualisation $\Delta\theta$ to quantify the difference in phenotypic response between cell lines when treated with barasertib. **(A)** Circular histogram of θ values of barasertib calculated for eight cell lines. **(B)** Phenotypic direction of cell lines treated with barasertib stratified by cell line. **(C)** Representation of $\Delta\theta$ for the difference between HCC1569 and MDA-MB-231 cell lines. Note that in this case $\Delta\theta$ is relatively small.

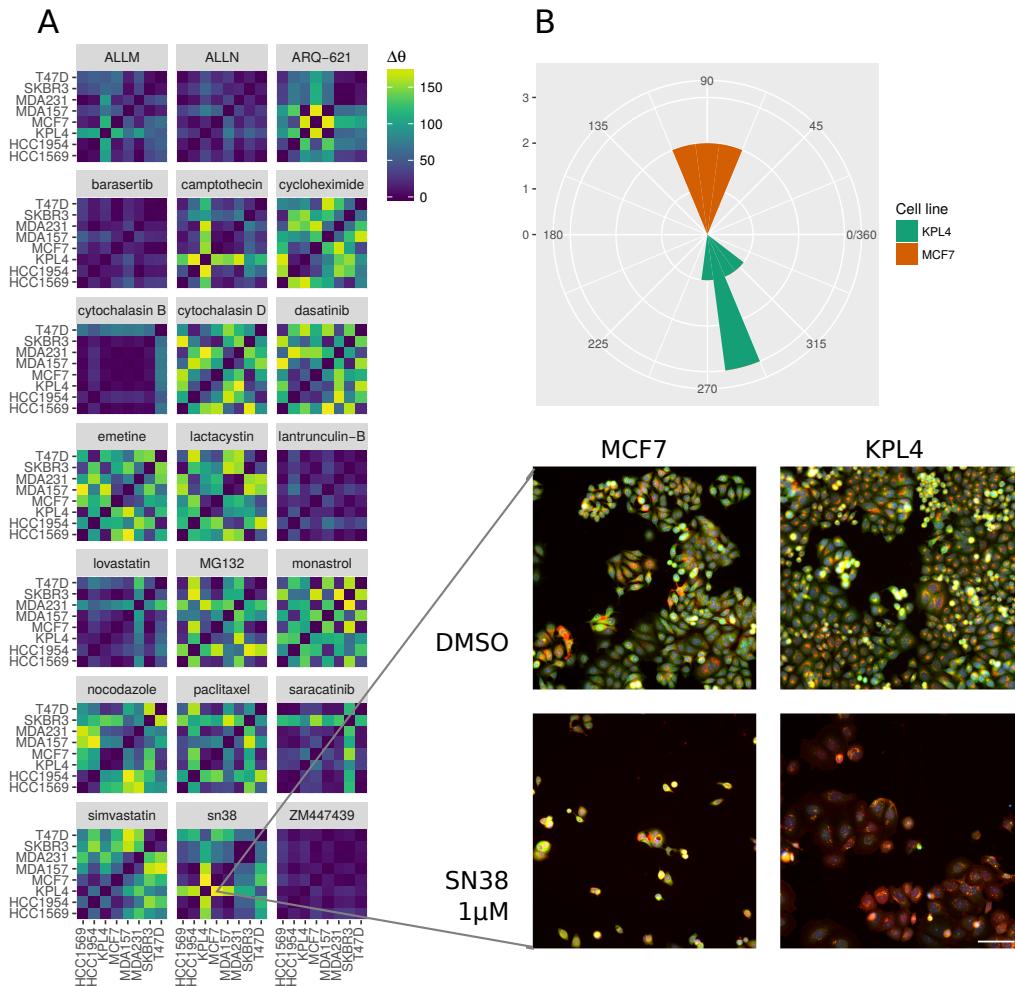


Figure 4.6: Heatmap of $\Delta\theta$ values between pairs of cell lines for separate compounds. **(A)** $\Delta\theta$ calculated between pairs of cell lines treated with 21 compounds as 1 μM concentration. Images show differential response between KPL4 and MCF7 cell lines treated with 1 μM SN38. MCF7 cells are observed to decrease in cell area with bright staining for the endoplasmic reticulum, whereas KPL4 cells produce a ‘fried egg’ morphology with large spread cells and weak endoplasmic reticulum staining. Channels used are as follows: *Red* - MitoTracker DeepRed (mitochondria); *Green* - Concanavalin A (endoplasmic reticulum); *Blue* - Hoechst33342 (nuclei). Scale bar: 100 μm . **(B)** Histogram of θ values calculated for MCF7 and KPL4 cells treated with 1 μM SN38. $\Delta\theta = 179^\circ$

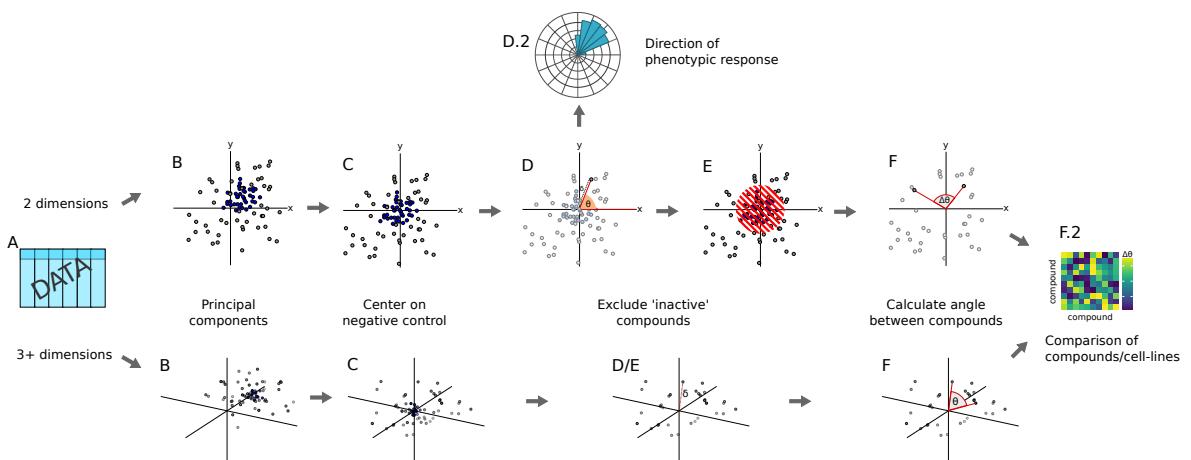


Figure 4.7: Theta comparative cell scoring (TCCS) workflow. **(A)** Normalised and standardised numerical data. **(B)** Principal component analysis, negative control values coloured in blue. **(C)** Centering of principal component values to the negative control centroid. **(D)** Calculation of distance from the origin to each data point, an activity cutoff is derived from the standard deviation of the distance to the negative control values. **(D.2)** In two-dimensional space, a directional histogram can be created by the angle of each vector against a reference vector. **(E)** Inactive compounds excluded based on distance from the origin. **(F)** Determining the angle between compounds/cell-lines. **(F.2)** Visualisation or clustering of compounds based on θ values.

4.3 Discussion

A number of methods exist to classify drug MoA and profile drug response in the context of high-content imaging studies, most of these have only been applied to a single cell type. The method described in this chapter, named as theta comparative cell scoring (TCCS), was developed to provide a pragmatic way to perform comparative high-content imaging studies across genetically and morphologically distinct cell lines. TCCS should be viewed as an extension to the common distance-in-PCA approach taking directionality into consideration in addition to distance from controls. The benefits of TCCS over previous methods are as follows: (1) the use of distance from the negative control to remove inactive compounds as one of the first steps prevents spurious differences that would be present in measures such as correlation or simple cosine similarity; (2) The comparison of each data point to a common reference vector enables visualisation of a phenotypic direction.

When comparing compound response between cell lines the most critical step, regardless of subsequent methods, is to account for the inherent morphological differences between untreated cell lines. Without this normalisation step morphologically distinct cell lines are not directly comparable as their large scale morphological differences will mask any difference in morphological response to a compound.

The TCCS method removes compounds which are deemed to be inactive if they are not sufficiently distant from the negative control (see figure 4.7). While this increases the robustness of the calculation by removing spurious differences in direction, it also introduces a new problem when compounds elicit large differences in potency between cell lines. This would result in the removal of

such compounds from the analysis despite producing a genuine, and potentially biologically interesting, differential response between cell lines. This can be rectified by identifying these compounds when computing compound distances from the negative control in principal component space – any compounds that show large differences in this distance between cell lines can be flagged for further analysis before removal.

When using high-content imaging data with a lot of morphological feature measurements, using the first two principal components as depicted in this chapter may only account for a small proportion of variation in the data. This may lead to potentially missing interesting differences which are only evident in later principal components.

Fortunately, as part of the TCCS algorithm the cosine similarity equation uses the dot product of the two vectors reducing any two equal length vectors to a single number, enabling the use of 3 or more principal components. Therefore the proportion of variance to keep in the data can be specified beforehand, and the dimensionality of the data reduced in a way to suit the statistical properties of different datasets.

An interesting prospect of ‘phenotypic direction’ is relating directions back to combinations of morphological features to provide more interpretability to the results. This is possible with PCA by using the feature loadings describe the contributions of original features used to construct each principal component. However, as PCA uses arbitrary positive and negative weights for these feature loadings, other dimensional reductions techniques might be better suited for generating more interpretable results. One example is non-negative matrix factorisation which would return only positive weights for the morphological features, making the contribution of morphological features to the phenotypic direction more interpretable.

Multiple concentrations are not often used in high throughput cell based screening assays despite providing useful information to detect off-target effects as well as reducing false negatives by screening at incorrect concentrations. A potential improvement of the TCCS method is to incorporate data from compound titrations as in figure 4.3 and fitting a linear model to the data points providing information relating to goodness of fit. This could potentially be used to identify compounds with off-target effects at higher concentrations if they do not fit a linear model well which indicates the data points going off at a tangent at higher concentrations towards phenotypic space indicative of cell death (e.g figure 4.1 B compound A).

In conclusion, the TCCS method presents an alternative to (dis)similarity measures such as correlation and cosine distance with important prior steps to account for peculiarities in high-content screening data, enabling high-content screening studies for quantifying distinct phenotypic response between morphologically diverse cell types.

4.4 Methods

4.4.1 Data pre-processing

Tabular data from Cellprofiler measuring 309 morphological features for each cell was aggregated to an image median. To remove batch effects and to remove inherent cell-line specific morphologies

data was normalised by dividing each morphological feature by the median negative control value for that feature per plate. Each feature was then standardised to a mean of zero and unit variance on the pooled data.

4.4.2 Principal component analysis

Principal components were calculated using the `prcomp` function in R v3.2, with no centering or scaling as this was performed manually beforehand.

4.4.3 Selecting the number of principal components

The number of principal components to used in the analysis can be determined by specifying beforehand the proportion of variance in the data that should be kept, and then finding the minimum number of principal components that account for that proportion of variance in the dataset.

E.g in R:

```

1 threshold = 0.8
2 pca_output = prcomp(data)
3 pc_variance = pca_output$stdev^2
4 cumulative_prop_variance = cumsum(pc_variance) / sum(pc_variance)
5 n_components = min(which(cumulative_prop_variance >= threshold))

```

where `data` is numeric dataframe of morphological features.

4.4.4 Centering the data on the negative control

In order to centre the principal component data so that the mediod of the negative control was positioned on the origin, the median value for each feature columns for the negative control data was calculated. Then finding how much this differs from the origin for each feature, all principal component values were adjusted by this difference.

1. Calculate the median value m for each principal component for the negative control data (medioids).
2. Subtract each medioid from 0 in order to find the difference from the origin to δm_i , where i is the i^{th} principal component.
3. Add δm_i to each value in the i^{th} principal component.

For example in R, given a dataframe `data` containing a metadata column "compound_name" of compound names, with "DMSO" as a negative control, and `feature_cols` as a list of non-metadata column names:

```

1 medioids = apply(data[data[, "compound_name"] == "DMSO"], 2, median)
2 delta_m = 0 - medioids # δm
3 for (i in seq_along(feature_cols)) {
4   feature = feature_cols[i]
5   # feature_column_i := feature_column_i + δm_i
6   data[, feature] = data[, feature] + delta_m[i]
7 }

```

4.4.5 Identifying inactive compounds

Inactive compounds were identified by determining a minimum cut-off distance to the negative control centroid in principal component space. This was calculated by first finding the l_1 normⁱⁱ from each compound at all concentrations to the negative control centroid. The standard deviation of all these distances was calculated and any compound which was within 2 standard deviations of the negative control centroid at 1 μM was deemed inactive, if a compound was found to be inactive in any one of the eight cell lines it was removed from the analysis.

4.4.6 Calculating θ and $\Delta\theta$

θ was calculated by taking cosine dissimilarity between two vectors (u and v) in principal component space and converting into degrees.

$$\theta = \cos^{-1} \left(\frac{\mathbf{u} \cdot \mathbf{v}}{\|\mathbf{u}\| \|\mathbf{v}\|} \right) \cdot \frac{180}{\pi} \quad (4.1)$$

When v is a common fixed reference vector, $\Delta\theta = |\theta_i - \theta_j|$ where θ_i and θ_j are theta values for 2 vectors. As opposite phenotypic directions are at 180° , $\Delta\theta$ values greater than 180° should be thought as converging towards similar phenotypes. Therefore $\Delta\theta$ values were constrained to a maximum value of 180° by subtracting any value greater than 180° from 360° .

$$\theta = \begin{cases} 360 - \theta & \text{if } \theta > 180 \\ \theta & \text{otherwise} \end{cases} \quad (4.2)$$

ⁱⁱA.K.A Manhattan or city-block distance

5

LARGE COMPOUND SCREEN ACROSS 8 BREAST CANCER CELL LINES

5.1 Introduction

5.1.1 subsection

5.2 Results

5.2.1 Hit selection

5.2.2 Serotonin related compounds

5.2.3 Spheroids

5.2.4 RPPA

5.3 Methods

5.3.1 Identifying hits

5.3.2 Spheroids

5.3.3 RPPA

6

CHEMINFORMATICS AND HIGH-CONTENT IMAGING

6.1 Introduction

6.1.1 Cheminformatics

6.1.2 Structure activity relationships

6.1.3 Chemical similarity

6.1.4 Previous work in this field

6.2 Results

6.2.1 The BioAscent library contains clusters of phenotypically similar compounds

In order to compare the phenotypic profiles produced by compounds in the BioAscent library, active compounds were selected based on the L_1 norm distance from the negative control centroid (figure (6.1)). As many of the compounds were cytotoxic and produced images containing only a few dying cells which do not produce robust morphological measurements, an activity window was used to exclude cytotoxic compounds.

Hierarchical clustering of morphological profiles produced by these phenotypically active compounds showed that despite the chemical diversity of the BioAscent library, the active compounds formed distinct clusters of compounds which produced similar cellular morphologies (figure 6.2 A).

To confirm the validity of the clustering, the hierarchical labels were compared with clusters found in an unsupervised algorithm. The morphological profiles were embedded into lower dimensional space using the t-SNE algorithm^{tnse_paper} which aims to preserve local structure within the data and reveals clusters of similar points in an unsupervised approach. When these points were coloured by the cluster labels identified by hierarchical clustering they appeared to match up with the tSNE embedding (figure 6.2 B).

6.2.2 The BioAscent library is chemically diverse

The BioAscent library is marketed as chemically diverse, yet I still wanted see to what degree this is true, and if there are clusters of chemically similar compounds such as those based around a common scaffold. All 13,000 BioAscent compounds were converted into molecular fingerprints

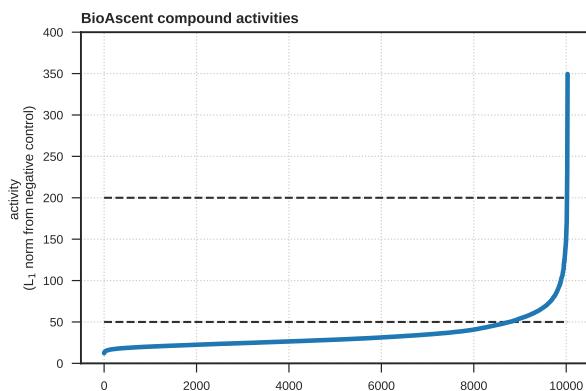


Figure 6.1: Selection of active BioAscent compounds based on the L_1 norm distance from the DMSO negative control centroid in PCA space. Lower and upper bounds of the selected compounds are indicated by dashed lines. In total 1244 compounds were selected.

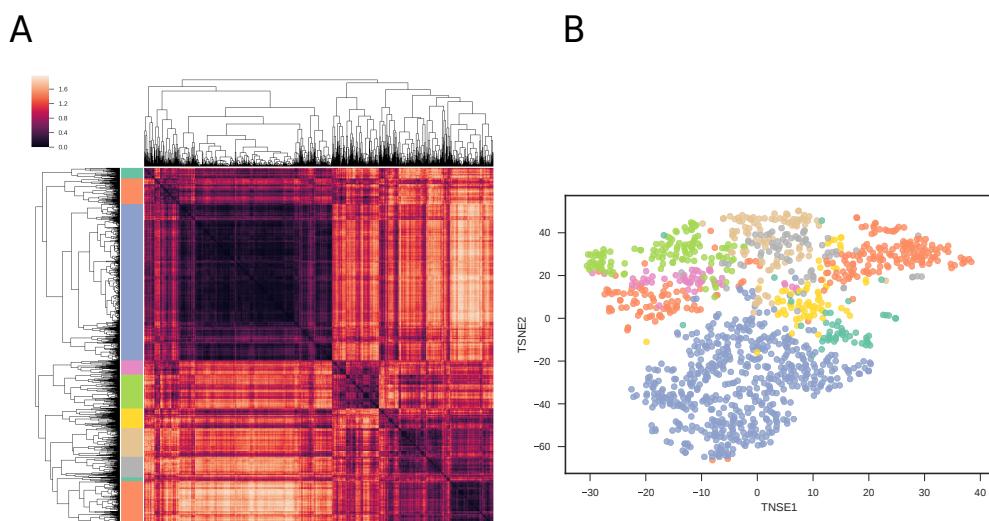


Figure 6.2: Morphological clustering of active compounds within the BioAscent library. **(A)** Hierarchical clustering of the 1244 active BioAscent compounds based on a distance matrix of principal components. Clusters formed by cutting the produced dendrogram. **(B)** Unsupervised t-SNE clustering of active BioAscent compounds based on principal components of morphological features. Points are labels derived from the hierarchical clustering.

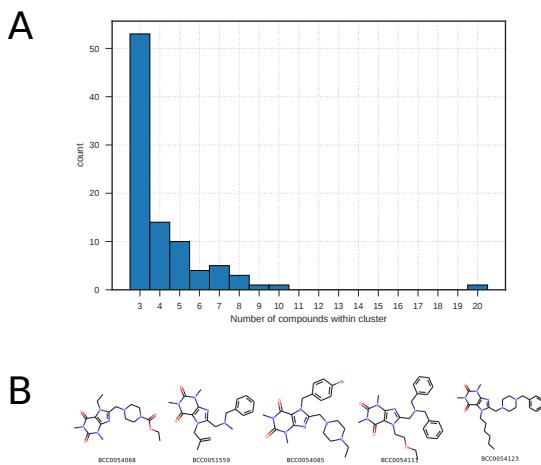


Figure 6.3: (A) Histogram of number of compounds within structurally similar clusters, with most clusters only containing 3 molecules. (B) An example of one of the structurally similar clusters as found with the Butina clustering algorithm.

to produce a distance matrix between all pairs of compound fingerprints, this was then clustered using agglomerative hierarchical clustering. As could be predicted, the heatmaps and dendograms did not reveal any large clusters of structurally similar compounds in the 13,000 compound library. This chemical diversity continued when the compounds were filtered to only contain the phenotypically active molecules. The use of more novel compound fingerprinting techniques such as USRCAT^{usercat} and autoencoded features^{autoencoder} did not increase the degree of clustering.

Rather than looking at large-scale clustering of many thousands of compounds with hierarchical clustering, I tried the Butina clustering method to identify small collections of structurally similar compounds. This method does not return similarity measures, but rather groups compounds into bins of similar compounds⁶⁵. After removing clusters which contained fewer than 3 compounds, this left 96 clusters, with the largest cluster containing 20 compounds and 58% of the clusters containing only 3 compounds (figure ??).

6.2.3 There is little evidence that structurally similar molecules produce similar cellular morphologies

Following the premise of SAR, structurally similar molecules are likely to share the same protein binding site, therefore activating the same or similar signalling pathways and producing similar cellular morphologies. I investigated to what extend structurally similar molecules in the BioAscent library produce similar cellular morphologies, and also how structurally similar are compounds which were shown to produce similar phenotypes. Using the phenotypic clusters as defined in fig.6.2, I compared the structural similarity between compounds within these phenotypic clusters compared to a null distribution of compounds picked at random. I found that compounds within phenotypic clusters were very slightly more structurally similar than compounds picked at random (figure 6.4 A, $p = 1.81 \times 10^{-15}$, $D = 0.011$, 2-sample Kolmogorov-Smirnov test). In addition, I approached the problem from the opposite direction and investigated the phenotypic similarity within

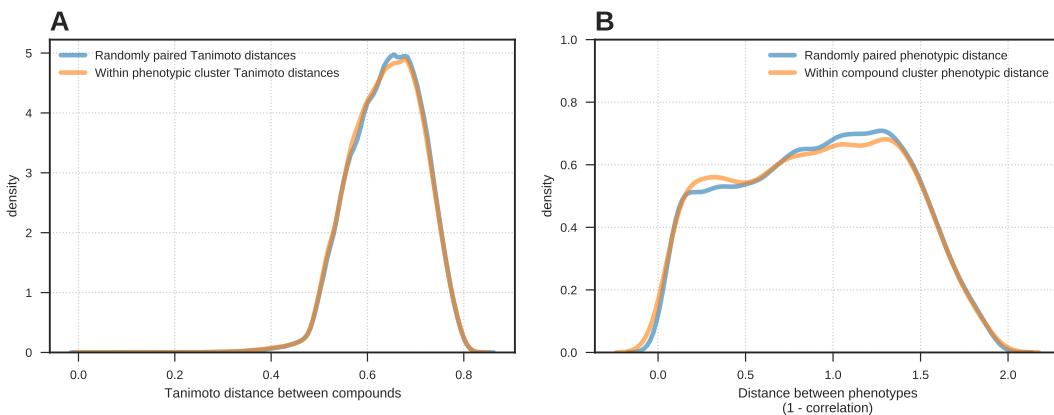


Figure 6.4: (A) Tanimoto distance between compounds from within phenotypic clusters (as found in fig. 6.2) and between randomly paired active compounds. ($p = 1.81 \times 10^{-15}$, $D = 0.011$, 2-sample Kolmogorov-Smirnov test) (B) Phenotypic distance between compounds from within structurally similar clusters and between randomly paired phenotypic profiles. ($p = 0.037$, $D = 0.018$, 2-sample Kolmogorov-Smirnov test)

clusters of structurally similar molecules as found with the Butina clustering algorithm, compared to the phenotypic similarity between compounds picked at random from the pooled compound list of those contained within Butina clusters. I again found that structurally similar molecules are more likely to produce similar cellular morphologies than compounds picked at random (figure 6.4 B, $p = 0.037$, $D = 0.018$, 2-sample Kolmogorov-Smirnov test).

Another approach is to see how well the distance matrix of phenotypic profiles correlates with the distance matrix of chemical structures. Using Mantel's test of correlation between two distance matrices⁶⁶, I found no significant correlation between the phenotypic and structural distance matrices for the active 1244 compound subset ($r = 0.02$, $p = 0.116$).

6.2.4 Identifying the putative MoA of phenotypic hits with ChEMBL structure queries

Another way to utilise the chemical structure data available with the BioAscent library is through querying publicly available databases such as ChEMBL for exact compounds matches or structurally similar compounds. This returns large amounts of data from a variety of assays in which the compound or a structural analogue was screened against such as targets, EC/IC₅₀ values, binding affinities etc. I set about to see if this historical data could be used to suggest putative MoAs of hits from target agnostic phenotypic screening assays.

For this I used the compounds within 10 phenotypic clusters (figure 6.2), and for each cluster queried ChEMBL based on a structure similarity search to identify records for either the query compound, or structural analogues. Then using these compounds identifying which human proteins they have been screened against, and filtering these protein based on EC/IC₅₀ values. This returns a list of Uniprot accession codes which were used with interpro⁶⁷ to test for enrichment compared to a background for each cluster.

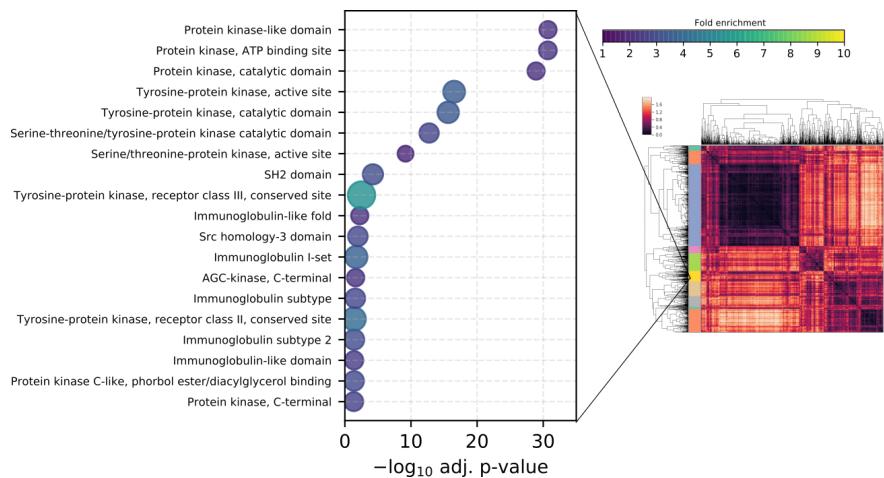


Figure 6.5: Enriched InterPro targets associated with compounds within one phenotypic cluster.

Eight out of the ten phenotypic clusters returned at least one significantly enriched target with fold-enrichment ranging between 1.5 and 10. The most significantly enriched target in 6/8 of the clusters was related to protein kinases, whereas the remaining two were rhodopsin-like GPCRs and adrenergic receptors.

6.2.5 Finding phenotypic hits to target “dark chemical space”

An area of interest in drug discovery is finding new pharmacologically active compounds which occupy new areas of chemical space.⁶⁸ One way to incorporate the phenotypically active hits from the BioAscent library is to query historical screening databases by structural similarity. To do this I took the list of 1244 phenotypically active BioAscent compounds and performed a structural similarity search on the ChEMBL database to look for those BioAscent compounds which have a large Tanimoto distance from all compounds deposited in the database.

From the 1244 active BioAscent compounds 59 (4.7%) were found to have no structurally similar analogues in the ChEMBL database (figure 6.6). To assess if these 59 compounds contained undesirable physiochemical properties which would limit their inclusion in screening libraries explain their absence from historic screening databases I used a quantitative estimate of drug-likeness (QED),⁶⁹ to compare the 59 compounds from ‘dark chemical space’ to the 1244 active BioAscent compounds. The QED metric did not reveal any significant differences in desirable physiochemical properties ($\text{QED}_{\text{dark compounds}} = 0.57$, $\text{QED}_{\text{all active}} = 0.60$, 2 sample t-test $t = 0.85$, $p = 0.39$).

6.3 Discussion and Conclusions

TODO

6.4 Methods

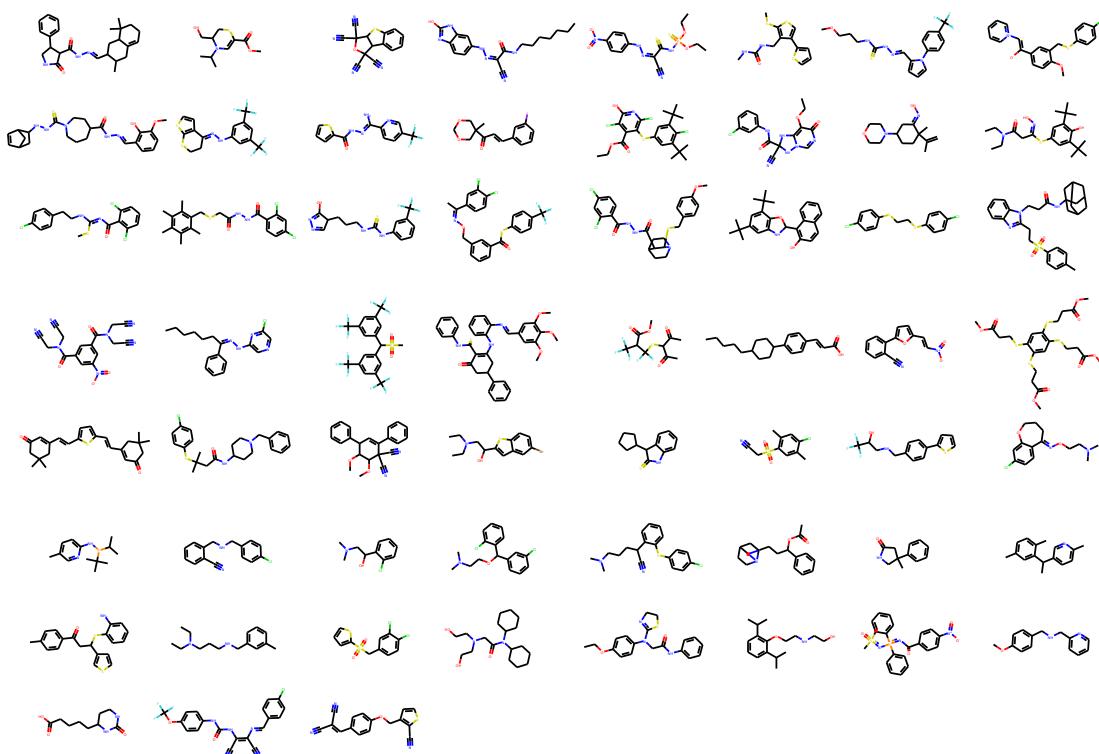


Figure 6.6: BioAscent hits from dark chemical space. 59 phenotypically active BioAscent compounds which had no structurally similar compounds listed in the ChEMBL database as measured.

6.4.1 Chemical similarity

Compound structural information was in the form of .sdf files provided by BioAscent. To create daylight-like compound fingerprints the RDKit library was used to convert .sdf entries into an RDKit's implementation of the daylight fingerprint using the 'rdkit.Chem.Fingerprints.FingerprintMols' function with default parameters.

USRCAT features were generously calculated and supplied by Dr. Steven Shave (Edinburgh).

Latent representations of chemical structure features were calculated using a molecular autoencoder pre-trained on the ChEMBL22 datasetⁱ, based on the work published by Gomez-Bombarelli *et al.*⁷⁰ using one-hot encoded SMILE strings of the molecules.

To compute the distance between RDKit daylight fingerprints the Tanimoto/Jaccard distance was used, in the case of USRCAT and autoencoded features I used the Euclidean distance. Hierarchical clustering was performed on the distance matrix using the complete linkage method and euclidean distance. To define clusters from the calculated dendrogram, a threshold was defined as 70% of the maximum linkage distance which produced 10 clusters. Butina clustering was implemented using RDKit with Tanimoto distances calculated from daylight fingerprints, with a cutoff value of 0.2.

Mantel's test for comparing two distance matrices was implemented with scikit-bio's implementation using Pearson's correlation coefficient and 999 permutations for testing significance. The distance matrices used were standardised Euclidean distance for the morphological profiles and

ⁱwww.github.com/cxhernandez/molencoder

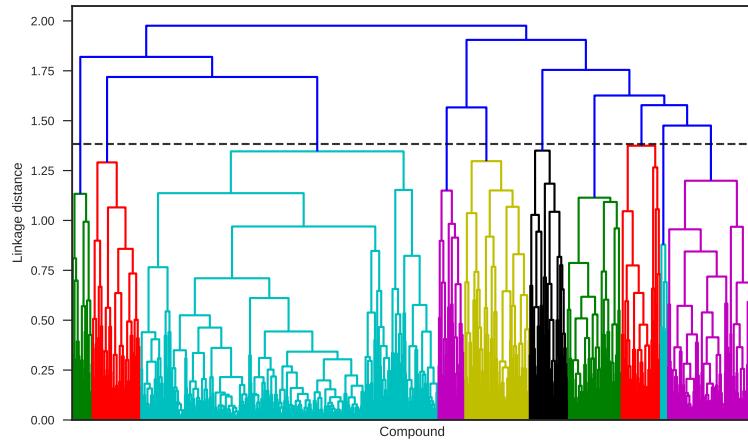


Figure 6.7: Dendrogram thresholding to determine the number of phenotypic clusters in the active BioAscent compounds. Dashed line indicates cutoff of 70% of the maximum linkage distance, resulting in 10 clusters.

standardised Tanimoto distances of the daylight fingerprints for compound structure profiles.

6.4.2 BioAscent library screen

Compound activity window

Data was normalised to plate-based controls and features standardised, then transformed with PCA to the minimum number of principal components which accounted for 80% of the variance in the data. L_1 norm distances were calculated from the DMSO negative control centroid in PCA space. The lower bound of the activity window was defined visually using a plot of ranked L_1 distances. The upper bound was chosen based on images containing at least 10 cells and visual assessment of images produced by higher L_1 distances ensuring images did not consist entirely of dying cell (small, rounded and bright cytoplasmic staining).

6.4.3 Phenotypic similarity

Clustering of morphological profiles was carried out by first calculating a correlation matrix between all pairs of active compound morphologies. Hierarchical clustering was performed on the correlation matrix using the complete linkage method and euclidean distance. To define clusters from the calculated dendrogram, a threshold was defined as 70% of the maximum linkage distance which produced 10 clusters (figure 6.7)

t-SNE clustering was performed using sklearn's 'manifold.TSNE' implementation using the Barnes-Hut approximation with the default parameters.

6.4.4 ChEMBL structure searches

To query the ChEMBL database I used the ChEMBL webresource client ⁱⁱ. In order to identify records for similar compounds I first queried structures based on SMILE strings of the BioAscent compounds with a filter to return only compounds with a Tanimoto distance less than 0.1, recording the similar compounds as ChEMBL identifiers. Then in a second query using the ChEMBL identifiers, I searched for historical screening results against human protein targets and returned a list in the form of Uniprot accession codes. As this returned a list of all protein targets which had been screened against, I filtered this list to protein targets with an assay EC/IC₅₀ value less than 1 μ M. This was repeated for each cluster of BioAscent compounds returning a list of Uniprot accession codes for each cluster.

To search for active compounds in the BioAscent library which are structurally distinct from any compounds in the ChEMBL database I queried the ChEMBL webresource with the 1244 active BioAscent compounds, returning ChEMBL compounds with a similarity of 70% relating to a Tanimoto distance of the daylight fingerprints of within 0.3 (the minimum similarity value allowable with the ChEMBL API). Any BioAscent compound that failed to return any structurally similar ChEMBL record was listed as a ‘dark SMILE’ ⁱⁱⁱ. QED values were computed using RDKit’s Chem.QED.qed function on molecules computed from the supplied .sdf file.

6.4.5 Interpro analysis

Interpro analysis was carried out using DAVID 6.8.⁷¹ DAVID was chosen despite more up-to-date alternatives, as DAVID allows uploading a custom background list. Therefore I created a background list of protein targets by repeating the Uniprot lookup as before but with a list of all 12,000 BioAscent compounds, which was used as a background for each cluster. Significantly enriched interpro targets were selected based on a Benjamini-Hochberg corrected p-value with an α of 0.05.

ⁱⁱhttps://github.com/chembl/chembl_webresource_client

ⁱⁱⁱA thanks to Michał Nowotka from EMBL-EBI for making changes to the ChEMBL servers and API to allow for such time-intensive queries.

7 | DISCUSSION AND CONCLUSION

7.1 Section name

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8 | APPENDIX

Next-generation phenotypic screening

Phenotypic drug discovery (PDD) strategies are defined by screening and selection of hit or lead compounds based on quantifiable phenotypic endpoints without prior knowledge of the drug target. We outline the challenges associated with traditional phenotypic screening strategies and propose solutions and new opportunities to be gained by adopting modern PDD technologies. We highlight both historical and recent examples of approved drugs and new drug candidates discovered by modern phenotypic screening. Finally, we offer a prospective view of a new era of PDD underpinned by a wealth of technology advances in the areas of *in vitro* model development, high-content imaging and image informatics, mechanism-of-action profiling and target deconvolution.

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Background

During the past 5 years, the drug discovery field has witnessed a re-emerging interest in phenotypic drug discovery (PDD) strategies and increased research activity in phenotypic assay development and screening. PDD describes the screening and selection of hit or lead compounds based on quantifiable phenotypic endpoints from cell-based assays or model organisms without prior knowledge of the drug target. The renewed interest in phenotypic screening may be attributed to several factors including: the demand to identify high-value novel drug targets to feed contemporary target-directed drug discovery (TDD) capabilities and commercial drug discovery pipelines; high attrition rates in late stage clinical development and an overall decrease in pharmaceutical R&D productivity, while not directly attributed to limitations of TDD, nevertheless, correlate with the widespread adoption of the TDD operating model in favor of PDD strate-

gies [1–5]; significant duplication of effort and focus upon a relatively small number of well-characterized targets across industrial and academic drug discovery groups; urgent unmet medical need in complex human conditions such as heterogeneous solid cancers and neurodegeneration, where target biology is poorly understood; recent retrospective analysis of all drugs approved by the US FDA since 1999 indicating significant success rates in development of novel, first-in-class, small-molecule drugs by PDD approaches [6–8].

While the three recent retrospective studies of drug approval rates present discrepancies in the number of drug approvals attributed to PDD and TDD strategies, primarily because of differences in terminology, disease area focus and period of analysis, all three studies demonstrate that PDD approaches are providing a significant contribution to clinical approval rates of first-in-class drugs [6–8]. This recent clinical success of PDD is con-

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sidered by many as remarkable given the relatively low investments in PDD in comparison to TDD by translational funding bodies in academia and industry over the past three decades. PDD, however, does not represent a new drug discovery strategy and was indeed the preferred drug discovery approach prior to increased understanding of human disease at the genetic level and the emergence of molecular biology techniques, which advanced elegant molecular pharmacology studies and high-throughput screening of specific targets [2]. Traditional PDD approaches have utilized a variety of biological model systems such as *in vivo* physiological and behavioral models, *ex vivo* tissue-based assays and basic *in vitro* cellular assays to guide drug development. While many drugs successfully used in the clinic today were discovered using such early PDD approaches, traditional PDD methods were laborious and did not provide ample mechanistic information and thus tend to favor the discovery of less selective agents including cytotoxics rather than novel classes of targeted therapies. Given the duration of time between early-stage drug discovery and clinical approval, many of the example first-in-class medicines attributed to PDD described in the three recent retrospective articles [6–8] are somewhat historical. They utilize, by modern standards, rudimentary phenotypic assays, and thus such retrospective analysis may indeed underestimate the true value of modern phenotypic screening strategies, with regard to identifying novel targets and translation into clinical success.

A significant driving force behind the resurgence of PDD may be attributed to substantial technology developments across several inter-related areas, which advance the PDD paradigm. Such advances include more sophisticated cell-based and small model organism-based automated screening platforms [9–11]. Advances in the

development of more complex and more disease-relevant phenotypic assays incorporating: multicellular co-cultures, 3D models, patient-derived primary and Induced Pluripotent Stem Cell (iPSC) models, including gene-edited and isogenic controls, which recapitulate key disease driver mutations, are all well-placed to advance the molecular and pathophysiological relevance of phenotypic screening assays. Improvements in cell-based assay technologies are further complemented by advances in target deconvolution strategies including affinity mass spectrometry, cellular thermal shift assays and cDNA expression microarray technologies among others (Box 1) [12–14]. Also the development of new methodologies, which enable profiling drug mechanism-of-action (MOA) in complex biological samples at genomic, proteomic and phenotypic levels at scale [15–17], supports informed mechanistic classification and triaging of phenotypic hits to assist further target deconvolution or progress preclinical development of phenotypic hits in the absence of target knowledge.

In this article, we attempt to address some common misconceptions and challenges associated with phenotypic screening. We highlight both historical and recent success stories of approved drugs and new drug candidates discovered by PDD. We describe some of the challenges and pitfalls of poorly designed phenotypic screening and target deconvolution strategies and how these may be resolved by the application of new technologies. We place specific emphasis upon the evolution of new gene transcription, pathway profiling and multiparametric high-content screening technologies, which support more advanced phenotypic screening and MOA studies. We provide specific examples and discuss the advantages and limitations of each new approach. Finally, we conclude by discussing how the

Box 1. Target deconvolution methods.

Chemical proteomics

- Affinity chromatography and mass spectrometry [12,18–20]
- Quantitative proteomic and silac labeling [21]
- Thermostability shift assays: *in vitro* and in cells [13,22]

Expression cloning

- Phage display [23]
- Yeast three-hybrid assays [24,25]
- cDNA cell microarray [26]

Genetic-based screens

- Yeast deletion collections [27]
- Haploinsufficiency profiling [28]
- Resistance screens combined with Next-Generation Sequencing (NGS) profiling of resistant clones [29]
- Small model organism knock-out (KO) and genetic mutant collections (under development in Zebrafish, *Caenorhabditis elegans* and *Drosophila*)
- Modifier screens: si/shRNA or CRISPR-Cas9 library screens to identify modulators of small-molecule activity [30,31]
- Activity-based protein profiling [32]

This is a nonexhaustive list of target deconvolution methods and reflects some of the most common approaches selected by the authors.

combination of new technology developments such as more advanced primary and induced pluripotent stem cell (IPSc) culture techniques, gene editing, high-throughput gene transcription, pathway profiling and multiparametric high-content screening technologies are well-placed to advance phenotypic screening toward increased success across multiple disease areas.

Historical examples of drugs discovered by phenotypic screening

Comprehensive discussion of approved drugs originating from PDD strategies have been reviewed previously [6–8,33]. In this article, we highlight specific examples of PDD drugs currently used in the clinics, which challenge conservative views on the necessity for target deconvolution to progress candidate drugs through clinical development. We further describe new lead compounds and candidate drugs discovered by more modern phenotypic screening strategies, which guide chemical design toward specific MOA and which can integrate with ligand-based drug design and TDD strategies to develop highly potent and selective lead compounds and drug candidates.

Metformin (Figure 1, structure 1) belongs to the biguanide class of compounds and represents the first-line standard-of-care therapy for Type 2 diabetes by virtue of its confirmed physiological effects upon decreased glucose production by the liver. Approved in Europe in 1957, metformin has been used for decades as a safe and efficacious medicine to manage the morbidity and mortality associated with Type 2 diabetes and represents a core component of new drug combination therapies for diabetes [34,35]. It is, however, only recently that the MOA by which metformin regulates glucose levels has been revealed. In mouse hepatocytes, metformin leads to the accumulation of AMP and related nucleotides, which inhibit adenylate cyclase, reduces levels of cyclic AMP and PKA activity, abrogates phosphorylation of downstream protein targets of PKA and blocks glucagon-dependent glucose output from hepatocytes [36]. These new insights into metformin MOA will most likely pave the way to development of novel antidiabetic drugs.

Further examples of approved drugs derived from compound library screening in phenotypic models were the molecular target of the drug is not known include, daptomycin (Figure 1, structure 2), a naturally occurring antibiotic targeting cell membrane function of Gram-positive bacteria to treat systemic and life-threatening infections [37]. Pemirolast (Figure 1, structure 3) is an antiallergic drug therapy that is proposed to work through suppression of mast cell degranulation, histamine release and eosinophil activation, although precise target mechanism remains to be confirmed [38]. Rufinamide (Figure 1, structure 4) is a tri-

azole derivative used as an anticonvulsant/antiepileptic medication to treat several seizure disorders including Lennox–Gastaut syndrome [39]. The specific molecular target or targets of rufinamide remain to be established.

These examples, described in Figure 1, serve to highlight that if target deconvolution was always a prerequisite for drug development, valuable treatments for such serious human disorders would not have been developed and would not progress the next generation of therapies for many of the most serious and life-threatening conditions.

Sirolimus also known as rapamycin, (Figure 1, structure 5) is a macrolide derived from the bacterium, *Streptomyces hygroscopicus* and discovered through PDD to possess immunosuppressive, antifungal and anticancer properties [40–42]. The National Cancer Institute (NCI) Developmental Therapeutics Program demonstrated that rapamycin inhibited cell growth in panels of tumor cell lines [43]. Subsequent mechanistic studies indicated that the MOA was mediated through inhibition of a serine/threonine protein kinase critical to cell growth, proliferation and survival, the subsequently named mammalian target of rapamycin (mTOR) [44]. Inhibition is mediated through forming a complex between rapamycin bound FKBP12 with mTORC1 [45]. It is worth noting that while rapamycin has been clinically approved, it violates the Lipinski rule of 5 defining optimal lead and drug like properties and thus may never have been developed through a conventional small molecule drug discovery program. The development of rapamycin through PDD and subsequent understanding of mTOR signaling and the target of rapamycin within preclinical and clinical settings provided important target validation data to support the development of several rapamycin analogs known as rapalogs and second generation ATP-competitive mTOR kinase inhibitors targeting mTOR catalytic activity associated with both mTORC1 and mTORC2 complexes [46,47].

Recent examples of phenotypic screening outcomes

We recently reported application of an iterative process consisting of ligand-based design and phenotypic screening of focused chemical libraries to develop novel antiproliferative inhibitors. The strategy employs promiscuous kinase inhibitors as templates to design high-quality small-molecule collections to facilitate the concurrent search for enhanced physicochemical properties and novel pharmacological features. Using this method, target deconvolution of identified hits and leads is largely simplified (for example, focused kinase screening), thereby assisting subsequent lead optimization campaigns [47]. The application of this strategy resulted in the discovery of the first subnanomolar SRC

inhibitor with 1000-fold selectivity over ABL [48] and highly potent dual mTORC1 and mTORC2 inhibitors (eCF309 – **Figure 2**, structure 6) with high selectivity over other family kinases [47]. A further example of a highly selective kinase inhibitor derived from a phenotypic screen is the allosteric inhibitor of MEK, Trametinib (**Figure 2**, structure 7), which was initially identified by screening for increased mRNA expression of the cyclin-dependent kinase inhibitor p15 and cell proliferation [49].

Modern high-content phenotypic screening assays, which quantify specific functional endpoints, can also be used to identify compounds with precise target MOA such as the identification of novel Eg5 kinesin inhibitors which induce the monopolar and monaster phenotype [50]. Similar approaches were used to discover and confirm the MOA of second generation Eg5 kinesin inhibitors (AZD4877), which have progressed into clinical development (**Figure 2**, structure 8) [51,52]. Olesoxime (**Figure 2**, structure 9) was originally discovered by performing a screen of 40,000 small mol-

ecules in an *in vitro* cell-based assay to identify compounds capable of preventing motor neuron cell death in the absence of trophic support [53].

The historical exemplars of approved drugs discovered by PDD chosen (metformin, daptomycin, pemirolast and rufinamide, **Figure 1**, structures 1–4) highlight that clinically useful and safe medicines can be developed without precise knowledge of the target mechanism. Examples of approved drugs discovered by PDD also serve to highlight that compound structures, which lie out with conventional characteristics of drug likeness can be proved effective in patients (rapamycin, **Figure 1**, structure 5). Further recent examples of approved drugs discovered by phenotypic screening demonstrate that highly selective targeted therapies can be discovered by phenotypic screening. These examples include drugs targeting ubiquitously expressed regulators of critical cellular functions such as protein synthesis (mTOR inhibitors, eCF309, **Figure 2**, structure 6), MAPK/ERK signaling (trametinib, **Figure 2**, structure 7), Eg5 kinesin and mitotic spindle assembly

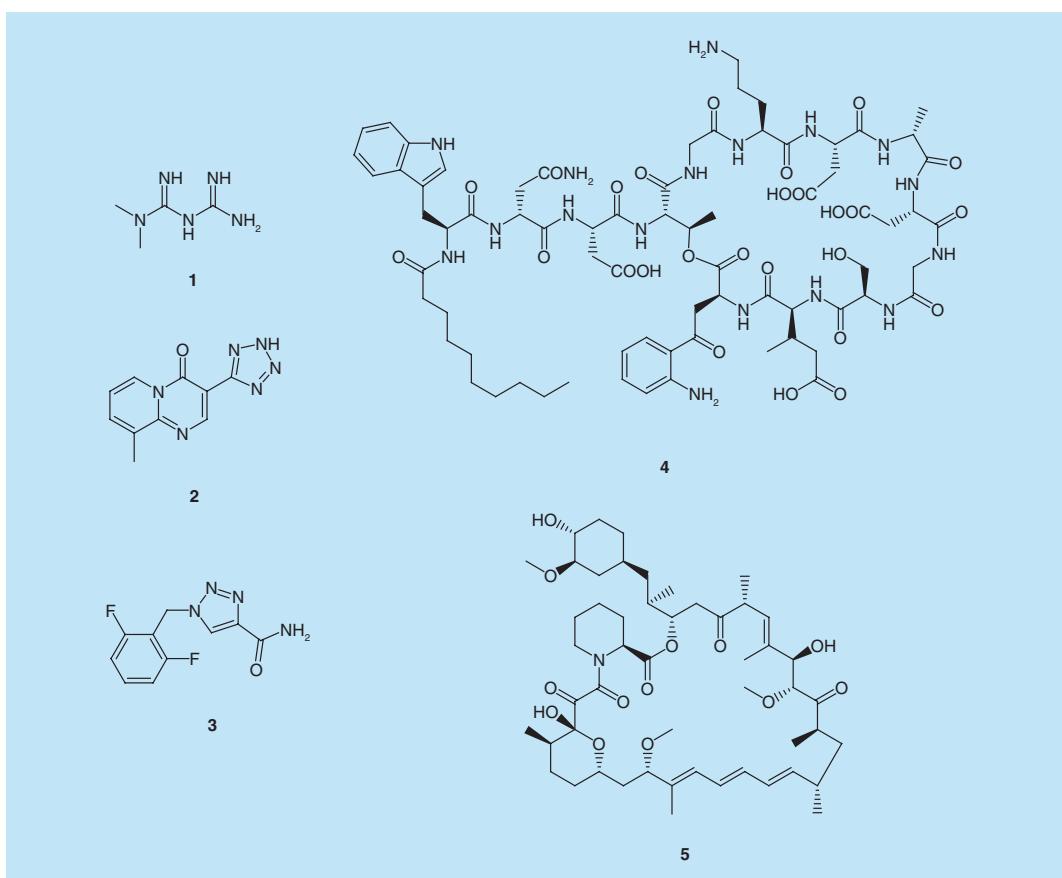


Figure 1. Compound structures of historical examples of drugs discovered by phenotypic drug discovery.
1: Metformin; 2: Daptomycin; 3: Pemirolast; 4: Rufinamide; 5: Rapamycin/sirolimus.

(AZD4877, Figure 2, structure 8) and mitochondrial function (olesoxime, Figure 2, structure 9). Such target classes are unlikely to be prioritized by current drug target review or translational funding committees using conventional target selection criteria to support investment in novel therapeutic targets. Thus, PDD approaches have resulted in the development of many clinically valuable drugs, which would not be developed by TDD programs. The recent examples, which we highlight in Figures 1 and 2 represent a small number of drugs and drug candidates discovered by PDD. For more comprehensive listings of drugs approved by PDD, we direct readers to three recent review articles providing in depth description on the origins of drugs discovered by PDD [6,8,33].

While the overwhelming development of modern targeted therapies has been derived from TDD approaches, these recent examples highlight how advanced phenotypic screening can efficiently direct structure–activity relationships (SAR) and identify novel chemotypes with high potency and selectivity. The above examples further highlight how PDD and TDD approaches complement one another and how new opportunities for combining PDD and TDD strategies are supported by more advanced phenotypic screening, MOA profiling and target deconvolution technologies.

Pitfalls of poorly designed phenotypic screens & black box assays

The phrase ‘phenotypic screening’ is a broadly used term to describe the extraction of quantifiable readouts of biological relevance from any cell-, tissue- or organism-based system suitable for medium- to high-throughput chemical or functional genomic screening in a target agnostic fashion. Phenotypic screens can range from simplistic 2D cell line viability or reporter assays/pathway screens to more complex multicellular, 3D and multiparametric assays. Phenotypic screening is applied in both the industrial and academic research settings to support functional genomic studies, discover novel candidate drugs and/or useful chemical probes and pharmacological tools for further exploring biology. Thus, analysis and debate on success and challenges of phenotypic screening and target deconvolution strategies must be placed into appropriate context of the value and information provided by the primary phenotypic screen. Traditional single endpoint cell viability and reporter-based cellular assays provide limited information of drug MOA and thus limited opportunity to triage and precisely direct further development of phenotypic hits prior to target deconvolution. Such traditional phenotypic assays, which provide limited mechanistic data, so called ‘black box’ assays may

amplify phenotypic screening challenges and common pitfalls such as, preferential selection of cytotoxic compounds, pan-assay interference compounds or PAINS and sharp activity cliffs, which confound SAR studies. Such pitfalls can largely be avoided by development of information-rich phenotypic screening assays such as multicellular co-culture assays to discriminate phenotypic effect between distinct cell types or multiparametric high-content phenotypic profiling assays, which provide more informative insights into cellular pharmacology. Such high-content assays can classify MOA based upon specific cell targeting or by phenotypic fingerprint similarity with compounds of known MOA and target binding [54]. High-content screening in co-culture assays incorporating target and nontarget cell types may help guide hit selection and chemical design away from toxicity toward enhanced efficacy and novel target space within a single primary high-throughput phenotypic screen [55]. While many ‘black box’ phenotypic assays represented the state-of-the-art at the time of their development and have had many notable successes in supporting the development of novel drugs, including many of the examples described in Figures 1 and 2. In contrast to modern high-content phenotypic assays, ‘black box’ assays provide limited opportunity to design screens, which guide selection of hits and leads toward increased therapeutic index and novel phenotypic and target space.

Several review articles, editorials and commentators also suggest that phenotypic screening may help reduce high attrition rates observed during late-stage clinical development specifically the high failure rate observed during Phase II clinical trials resulting from lack of efficacy [4,56,57]. However, the ability of a phenotypic screen to reduce attrition from poor efficacy is directly related to the ability of the primary phenotypic screening assays and any secondary phenotypic assays used for hit selection to predict clinical outcomes. For many complex diseases it is unlikely that the primary screen will recapitulate the full complexity of human disease. Thus, phenotypic screening assays must be developed that ask specific clinical questions or recapitulate key segments of disease pathophysiology to inform subsequent decision-making and effectively guide the next stages of preclinical development and validation. This approach is supported by recent advances in cell-based assay methodology and technologies. Examples in the oncology area include techniques for culturing glioma progenitor cells representing the cancer stem cell niche [58], 3D tumor and fibroblast co-culture organotypic assays, which recapitulate the dense fibrosis and poor drug penetration of poorly vascularized tumors [59] and 3D tumor spheroid cultures, which recapitulate the hypoxic and host cell stromal microenvironment

of many tumors [60]. Screening phenotypic hits across suites of such assays raises the bar with regard to early assessment of the clinical relevance of hit and lead compounds, and also informs subsequent preclinical and clinical development strategies. Ongoing advances in iPSC, gene editing and microfluidic technologies support the development of more physiologically relevant assays across disease areas further advancing more robust approaches to prioritizing phenotypic hits.

Challenges in target deconvolution

An emerging simplistic view of phenotypic screening is that it is an effective strategy for identification of new therapeutic targets from physiological-based models to feed TDD. However, as discussed above, it is unlikely that a primary phenotypic screening assay by itself will predict clinical efficacy and it is also unlikely that initial chemical hits from a large chemical library phenotypic screen will have sufficient potency or selectivity to support rapid and robust target deconvolution. Caution should, therefore, be taken to ensure that poorly designed phenotypic screening and target deconvolution strategies do not create expensive new drug discovery bottlenecks in target deconvolution and further investment of significant chemistry resources on poorly validated targets.

As discussed below, target deconvolution is a challeng-

ing and expensive endeavor with limited success rates, we therefore propose that the pathway from phenotypic screening to target deconvolution should not directly follow one another. Rather phenotypic hits should be carefully triaged through increasingly more complex and disease relevant secondary phenotypic assays to build further confidence in the translational potential of the phenotypic hit. Further panel screening across *in vitro* toxicity assays, physiologically relevant assay formats and phenotypic profiling against reference compound libraries will help select the most novel and desirable compounds for target deconvolution. Further experimental medicine studies, including transcriptomic and proteomic analysis, across genetically defined cell assays to prioritize biomarker and drug combination strategies support subsequent chemical optimization using specific pathway reporter assays, target deconvolution and preclinical development. This more in-depth biological investigation will then shift the PDD bottleneck from target deconvolution toward increased disease relevance, novelty, safety and hopefully improved efficacy and drug discovery productivity.

Target deconvolution

Following careful triaging and selection of high-value lead compounds identified by PDD, a number of dis-

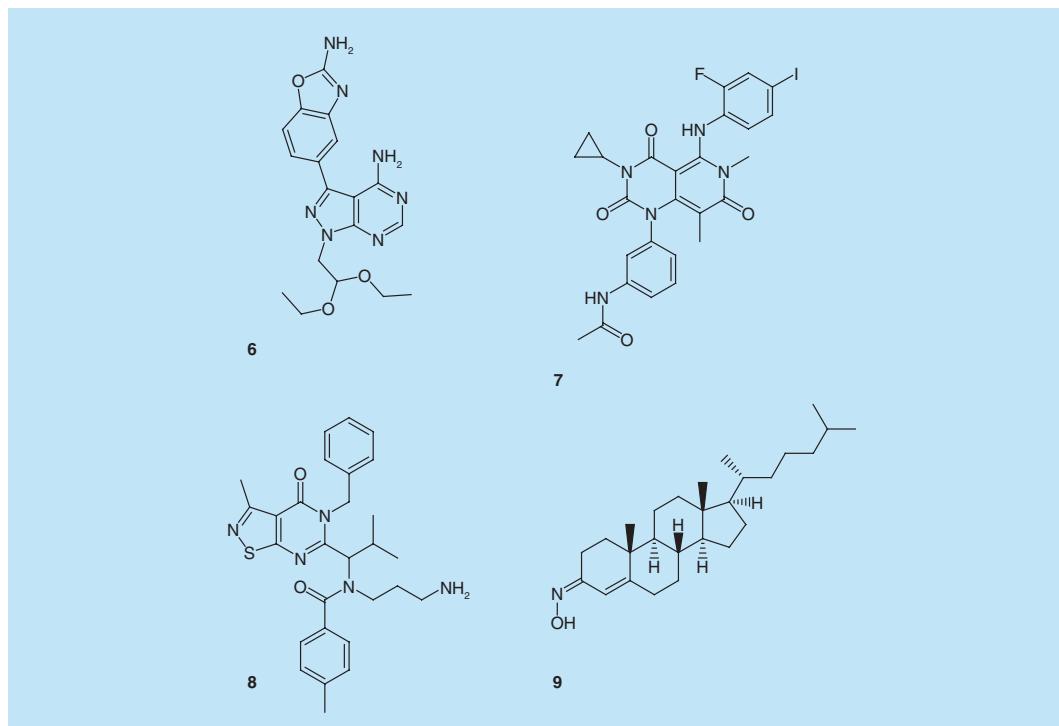


Figure 2. Compound structures from recent examples of phenotypic drug discovery and modern phenotypic screening. 6: eCF309; 7: Trametinib; 8: AZD4877; 9: Olesoxime.

tinct and complementary target deconvolution strategies can be employed (Box 1). Many early target deconvolution studies relied heavily upon affinity-based chemical proteomics approaches which have demonstrated success in identifying targets for a variety of novel inhibitors including hedgehog pathway, bromodomain and N-acetyltransferase inhibitors derived from phenotypic screens [18–20]. However, despite such examples of clear target deconvolution success stories, affinity-based chemical proteomics are often hampered by nonspecific binding of proteins [61–63]. The recent development of publicly available databases characterizing nonspecific protein binding contaminants associated with affinity-based proteomics methods attempts to address the background noise associated with affinity-based proteomics [62]. Competition assays were parent compound is preincubated with cell lysates prior to adding the conjugated affinity capture compound have been developed to determine nonspecific binding to affinity capture reagents and can be combined with databases describing common background contaminant profiles to increase confidence in identifying specific drug-target interactions [61,62]. Such approaches, however, do not completely resolve the issue of nonspecific binding, and affinity-based chemical proteomics is limited to providing lists of potential target binders rather than conclusive evidence of which target is responsible for the phenotypic response, thus further target confirmation studies are required. Several new and complementary target deconvolution strategies are rapidly emerging (Box 1), although no target identification method provides conclusive evidence of which target is responsible for the complete pharmacological profile of a compound. The application of distinct target deconvolution methods (Box 1) combined with other MOA profiling tools may provide strong corroborative evidence to prioritize target hypothesis, which may be responsible for phenotypic response. However, validation of target hypothesis will only be confirmed through further biochemical and cell pharmacology studies. Established and emerging target deconvolution strategies have been reviewed in depth elsewhere [64,65] and so will not be covered in further detail here; however, we do highlight the latest trends in target deconvolution strategies in Box 1.

Mechanism-of-action profiling

A critical success factor in any drug discovery project is the understanding of candidate drug MOA within complex and physiologically relevant biological settings. Several new technologies enable rapid MOA profiling in complex cell models at genetic, proteomic and phenotypic levels at scale. Such higher throughput MOA profiling can facilitate the selection of appropri-

ate phenotypic hits to take forward the further pre-clinical development, identify new assay endpoints and biomarkers to support early hit-to-lead chemical optimization, provide corroborative evidence for target deconvolution studies and support further pre-clinical development and translation toward clinical studies with or without conclusive target identification. Recent advances in MOA profiling technologies include: high-throughput gene transcription profiling, pathway profiling at the post-translational level and high-throughput phenotypic imaging and image informatics [15–17,66]. The latest developments and application of these approaches in PDD are described in further detail in the following sections.

High-throughput gene transcription profiling

Gene transcription-based profiling approaches using whole genome expression arrays provide a comprehensive overview of gene activity in biological samples. Common applications of gene expression arrays include genome-wide differential expression studies, disease classification and drug MOA analysis. The concept of using gene transcription profiling to elucidate drug MOA and deconvolve therapeutic targets was first applied by Hughes *et al.* who created a compendium of 300 yeast deletion strains and associated transcription profiles [27]. By correlating similarity of transcription profiles from drug-treated cells with those derived from each individual yeast deletion they identified the C-8 sterol isomerase, ERG2 as the target for the anesthetic Dyclonine [27]. To progress a more systematic comparative bioinformatics analysis of gene expression profiles, the Connectivity Map concept and public repository of transcription profiles was developed [14]. Connectivity Map combines a catalog of gene expression profiles from large panels of compound perturbed samples with computational and statistical methods to support similarity profiling of gene expression patterns to infer compound MOA [14,67]. As a proof-of-concept study, connectivity map gene expression profiling was applied to identify the MOA of the compound, Gedunin, identified as a hit from a screen for androgen receptor inhibitors. Gene transcription profiles of LNCaP prostate cancer cells treated for 6 h with Gedunin were used to query the Connectivity Map database, which identified high similarity with multiple HSP90 inhibitors; subsequent studies further support Gedunin as an inhibitor of HSP90 function [14]. The Connectivity Map approach has proven particularly useful for discovering the MOA of natural products from traditional remedies. A recent example used Connectivity Map to identify the MOA of Berberine, an isoquinoline alkaloid used in traditional Chinese

herbal medicine and which has demonstrated anticancer properties in phenotypic assays [68]. Transcription profiles of HepG2 cells treated with Berberine for 4 h demonstrated similarity with gene expression profiles of the protein synthesis inhibitor cycloheximide as well as several mTOR and HSP90 inhibitors. Subsequent cellular pharmacology studies demonstrated that Berberine inhibits protein synthesis, Akt activity but not mTOR activity and induces AMPK-mediated endoplasmic reticulum stress and autophagy [68]. Therefore, in this case, the initial application of Connectivity Map and gene transcription similarity profiling identified mechanistically similar compounds with known target activities to guide subsequent studies to further elucidate the MOA of Berberine.

Recent technical advances in gene expression profiling include the development of higher throughput and low-cost gene-expression methods such as the L1000TM platform. L1000TM Expression Profiling is based upon the rapid quantification of a reduced number of landmark transcripts in 384-well plate format and a computational model to infer expression across the genome [15]. The L1000TM technology underpins the Library of Integrated Cellular Signatures (LINCS) NIH program, which funds the generation of perturbed gene expression profiles across multiple cell and perturbation types supporting drug MOA profiling at scale [15,69,70]. While gene transcription profiling has proven effective in elucidation of compound MOA, success is dependent upon the use of appropriate biological assays where the relevant target pathway for any given compound is activated. A further dependency is the cross referencing to a comprehensive and well-annotated reference set of compound signatures also generated under appropriate biological context. An alternative approach to inferring MOA from gene expression signatures is the comparison of drug sensitivity/phenotypic response across large panel of cells with their basal gene expression profiles. A recent study used correlation-based analyses to associate the sensitivity of 481 compounds tested across 860 human cancer cell lines with the basal gene expression profile of each cell line [69]. The study included 115 small molecules of unknown mechanism with the aim of identifying novel targets for these compounds; correlation analysis was focused on single-transcript correlation outliers to prioritize potential target hypothesis [69]. Cancer cell sensitivity to the compounds BRD5468 and ML239 correlated with high expression of the monoglyceride lipase MGLL and the fatty acid desaturase FADS2, respectively [69]. Treatment with the MGLL inhibitor, JZL184 or shRNA knockdown of MGLL attenuated the cytotoxicity of BRD5468 and FADS2 knockdown and cotreatment with the selective FADS2 inhibitor

SC-26196 reduced ML239 cytotoxicity [69]. These studies demonstrate that correlation of drug sensitivity profiles with basal gene expression patterns across large cell panels can reveal specific target hypothesis. An advantage of correlating transcription profiles across large panels of cells is the ability to distinguish between distinct transcript correlations with drug sensitivity from coregulated transcripts thereby prioritizing the most likely targets. However, limitations of this approach include the prerequisite for compounds that display distinct sensitivity across cell panels, which also display differential gene expression patterns and confounding correlation with mechanisms of metabolism or indirect regulators of compound sensitivity. Indeed the analysis by Rees *et al.* demonstrated that for 57% of the compounds tested, no significant correlation with any target could be detected [69]. Despite the recent advances in transcription-based profiling technologies, the costs associated with such analysis limit high-throughput application to larger compound sets and dose-response and temporal studies. Transcription-based profiling may also only reveal the downstream effects of compound exposure rather than the direct therapeutic targets.

Pathway profiling across panels of primary cell-based assays

Profiling compound response at the post-translational pathway level across panels of primary cells and pathway targets has also demonstrated success in determining drug MOA, confirming selectivity, identifying toxicity liabilities and guiding SAR [71]. For example the BioMAP® – Human Primary Cell Phenotypic Profiling Services provided by DiscoverRX consists of panels of primary human cell-based assay systems, a database of reference compound profiles, and computational data mining and analysis tools to support drug MOA analysis [72]. The comparison of BioMAP profiles from testing of two p38MAPK inhibitors, PD169316 and SB203580 revealed activity features unique to SB203580 including inhibition of VCAM-1, E-selectin, IL-8 and P-selectin expression [71]. To further explore the structural determinants of the unique activities of SB203580, the BioMAP profiles of several well-studied p38MAPK inhibitors and SB203580 analogs were generated for comparison. These studies reveal that many of the unique activities of SB203580 represent secondary off-target activities independent of catalytic activity [71]. The BioMAP approach is applicable to large numbers of compounds tested across dose-response and time-series studies supporting precise SAR studies upon pathway responses. While the assays and core pathways tested represent highly sensitive readouts for multiple biological mechanisms,

the biological space covered will not be appropriate for elucidating the MOA of all molecules.

Reverse phase protein microarray

Reverse phase protein microarray (RPPA) represents a highly sensitive and quantitative high-throughput antibody-based proteomics methodology for measuring abundance of multiple proteins and phospho-proteins across large sample sets [73]. Key applications of RPPA include, dynamic pathway profiling at the post-translational network level following chemical or genetic perturbation, screening modulators of key pathway markers and protein biomarker discovery in clinical and preclinical studies [73–75]. Recent advances in RPPA technology include more sophisticated sample handling, quality control, better quality affinity reagents and optical detection, including planar waveguide detection systems providing femtomole to zeptomole sensitivity in protein analyte detection in formats suitable for medium-throughput applications [76]. The development of ultra-sensitive RPPA facilitates large-scale multiplex analysis of multiple post-translational markers across small samples from *in vitro*, preclinical or clinical biopsies. Thus, RPPA technology is particularly suited to proteomic analysis of miniaturized assay formats of a few thousand cells from an individual well of a microtiter plate and microfluidic devices. Similar to the BioMAP and gene-expression approaches, multiple pathways can be monitored across large sets of assay panels and RPPA profiles compared with reference compound can help predict MOA and triage common/nonnovel pathway inhibitors or highly promiscuous pathway inhibitors with toxic liabilities. Retrospective analysis of esophageal adenocarcinoma patients who were also under treatment with metformin (Figure 1, structure 1) for diabetes demonstrated a better response to chemoradiation therapy compared with patients who were not receiving metformin [77]. However, the MOA of metformin in esophageal cancer was unknown. RPPA analysis applied to esophageal cancer cells treated with metformin revealed inhibition of PI3K/mTOR signaling pathway, which correlated with reduced cell growth and increased apoptosis [78]. In a similar approach, a Danish study comparing recurrence rates for breast cancer between Simvastatin users and nonusers demonstrated a significant reduction in recurrence rates in the statin users [79]. RPPA analysis of triple-negative breast cancer cell lines following Simvastatin treatment demonstrated decreased phosphorylation of FOXO3a. Subsequent knockdown of FOXO3a attenuated the effect of Simvastatin on mammosphere formation and migration [80]. Corilagin has recently been identified as a major active component in a well-known herbal medicine (*Phyllanthus niruri L.*) with antitumor activity although the antitumor mechanism

has not been clearly defined. RPPA analysis of a panel of ovarian cancer cell lines treated with Corilagin demonstrated inhibited activation of canonical Smad and non-canonical ERK/AKT pathways, which correlated with inhibition of TGF- β secretion and TGF- β pathway activation [81]. Similar to correlation of drug sensitivity across cell panels with basal gene expression profiles, drug sensitivity across cell panels have also been correlated with basal protein levels and pathway activation states by RPPA to identify both MOA and mechanism-of-resistance [82,83]. Correlation of sensitivity of a panel of small-cell lung cancer lines treated with the PARP inhibitor BMN 673 with RPPA analysis indicated the compound sensitivity is associated with elevated baseline expression levels of several DNA repair proteins [83]. This study identified a novel 'DNA repair score' consisting of a group of 17 DNA repair proteins, which predict sensitivity to BMN 673 [83]. Small-cell lung cancer insensitivity or resistance to BMN 673 correlated with baseline activation of the PI3K/mTOR pathway identifying a potential drug combination hypothesis [83]. While the majority of exemplar studies describing RPPA applications in drug MOA analysis have been applied to late-stage drug candidates or approved drugs, many of which have come from target-directed drug discovery, the success of this approach indicates that it will also be a useful method for uncovering the MOA of hits and lead compounds derived from phenotypic screens. A significant advantage of antibody-based proteomic profiling approaches is that they can help identify translatable pharmacodynamic or predictive biomarker reagents to guide appropriate preclinical proof-of-concept studies and clinical development strategies of drug candidates with or without conclusive target deconvolution.

High-content image-based multiparametric phenotypic profiling

Advances in automated microscopic image acquisition and image analysis tools enable the extraction of functional phenotypic endpoints from complex assay formats including 3D and co-culture models. Integration of high-throughput imaging assays with new image informatics resources enable high-throughput phenotypic profiling and classification of MOA across multiple assays, dose-response and time-series studies. We outline below the development in high-content imaging and image informatics methods and the new opportunities they present to phenotypic screening.

Evolution of high-content imaging & image informatics methods applicable to phenotypic screening

The rapid development of automated microscope platforms has enabled the ability to generate tens of thou-

sands of images a day on a single platform supporting medium- and high-throughput image-based phenotypic screening. With image analysis software capable of extracting several hundred measurements per cell from these images, researchers can detect and quantify subtle phenotypic changes that would otherwise be missed with the naked eye or from a single endpoint assay. These developments have stimulated a new field of biological profiling in cell-based assay systems called high-content analysis [9,84]. However, due to the high-dimensional nature of the high-content datasets, tried-and-tested methods to determine hits and guide SAR developed in TDD are no longer applicable. This means new methods for hit selection and triaging are required, and with the parallel developments in machine learning and other quantitative fields there are many options open to researchers.

Image-based phenotypic measurements can be recorded on two levels: an average of whole-well/-cell population measurements or individual cell measurements. Whole-well measurements are less computationally intensive and easier to obtain and can prove useful when individual cell segmentation is not feasible. Measurements taken from individual cells can be much more detailed, such as individual cell areas or number of organelles per cell. However, individual cell measurements generate large datasets that can become unwieldy and difficult to analyze without significant computing power and data handling pipelines. Therefore, many image-based phenotypic assays use well or population averages of data obtained from individual cell measurements, describing the mean or median cell within each image. While this reduces the amount of data, and allows for more simple analyses, calculating a population average removes any information about heterogeneity or possible phenotypic subpopulations. In instances of two equal sized subpopulations, a well average phenotypic measurement may be a representative of few cells within that image and thus does not accurately record phenotypic response across the cell population. A method to quantify cellular heterogeneity within cell populations has recently been suggested based on three simple statistic procedures: percentage of outliers; the Kolmogorov–Smirnov (KS) test of normality; and quadratic entropy. This method can then be used to classify a cellular population according to the type of heterogeneity observed [85].

The development of such cellular subpopulation analysis methods is important as the origins behind heterogeneity within clonal populations are not well-understood and the diverse response to therapeutics can be a driver underlying clonal selection, a well-known contributor to the evasion of anticancer therapeutics observed in many tumors. New methods calculating

heterogeneity and the impact of pharmacological intervention upon heterogeneous cell populations are thus especially relevant to anticipating therapeutic response and monitoring evolution of the disease in response to treatment within complex tumor microenvironments. Several studies have also reported that the expression of specific transcription factors associated with stem cell pluripotency are expressed in a heterogeneous fashion in embryonic stem cell cultures. For example, approximately 80% of embryonic stem cells express Nanog, while 10–20% do not [86]. Stem cell heterogeneity and conversion between distinct pluripotent or differentiated stem cell fates also impact upon therapeutic areas dependent upon endogenous stem cell differentiation and reprogramming such as tissue regeneration and repair. The evolution of image-based methods monitoring cell heterogeneity and classification of subpopulation responses at the single-cell level support the development of more complex and clinically relevant heterogeneous and multicellular models for automated cell-based screening. However, the challenge remains in how to distill such complex multiparametric data to enable key decision-making. Advances in the fields of multivariate statistics and machine learning offer potential solutions.

Development of multivariate high-content methods to predict compound MOA

In 2004, Perlman *et al.* published a landmark paper describing the use of compound ‘fingerprints’ derived from phenotypic measurements. It was shown that compounds with known similar MOA exhibited similar phenotypic fingerprints [17] and this could be used to predict the MOA of unknown compounds by their similarity to that of known compounds. In order to create the compound fingerprints a modified KS test was developed to compare the distribution of every measurement against the same measurement for the negative control, producing a list of numbers for each compound [87]. These vectors were aligned to other compound vectors in order to maximize correlation to account for differences in potency across ranges of concentrations. The pairwise Euclidean distance was calculated to create a similarity matrix between all the tested compounds; following hierarchical clustering, compounds with similar MOA were found closely aligned to one another. This was the first published demonstration that image-based phenotypic information proved descriptive enough to discern compounds from one another [17]. Further development on multiparametric phenotypic assays combined with different compound profiling methods utilizing multivariate statistics, machine learning and artificial neural networks have steadily evolved [88–92]. In a recent study, 2725

compounds were profiled in a multiparametric high-content assay measuring phenotypic effects upon the nucleus, cytoplasm, endoplasmic reticulum, golgi and cytoskeleton of the U2OS osteosarcoma cell line [54]. The high-content phenotypic fingerprints subsequently generated were used to cluster mechanistically similar compounds using the Markov Clustering Algorithm and then each compound cluster was analyzed for enrichment of individual targets and gene sets to facilitate MOA analysis [54]. Individual target annotations for compounds were obtained from public and commercial drug target databases such as, ChEMBL, Drugbank, GVK (GOSTAR), Integrity and Metabase. Gene set enrichments were obtained from the following databases: Biosystems, Metabase, Integrity, Metabase pathway-derived gene sets (Metabase noodles) and Gene Go Ontologies [54]. Two compounds, 6-[6-(diethylaminopyridin-3-yl)-N-[4-(4-morpholinyl)phenyl]-9H-purin-2-amine and Silmitasertib clustered with each other and a collection of other compounds inducing similar phenotypic response. In contrast to the majority of compounds in this cluster, which were associated with gene sets enriched in PI3K/Akt/mTOR, the previously described Jak3 inhibitor, 6-[6-(diethylaminopyridin-3-yl)-N-[4-(4-morpholinyl)phenyl]-9H-purin-2-amine and the Casein kinase II inhibitor, Silmitasertib had not previously been associated with direct inhibition of PI3K/AKT/mTOR pathway targets. Subsequent biochemical analysis revealed 6-[6-(diethylaminopyridin-3-yl)-N-[4-(4-morpholinyl)phenyl]-9H-purin-2-amine inhibited 3-phosphoinositide-dependent protein kinase 1 (PDPK1), a component of PI3K/AKT/mTOR signaling and Silmitasertib inhibited mTOR and PI3K- α with IC₅₀ of 390 nM and 461 nM, respectively [54]. These studies demonstrate that novel compound–target associations can be identified from image-based multiparametric high-content profiling. In contrast to transcription or post-translational pathway profiling methods (BioMAP and RPPA) previously discussed, multiparametric high-content profiling assays can run in high-throughput across arrayed whole genome screens, large chemical libraries and compound profiling studies incorporating dose response and time series if necessary.

Integrating phenotypes & SAR to predict MOA

The study of SAR by the generation and screening of compounds with similar chemical structures, is one of the fundamental methods used by medicinal chemists to determine which structural motifs are required for inducing a biological effect on a particular protein, cell or organism. In principle, compounds with analogous chemical structures often bind to the same or similar

protein targets, a principle that is used to develop derivatives with improved drug metabolism and pharmacokinetic (DMPK) properties, and as Perlman *et al.* demonstrated, compounds with similar MOA produce similar phenotypes. Young *et al.* then filled the gap in this reasoning by investigating if compounds with comparable chemical structures produce similar phenotypes [87]. They screened HeLa cells with a small molecule compound library and performed factor analysis on 36 features to produce a fingerprint for each compound, with which a pair-wise similarity matrix was created by the cosine distance between phenotypic fingerprints. In order to determine the similarity between chemical structures, they defined the molecular structure through radial atom neighbors and a structure similarity matrix was constructed through Tanimoto distances between the compounds. The two similarity matrices, one for phenotype and one for chemical structure, were clustered by phenotypic similarity, which revealed distinct phenotypic clusters that matched up to distinct groups of structurally similar compounds [87]. Performing SAR studies in cell-based phenotypic assays is significantly challenged by the fact that effects of compound modulation upon phenotypic activity are multifactorial, influenced not only by target engagement, but also cellular permeability (cLogP/D-mediated), subcellular distribution, cell transport mechanisms, membrane interactions and off-target activities. These issues increase the likelihood of obtaining sharp activity cliffs, which hinder directional SAR studies contributing to more complex and lengthy medicinal chemistry programs. In the study by Young *et al.*, it was found that small changes in chemical structure were associated with large phenotypic differences indicating that sharp chemical activity cliffs are retained in information-rich high-content screening data [87]. Further biological investigation into the distinct multiparametric profiles obtained between chemically similar analogs may reveal the underlying causes of activity cliffs. For example, multiparametric high-content analysis can help diagnose if loss of activity is a consequence of reduced potency on a specific target mechanism, impaired distribution and influence within specific subcellular compartments or completely distinct MOA indicative of new off-target activities. Thus, high-content analysis supports a more in-depth cellular pharmacology approach to guiding subsequent chemical library design from initial phenotypic hits.

High-content imaging quality control/assay standards

To gain meaningful results from any screen, including phenotypic-guided SAR, assay quality control is critical. For many, the lack of reliable metrics to determine assay robustness, such as the z-factor in high-throughput

biochemical screens [93] is a deterrent for widespread adoption of multiparametric high-content methods in industrial drug discovery. Despite criticism of the inappropriate use of the z-factor in high-content studies by many groups, there is still not a universally accepted replacement. Any metric suggested has to address three primary concerns: ability to work with multivariate data; assay independence; and ease of implementation and interpretation. Many attempts to develop such a method have used the z-factor as their basis [94,95], although none have addressed all the issues or gained widespread adoption. The same principles apply for identifying phenotypic endpoints to guide SAR. Feature extraction and selection methods can reduce the data to a single value analogous to an IC_{50} to guide chemical design toward specific areas of phenotypic space. Successful implement of such phenotypic-guided SAR is, however, critically dependent upon reproducible assay formats, appropriate feature extraction and selection methods and deep biological insight to ensure phenotypic features guide chemical design toward desired outcomes. The use of open datasets, such as the Broad Bioimage Benchmark Collection [96,97] enables researchers to compare image analysis and informatics methods on a common collection of annotated images, allowing iterative improvement of methods through collaboration and the replication of results. Further collaborative initiatives to develop common standards for HCS and image analysis methods

will promote further adoption and stimulate cross-collaboration between both academic and industrial groups to advance the field of high-content image-based phenotypic screening and profiling.

Conclusion

To date, the majority of phenotypic screening assays that have been implemented in chemical or si/shRNA library screening campaigns and examples of compounds and drugs developed through PDD strategies have used simple biological models and assay readouts. Historical success of PDD combined with acceptance of a significant contribution to recent drug approvals has stimulated renewed interest in PDD strategies. In this article, we describe limitations of traditional PDD approaches and highlight solutions and new opportunities for PDD presented by recent advances in assay development and image-based screening technology. With new advances in precise gene editing technologies such as CRISPR-cas9, primary patient-derived cell culture, iPSC differentiation combined with multiparametric high-content phenotypic profiling, all advance the applications of phenotypic screening under more relevant and well-defined biological contexts. We propose that further development and adoption of new phenotypic assay technologies are well-placed to advance a new era of next-generation phenotypic screening contributing to both PDD and TDD success rates.

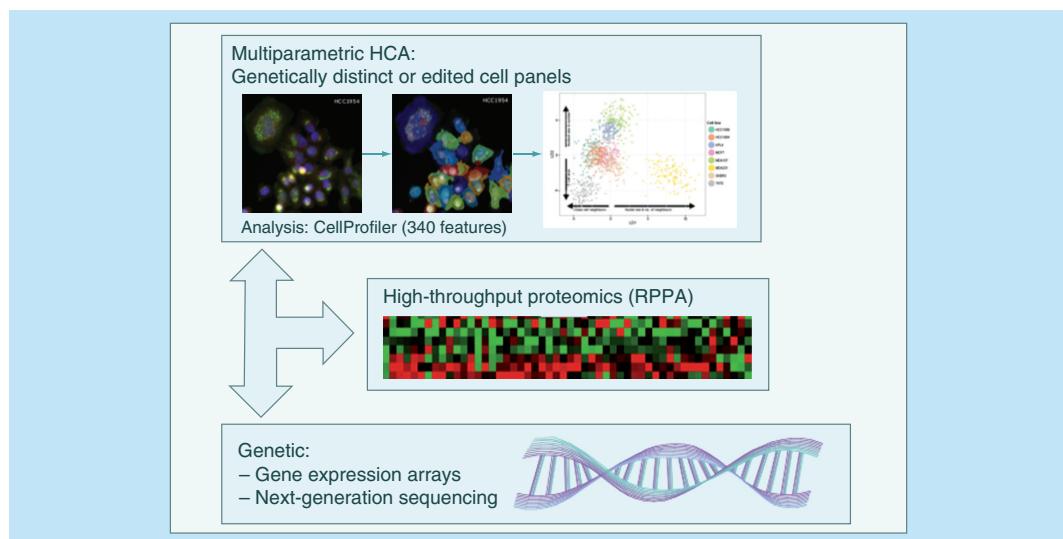


Figure 3. Integration of high-content multiparametric phenotypic profiles with proteomic and genetic datasets. Representative displays of multiparametric cell morphometry analysis using optimized cell staining and CellProfiler image-analysis protocols followed by correlation of distinct drug-induced phenotypes between cells with molecular data at post-translational and genetic levels. Application of these methods support understanding of drug mechanism of action; identification of resistance mechanisms/pathways to guide biomarker discovery; novel drug combination hypotheses and high-throughput pharmacogenomics incorporating more complex phenotypes across disease areas and across advanced multicellular or 3D models.
RPPA: Reverse phase protein microarray.

Future perspective

Despite over 10 years of research carried out with high-content phenotypic screening, the majority of studies have focused their efforts on a small selection of established cell lines, picked primarily due to amenable cell culture propagation and imaging properties rather than relevance to human disease. The reasons behind this are understandable, as cost and speed represent important criteria in medium- to high-throughput screening projects. Thus, selection of cell lines, which can be rapidly bulked up and accurately and reliably segmented into 2D cell culture assays using readily available image analysis methods, are attractive. An important advantage of image-based high-content screening over other screening platforms is the ability to extract functional endpoints from more complex *in vitro* assays, which extend beyond simple 2D cultures and may include 3D multicellular tissue models and small model organism screens, which exploit more complex biology. The development and adoption of more complex *in vitro* assays may benefit PDD in several ways:

- Application of assays which more accurately represent disease pathophysiology thus contributing to improved translation and clinical success rates;
- Identify novel target space including unbiased identification of novel target classes, which are not currently being pursued by drug discovery groups;
- Identify targets with more relevant functional validation, increasing confidence in target hypothesis to justify subsequent TDD investments;
- Recapitulate intact autocrine, paracrine and juxtacrine pathway signaling networks supporting discovery and development of novel multitargeted therapies and combination approaches.

The primary goal of PDD is to identify small molecules that beneficially modify a disease-associated phenotype, selecting a single cell line to model the disease can, however, prove risky. As demonstrated in cystic fibrosis disease models, there is little overlap between compounds that show efficacy in correcting the CFTR trafficking defect when the mutant CFTR protein is expressed across multiple cell lines [98]. This should lead us to question how well we place our trust in conclusions drawn from an experiment modeled in a single cell line. Application of high-content screening across genetically distinct primary cells or precise CRISPR-cas9 gene-edited cell panels can help elucidation of drug MOA by linking phenotype to genotype and also stimulate biomarker and drug combinations studies (Figure 3) [69,99].

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Executive summary

Background

Historical examples of drugs discovered by phenotypic screening

- Approved drugs with unknown target mechanism.
- Recent examples of modern phenotypic screening outcomes, including development of highly potent and selective targeted agents.
- Pitfalls of poorly designed phenotypic screens/black-box assays.
- Challenges in target deconvolution.
- New approaches in target deconvolution.
- New approaches in mechanism-of-action determination (genomic profiling, proteomics and high-content analysis).

Evolution of high-content imaging & image informatics methods applicable to phenotypic screening

- Early multiparametric high-content methods for compound classification.
- More advanced image analysis and image informatics, including integration of multiparametric phenotypic fingerprints with chemical similarity.
- Current limitations in high-content analysis and high-throughput image informatics.

Future perspective

- New disease models, incorporating 3D assays, induced pluripotent stem cell and gene editing technologies.
- New opportunities for application of phenotypic screening across genetically distinct/gene-edited cell panels linking phenotype to genotype to support high-throughput genomics and personalized healthcare strategies in new disease areas.

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Development of the Theta Comparative Cell Scoring Method to Quantify Diverse Phenotypic Responses Between Distinct Cell Types

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ABSTRACT

*In this article, we have developed novel data visualization tools and a Theta comparative cell scoring (TCCS) method, which supports high-throughput *in vitro* pharmacogenomic studies across diverse cellular phenotypes measured by multiparametric high-content analysis. The TCCS method provides a univariate descriptor of divergent compound-induced phenotypic responses between distinct cell types, which can be used for correlation with genetic, epigenetic, and proteomic datasets to support the identification of biomarkers and further elucidate drug mechanism-of-action. Application of these methods to compound profiling across high-content assays incorporating well-characterized cells representing known molecular subtypes of disease supports the development of personalized healthcare strategies without prior knowledge of a drug target. We present proof-of-principle data quantifying distinct phenotypic response between eight breast cancer cells representing four disease subclasses. Application of the TCCS method together with new advances in next-generation sequencing, induced pluripotent stem cell technology, gene editing, and high-content phenotypic screening are well placed to advance the identification of predictive biomarkers and personalized medicine approaches across a broader range of disease types and therapeutic classes.*

INTRODUCTION

The treatment of complex disease in human populations is often confounded by the broad heterogeneity in the mechanisms responsible for the generation and evolution of disease-affected cells. Within an individual patient and between genetically distinct patients, such heterogeneity in disease mechanisms contributes to poor drug responses and relapses observed in the clinic.^{1,2} Sequencing of

the human genome and advances in characterizing patient disease at genetic and proteomic levels support the personalized medicine concept of treating each individual patient with the most appropriate therapy for their disease.^{3,4}

Key to the personalized medicine approach is the identification of biomarkers, which can be readily measured in patient samples to predict drug response. Many such biomarkers, for example, BRAF V600E (Melanoma/Colorectal Cancer); EGFR (Non-small cell lung carcinoma); and HER-2 (Breast Cancer), are associated with monitoring activation state and mutation status of known drug targets to predict response to therapy.^{5–7} Thus, the personalized medicine approach is well suited to target-directed drug discovery strategies where target pathways are clearly defined. However, such target-directed personalized medicine strategies are unsuitable for many complex diseases and drugs discovered by phenotypic drug discovery, where they are not defined by a single target or the mechanism-of-action and therapeutic targets remain to be fully elucidated.^{8,9} Thus, more unbiased approaches to the identification of biomarkers, including genetic or pathway signatures, which predict drug response are required to expand the personalized medicine concept across complex disease types and therapeutic classes.

Comparative analysis of well-characterized panels of human cell lines derived from distinct individuals has many applications in basic research, drug discovery, and personalized medicine. Genomic and transcriptional profiling of cancer cell line panels, such as the National Cancer Institute 60 human tumor cell line drug screen collection, provide a genetic context to comparison of cell function and drug sensitivity, supporting biomarker discovery and drug mechanism-of-action analysis.¹⁰

High-throughput *in vitro* pharmacogenomic studies across larger cancer cell line panels have been established and provide valuable resources, such as the Cancer Cell Line Encyclopedia (CCLE) from the Broad Institute www.broadinstitute.org/ccle/home and the Catalogue of Somatic Mutation in Cancer Cell Lines project from the Sanger Institute http://cancer.sanger.ac.uk/cell_lines, which facilitate

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pharmacogenomic analysis. Such drug sensitivity profiling across genetically defined cell panels is now routinely implemented in academia and industry to identify biomarkers of response to support disease positioning and patient stratification strategies, or to further understand drug mechanism-of-action at genetic and proteomic levels.^{11,12}

To our knowledge, all examples of *in vitro* high-throughput pharmacogenomic studies carried out to date utilize either a concentration of a drug that gives half-maximal response (EC_{50}) or concentration of a drug that gives half-maximal inhibition of cell proliferation (GI_{50}) value obtained by standard cell viability assays as the primary phenotypic endpoint for correlating drug sensitivity with genomic or transcriptomic datasets. While the GI_{50} and EC_{50} measurements of cell viability provide the necessary univariate value for quantifying drug sensitivity across a panel of cell lines, this method has several limitations.

Accurate measurement of EC_{50} or GI_{50} values is dependent upon obtaining full sigmoidal dose-response curves for each drug or compound tested in the assay. Dose-response curves and thus the EC_{50}/GI_{50} calculations are prone to fluctuation dependent upon assay conditions, including cell culture media, atmospheric conditions, cell line health and cell line batch variation, and the type of viability assay reagents used. Indeed, comparative analysis of large pharmacogenomic studies published by the Broad and Sanger institutes have resulted in reports of inconsistency between the genetic signatures of drug sensitivity assigned to drugs shared between both studies.^{13,14} Cell viability assays and EC_{50}/GI_{50} values are also not suitable for the majority of disease models, which are not defined by a single viability endpoint, or for quantifying drug response in more complex and physiologically relevant cell assays such as three-dimensional (3D) coculture models.

High-content imaging enables the quantification of multiple phenotypic cellular endpoints with high spatial and temporal resolution supporting drug sensitivity testing across more complex *in vitro* assays including 3D and coculture models.¹⁵ Image-based phenotypic profiling combined with multiparametric analysis methods allows detailed characterization of drug mechanism-of-action and classification of phenotypic response, including identification of novel compound target associations based upon similarity of multiparametric phenotypic fingerprints with annotated reference compound sets.^{16–22}

The application of multiparametric biological profiling of compound libraries, by image-informatics and biospectra analysis methods, supports unbiased approaches to mechanism-of-action classification and identification of structure-activity relationships independent of target hypothesis.^{23–25} While multiparametric methods incorporating machine learning and artificial neural networks have steadily evolved to support phenotypic profiling across

several cell types,^{18,20,26} there are few studies that perform comparative multiparametric phenotypic analysis between distinct cell types in drug discovery. Thus, despite over 15 years of continued development in the high-content screening field, there are few reports of pharmacogenomic studies performed across the diversity of complex phenotypes that can be measured by multiparametric high-content analysis approaches. A number of challenges that must be overcome to apply high-content phenotypic profiling to pharmacogenomic or pharmacoproteomic strategies include the following: defining relevant phenotypic endpoints, which appropriately quantify drug sensitivity; quantifying diverse phenotypic response across a dose response; visualizing multiple diverse phenotypes elicited across dose response and distinct cell panels; and reducing multiparametric high-content analysis of cell phenotype to a robust univariate metric for correlating drug sensitivity with genomic or proteomic datasets.

The goals of this study were to develop a robust and scalable method for quantifying diverse multiparametric high-content phenotypes and distinct compound-induced phenotypic response across a panel of cell lines. We describe the optimization of a high-content cell-painting assay to enable analysis of a broad range of cell phenotypes across a panel of clinically relevant breast cancer subtypes. We present new methods for normalizing and displaying distinct and dose-dependent multiparametric high-content phenotypic response across multiple cell types. We introduce the development and application of the “Theta Comparative Cell Scoring” (TCCS) method for calculating distinct phenotypic response between cell types. We describe the broad utility of the TCCS method in providing a univariate metric for quantifying distinct phenotypic response between compounds tested in the same cell and for compounds tested across multiple cell types. We make available the source code to enable application of TCCS across large high-content datasets. We present proof-of-principle data from a small compound screen performed on a panel of eight breast cancer cells representing four well-characterized and clinically relevant subtypes. We demonstrate the ability of our TCCS method to cluster cell types, which have similar or distinct phenotypic response to individual compounds, to guide patient stratification hypothesis and facilitate pharmacogenomic or proteomic studies. We discuss the potential impact of this approach upon extending the application of *in vitro* pharmacogenomic and personalized medicine strategies across a wider range of disease areas and therapeutic classes.

MATERIALS AND METHODS

Cell Culture

Eight breast cancer cell lines were selected for their stratification of four well-characterized breast cancer clinical

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Table 1. Panel of Breast Cancer Cell Lines

Cell Line	Subclass	Mutation Status	
		PTEN ^a	PI3K ^b
MCF7	ER ^c	WT ^d	E545K
T47D	ER	WT	H1047R
MDA-MB-231	TN ^e	WT	WT
MDA-MB-157	TN	WT	WT
HCC1569	HER2 ^f	WT	WT
SKBR3	HER2	WT	WT
HCC1954	HER2	?	H1047R
KPL4	HER2	?	H1047R

^aPhosphatase and tensin homolog.

^bPhosphoinositide-3-kinase.

^cEstrogen receptor.

^dWild type.

^eTriple negative.

^fHuman epidermal growth factor receptor 2.

^gLack of consensus regarding the mutational status of those cell lines.

ER, estrogen receptor; HER2, human epidermal growth factor; PI3K, phosphoinositide 3-kinase; PTEN, phosphatase and tensin homolog; TN, triple negative; WT, wild type.

Imaging

We adapted the cell painting protocol from Gustafsdottir *et al.*²⁷ to optimize the cell staining across the eight selected breast cancer cell lines. Specific modifications to the original protocol by Gustafsdottir *et al.*²⁷ were implemented to circumvent morphological changes induced upon the MDA-MB-231 cell line, which was particularly sensitive to live cell staining. The modifications included using all stains on postfixed samples and adjusting concentrations of reagents to optimize staining across the cell lines. The following adapted cell painting protocol was therefore applied to our breast cancer cell panel.

After a 48-h incubation in the presence of compounds, an equal volume of 8% paraformaldehyde (PFA) was added to the culture media of each well resulting in a final concentration of 4% PFA fixation buffer; the plates were then incubated at room temperature for 20 min, followed by three washes in 100 µL PBS. Permeabilization was performed with the addition of 50 µL 0.1% Triton-X100 to each well and incubation at room temperature for 20 min followed by three washes in 100 µL PBS.

The staining solution was prepared in a blocking buffer consisting of 1% bovine serum albumin in PBS (Table 3). Thirty microliters of staining solution was added to each well and incubated in darkness at room temperature for 30 min followed by three washes in 100 µL PBS, with no final aspiration. Plates were then sealed (#PCR-SQ plate max) and imaged immediately.

Plates were imaged on a Molecular Devices ImageXpress[®] Micro XLS, six fields of view were captured per well using a 20× objective and five filters, DAPI (387/447 nm), FITC (482/536 nm), Cy3 (531/593 nm), TxRed (562/642 nm), and Cy5 (628/692 nm). Exposure, binning, and other image settings were not altered between cell lines.

Image Analysis

Images were analyzed using CellProfiler v2.1.1¹⁹ to extract 309 features (Supplementary Table S1; Supplementary Data are available online at www.liebertpub.com/adt). Briefly, cell nuclei were segmented from the nuclei image based on intensity and shape, and used as seeds to segment cell areas in the other channels. Subcellular structures such as nucleoli and endoplasmic reticulum speckles were segmented and assigned to parent objects. From these objects, measurements such as size, shape, and spatial distribution were measured. The final CellProfiler settings applied in this study were created by iteratively adjusting the parameters and assessing the performance of cell segmentation by eye across multiple drug treatments for all cell types under evaluation, to ensure the most robust segmentation

subtypes (Table 1). Authenticated cell lines were acquired from the American Type Culture Collection and carefully monitored for morphological changes to ensure authenticity. Cell lines were cultured in either Dulbecco's Modified Eagle's Medium (HCC1954, MCF7, KPL4, MDA-MB-231, MDA-MB-157, and SKBR3) or Roswell Park Memorial Institute-1640 (HCC1569 and T47D) supplemented with 10% fetal bovine serum and 2 mM L-glutamine and incubated at 37°C, 5% CO₂. Two thousand five hundred cells were seeded into each of the inner 60 wells of 96-well plates (#165305; Thermo) in 100 µL media and incubated for 24 h before compound treatment. Outer wells of plates were filled with 100 µL phosphate-buffered saline (PBS).

Compound Treatment

A panel of well-annotated compounds purchased from commercial suppliers (Table 2) were prepared as 10 mM stock solutions in dimethyl sulfoxide (DMSO). 1,000× compound plates were then created with semi-log dilutions in DMSO. Each plate contained six wells of 0.1% DMSO as a negative control and six wells of 200 nM staurosporine as a positive control. Following compound addition, cell assay plates were incubated at 37°C, in 5% CO₂ incubator for an additional 48 h before fixation, staining, and high-content imaging.

Table 2. Compounds

Compound	Class	Sub-Class	Supplier	Cat. No.
Paclitaxel	Microtubule disrupting	Microtubule stabilizer	Sigma	T7402
Epothilone B	Microtubule disrupting	Microtubule stabilizer	Selleckchem	S1364
Colchicine	Microtubule disrupting	Microtubule destabilizer	Sigma	C9754
Nocodazole	Microtubule disrupting	Microtubule destabilizer	Sigma	M1404
Monastrol	Microtubule disrupting	Eg5 kinesin inhibitor	Sigma	M8515
ARQ621	Microtubule disrupting	Eg5 kinesin inhibitor	Selleckchem	S7355
Barasertib	Microtubule disrupting	Aurora B inhibitor	Selleckchem	S1147
ZM447439	Microtubule disrupting	Aurora B inhibitor	Selleckchem	S1103
Cytochalasin D	Actin disrupting	Actin disrupter	Sigma	C8273
Cytochalasin B	Actin disrupting	Actin disrupter	Sigma	C6762
Jasplakinolide	Actin disrupting	Actin stabilizer	Tocris	2792
Latrunculin B	Actin disrupting	Actin stabilizer	Sigma	L5288
MG132	Protein degradation	Proteosome	Selleckchem	S2619
Lactacystin	Protein degradation	Proteosome	Tocris	2267
ALLN	Protein degradation	Cysteine/calpain	Sigma	A6165
ALLM	Protein degradation	Cysteine/calpain	Sigma	A6060
Emetine	Protein synthesis	Protein synthesis	Sigma	E2375
Cycloheximide	Protein synthesis	Protein synthesis	Sigma	1810
Dasatinib	Kinase inhibitor	Src-EMT	Selleckchem	S1021
Saracatinib	Kinase inhibitor	Src-EMT	Selleckchem	S1006
Lovastatin	Statin	Statin	Sigma	PHR1285
Simvastatin	Statin	Statin	Sigma	PHR1438
Camptothecin	DNA damaging agent	Topoisomerase 1 inhibitor	Selleckchem	S1288
SN38	DNA damaging agent	Topoisomerase 1 inhibitor	Selleckchem	S4908

Src-EMT, Src kinase and Epithelial-Mesenchymal Transition inhibitor.

for each distinct cell type, and drug-induced phenotype is achieved.

Data Preprocessing

Out of focus and low-quality images were detected and removed by filtering on saturation and focus measurements provided in the CellProfiler output. Image averages of single object measurements from CellProfiler were aggregated by taking the median of each measured feature per image.

Features were normalized and standardized on a plate-by-plate basis by dividing each feature by the median DMSO response for that feature and then scaled by a z-score to have a mean of 0 and a standard deviation of 1. Feature selection was performed by calculating pair-wise correlations of features and removing one of a pair of features that have correlation greater than 0.9 and removing features with very low or zero variance, using the findCorrelation and nearZeroVar functions in the caret R package.²⁸

Quantifying Differential Morphological Responses by TCCS

Principal component analysis (PCA) was performed and the data were then centralized to the DMSO centroid. This was carried out by calculating the mean of principal component (PC) 1 and 2 for the DMSO subset of the data, and then subtracting this from the PC values. With each data point as a vector in two-dimensional (2D) space formed by the first two PCs, the norm of each vector was calculated, returning a Euclidean distance of each data point from the DMSO centroid. Then, the angles between each vector and a reference vector (0, 1) were calculated and denoted as theta (θ). The reference vector is arbitrarily set as a vector along the x-axis and enables easy comparison

between the polar coordinate histograms of the PCA biplot in Cartesian coordinates. For replicates, median values of PCs were calculated before calculating vectors; this simple approach avoids the pitfalls in calculating the mean of circular quantities—for example the arithmetic mean of 1° and 359° is 180°, despite the close proximity of the values in polar coordinates.

As any perturbations that do not produce morphological changes will be indistinguishable from negative control values, these points were found clustered within the negative

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Table 3. Stains and Concentrations Used in the Modified Cell-Painting Protocol

Stain	Structure Labeled	Wavelength (ex/em [nm])	Concentration	Cat. No.; Supplier
Hoechst 33342	Nuclei	387/447	2 µg/mL	#H1399; Mol. Probes
SYTO14	Nucleoli	531/593	3 µM	#S7576; Invitrogen
Phalloidin 594	F-actin	562/624	0.85 U/mL	#A12381; Invitrogen
Wheat germ agglutinin 594	Golgi and plasma membrane	562/624	8 µg/mL	#W11262; Invitrogen
Concanavalin A 488	Endoplasmic reticulum	462/520	11 µg/mL	#C11252; Invitrogen
MitoTracker DeepRed	Mitochondria	628/692	600 nM	#M22426; Invitrogen

control cloud in a scatter-plot of the first two PCs. As these compounds are centered on the origin (0, 0), the angles calculated from their vectors are uniformly distributed in all directions and meaningless as a phenotypic direction. Therefore, a minimum distance from the DMSO centroid was determined as 1 standard deviation of the vector distances from the origin, and compounds within this distance were defined as inactive in our assay and not used in further calculations. Active compounds were only included if they fell beyond this minimum limit for all the eight cell lines.

To calculate the phenotypic difference between compounds tested within the same cell line or a compound tested across different cell lines using the vector analysis described above, the absolute difference between the two theta values can be used. However, as any difference greater than 180° and approaching 360° starts to reflect morphologies becoming more similar, the absolute difference values have to be constrained between 0° and 180°; this is carried out for values greater than 180 by subtracting the value from 360, for example, 190° will become 170°. We named the method "Theta-Comparative-Cell-Scoring" to reflect the use of vectors applied to multiparametric high-content data to quantify distinct phenotypic response between cell types.

Data and Code Availability

The CellProfiler pipelines, numeric data, and R code to run the analyses and generate the figures are available at github.com/swarchal/TCCS_paper

RESULTS

High-Content Phenotypic Comparisons Between Morphologically Distinct Breast Cancer Cell Subtypes

We have modified the cell painting assay previously applied to the osteosarcoma cell line U2OS cells²⁷ to a panel of breast

cancer cell lines representing clinically relevant subtypes. Eight breast cancer cell lines representing four pairs for each of the following clinical subtypes: estrogen receptor (ER)-positive, triple negative, human epidermal growth factor receptor 2 (Her2)-positive/Phosphatase and tensin homolog (PTEN) and phosphoinositide 3-kinase (PI3K) wild type, and Her2-positive/PTEN and PI3Kmut were selected for this study (*Table 1*).

The modified cell painting assay was optimized to enable the CellProfiler image analysis software to segment individual cells for each well and extract features, which provide detailed morphological analysis of individual breast cancer cell phenotypes. Representative images of the eight breast cancer cells stained with the modified cell-painting protocol are displayed in three channels in *Figure 1A* and respective cell segmentation masks generated by CellProfiler analysis are shown in *Figure 1B*. As the breast cancer cell lines look inherently different from one another (*Fig. 1*), detecting differential phenotypic changes between them requires normalization against the negative control phenotype for each cell line. This was performed by dividing each feature by the median DMSO value for that feature on a plate-by-plate basis followed by z-scoring each feature individually for all cell lines. Normalization in this manner achieved two objectives: (1) removing any batch effects that may be present across plates and (2) normalizing all phenotypic measurements as standardized fold changes from the negative control values per cell line. PCA was then performed on the normalized dataset of all cell lines using the prcomp function in R.

Quantifying Differential Morphological Response Between Cell Lines to the Same Compound

When the first two PCs are visualized as a 2D scatter plot, low concentrations of compounds are typically found near or within the DMSO cluster. However, with increasing concentrations, the points are often seen to proceed toward a given trajectory, describing decreasing phenotypic similarity to the negative control cells with increasing compound concentration. In the case of MDA-MB-231 cells treated with Cycloheximide and Barasertib, the compounds result in trajectories with opposing directions, describing opposite morphological changes (*Fig. 2*). The case of Barasertib and Cycloheximide provide a proof-of-principle example in the ability of the

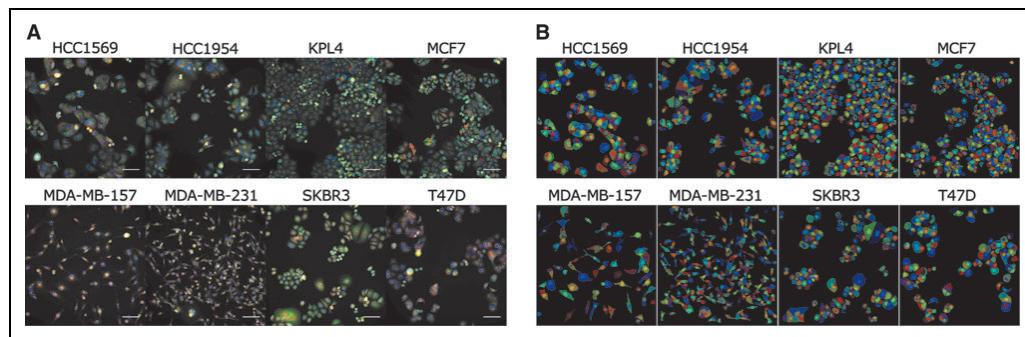


Fig. 1. Cell painting assay applied to eight distinct breast cancer cell lines. **(A)** Composite image of cell lines treated with 0.1% DMSO. Channels used: *Red*—MitoTracker DeepRed (mitochondria); *Green*—Concanavalin A (endoplasmic reticulum); *Blue*—Hoechst33342 (nuclei). Scale bars: 100 μ m. **(B)** Image masks from CellProfiler showing nuclei and cell body segmentation. DMSO, dimethyl sulfoxide.

method described to distinguish opposing phenotypes represented by enlarged and aneuploidy nuclei characteristic of cytokinesis defects elicited by inhibitors of Aurora kinase B (Barasertib) in contrast to the condensed nuclei characteristic of the protein synthesis inhibitor (Cycloheximide).

These distinct phenotypic trajectories have been quantified as theta values against a reference vector using Equation (1), where u is the PC1, PC2 vector, and v is the reference vector of

(0, 1) (*Fig. 2*). A circular histogram of the theta values can then be plotted to visualize the distribution of compound induced phenotypes. The circular histogram theta plots provide an intuitive indication of a phenotypic direction produced by a specific pharmacological perturbation, as well as any change in phenotypic direction across increasing concentrations that may indicate off-target effects. *Figure 3A* shows a circular histogram of the data pooled from all eight cell lines treated with an eight-point half-log dose response of the Aurora B kinase inhibitor Barasertib. Using the same directional histograms, data can also be split by cell lines to directly visualize differential phenotypic response across a panel of distinct cell lines (*Fig. 3B*).

The difference in theta values between cell lines can then be calculated for a given compound to provide a univariate theta metric of phenotypic dissimilarity between cell types (*Fig. 3C*). It is possible to rank similarity and dissimilarity of each compound-induced phenotype between cells or between other compounds on a scale of 0–180° where 0 describes the most similar phenotypes and 180 the most dissimilar phenotypes. We name this method “Theta Comparative Cell Scoring” and provide the formula below:

$$\theta = \cos\left(\frac{u \cdot v}{\|u\|\|v\|}\right) \times \frac{180}{\pi} \quad (1)$$

Screening for Differential Phenotypic Response Across the Panel of Breast Cancer Subtypes

To evaluate the TCCS method for the ability to identify compounds that induce differential phenotypic responses between the breast cancer cell lines, we calculated the difference between theta values for all eight breast cancer cell lines treated with 1 μ M of 24 different compounds. Compounds

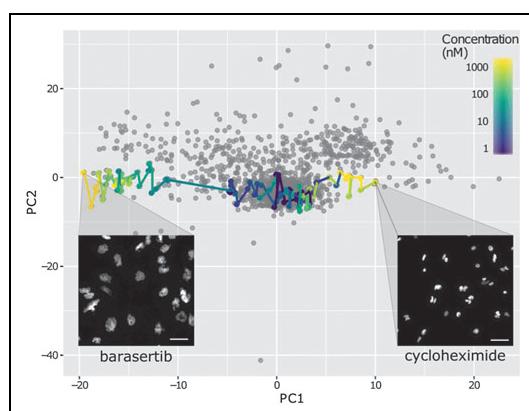


Fig. 2. Phenotypic directions in the first two PCs. Scatter plot of the first two PCs of MDA-MB-231 cells treated with a small compound library. Principal component analysis was carried out on 309 median normalized features extracted from cellular images. Barasertib and Cycloheximide compounds are colored by concentration demonstrating opposite phenotypic directions in PC space producing opposite nuclear phenotypes. Images show nuclei imaged with Hoechst, scale bars: 20 μ m. PC, principal component.

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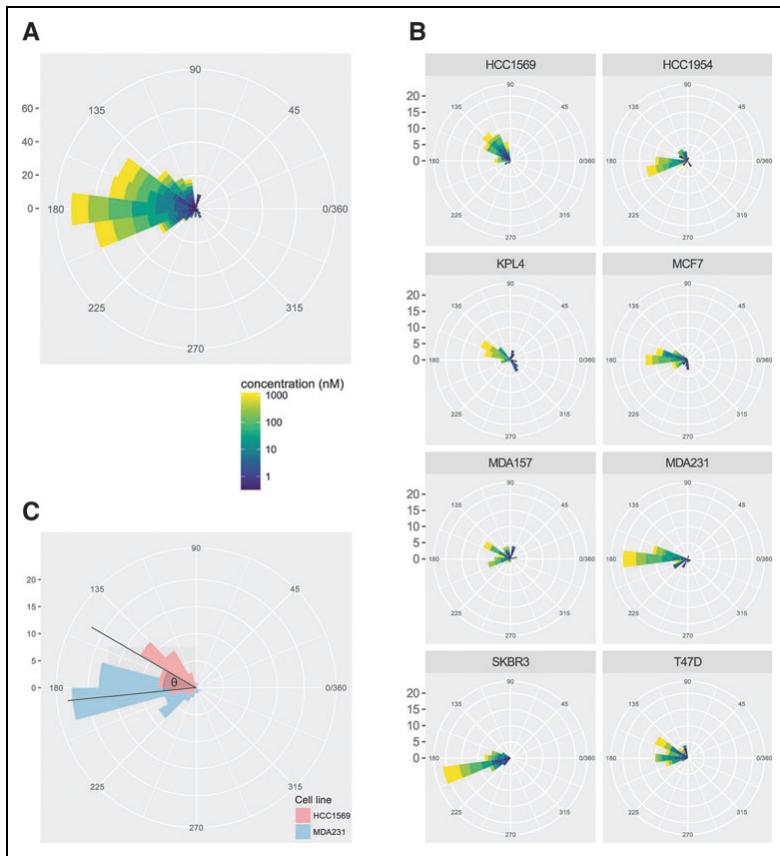


Fig. 3. Circular histograms of theta values. **(A)** Circular histogram of theta values of Barasertib calculated for all eight cell lines. **(B)** Phenotypic direction of cell lines treated with Barasertib stratified by cell line. **(C)** A diagrammatic explanation of the theta value showing the difference in theta values between HCC1569 and MDA-MB-231 cell lines treated with Barasertib.

were selected to represent 12 pairs of well-characterized mechanistic subclasses, 21 of these compounds elicited robust morphological changes in all eight cell lines.

To identify and quantify differential phenotypic responses, the difference between theta values was calculated for all pairs of cell lines, constrained to the maximum dissimilarity value of 180° and plotted as a heat map for each of the 21 compounds (Fig. 4). Compounds with high theta values indicate a differential response between pairs of cell lines for that particular compound. A representative image between KPL4 and MCF7 cells treated with $1\ \mu\text{M}$ of the topoisomerase I inhibitor SN38 is

an example of a compound that induces a distinct phenotypic response between these cell types ($\text{TCCS} = 179^\circ$), relative to the negative control for each cell line (Fig. 4). The majority of cell line comparisons returned low TCCS values, indicating that most of the breast cancer cell lines selected respond similarly to the compounds in our panel (Supplementary Fig. S1).

Differential Response of Breast Cancer Cell Lines Are Stratified by Molecular Subclass

To demonstrate the ability of the TCCS method to cluster high-content phenotypic response across breast cancer subtypes with a view to informing disease positioning and personalized medicine strategies, we used data from an exemplar molecular targeted therapy, the dual Src/Abl inhibitor Saracatinib (AZD0530).

To utilize the data present across multiple titrations, the mean PCs were taken across eight concentrations to create the 2D vector with which the difference between TCCS values across all pairs of cell lines is calculated. TCCS values are plotted as a heat map clustered by hierarchical clustering using Euclidean distance (Fig. 5A). This revealed that the divergent high-content phenotypic response in-

duced by Saracatinib across the breast cancer cell panel clustered together based on their molecular subclass. Figure 5B shows images of three cell lines treated with either DMSO negative control or $1\ \mu\text{M}$ Saracatinib. From Figure 5A the MDA-MB-231 cell lines are found to have responded differently to KPL4 and SKBR3 cell lines, which in turn elicited a similar response to one another. This can be seen predominantly through increased cell-cell contact in the Saracatinib-treated MDA-MB-231 cells compared to the other two cell lines, observed as an increase in normalized number of adjacent cells in MDA-MB-231 cells (Supplementary Fig. S2). Although far from

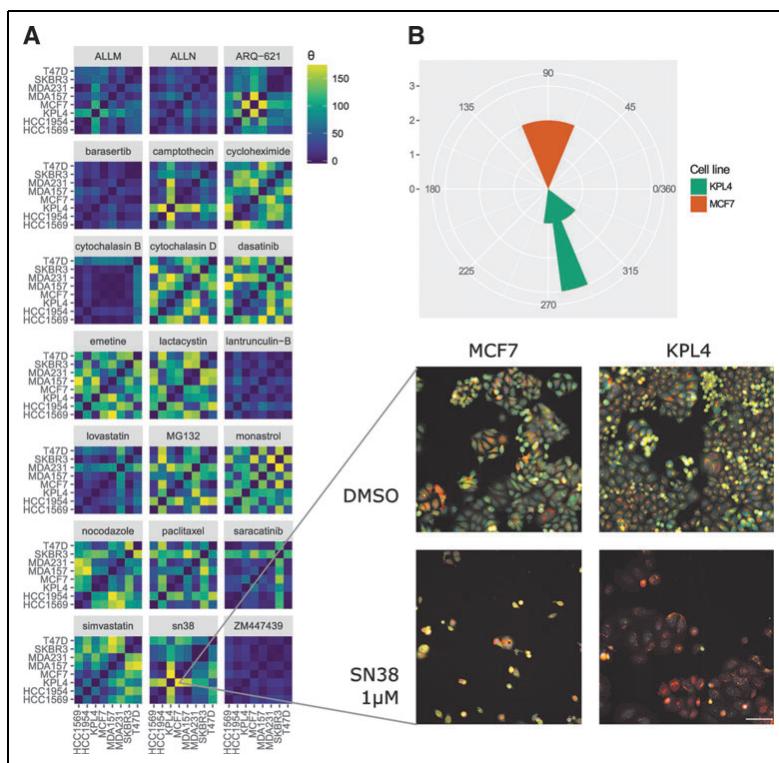


Fig. 4. Heat map of theta values between pairs of cell lines for separate compounds. **(A)** Difference in theta values calculated between pairs of cell lines treated with 21 compounds at 1 μ M concentration. Images show differential response between KPL4 and MCF7 cell lines treated with 1 μ M SN38. MCF7 cells are observed to decrease in cell area, with bright staining for the endoplasmic reticulum, whereas the KPL4 cells produce a “fried egg” morphology with large spread cells and weak endoplasmic reticulum staining. Channels used are as follows: Red—Mito Tracker DeepRed (mitochondria); Green—Concanavalin A (endoplasmic reticulum); Blue—Hoechst33342 (nuclei). Scale bar: 100 μ m. **(B)** Circular histogram of theta values calculated for MCF7 and KPL4 cells treated with 1 μ M SN38.

representative of all compound responses and disease subtypes, this example does indicate the potential of high-content cell-based phenotypic screening combined with application of the TCCS method across genetically defined cell panels to provide patient stratification hypothesis for both well-characterized candidate drugs or poorly characterized active compounds identified from phenotypic screens.

DISCUSSION

The rapid evolution and convergence of new technologies, including advances in image-based high-content phenotypic

screening, induced pluripotent stem cell (iPSC) technologies, and gene editing, are well placed to advance a new era of modern phenotypic screening in more informative and disease relevant cell-based models of disease.^{15,29,30} However, a limitation of phenotypic screening is the identification of hit molecules or candidate drugs without knowledge of the target mechanism.

The lack of information on target mechanism, while not required for drug approval, impedes the design of personalized healthcare strategies to combat disease heterogeneity. Several target deconvolution strategies have been applied to compounds discovered by phenotypic screening to elucidate target mechanisms.^{31–33} However, no target deconvolution method is conclusive, and such strategies are often based upon the assumptions that a compound will only inhibit a single target and monitoring the activity and inhibition of the elucidated target will guide personalized therapy.

For the majority of compounds discovered by phenotypic screens, and for many complex human diseases where the one-drug-one-target hypothesis is unrealistic, new nontarget-centric approaches are required to understand drug mechanism-of-action and guide

personalized healthcare strategies. *In vitro* pharmacogenomic or pharmacoproteomic profiling across well-characterized cell panels, representing specific disease subtypes, exemplifies one approach for informing drug mechanism-of-action and guiding personalized healthcare strategies in the absence of target knowledge. Breast cancer is separated into four major molecular subtypes; Luminal A (ER-positive and/or progesterone receptor (PR)-positive and HER2-negative and Low Ki67); Luminal B (ER-positive and/or PR-positive and HER2-positive or HER2-negative with high Ki67); Triple negative/basal like (ER- PR- and Her2-negative); and HER2 type (ER- PR- negative and

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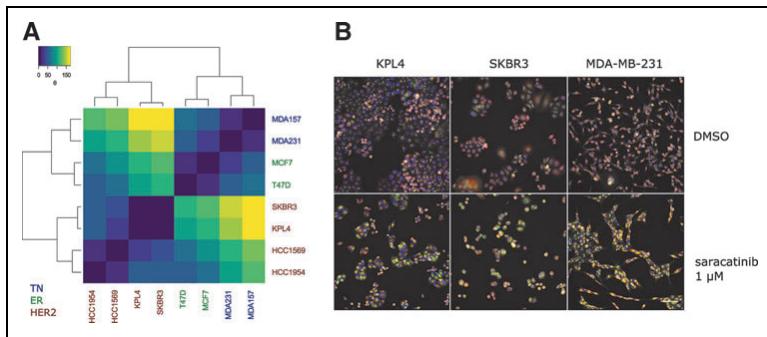


Fig. 5. Heat map and hierarchical clustering of cell lines treated with Saracatinib. **(A)** Heatmap of TCCS values calculated between all pairs of cell lines treated with Saracatinib with hierarchical clustering by complete linkage of the Euclidean distance. **(B)** Images demonstrating two similar phenotypic responses—KPL4 and SKBR3—and the dissimilar phenotypic response of MDA-MB-231 cell lines to $1\text{ }\mu\text{M}$ Saracatinib treatment. Channels used: Red—MitoTracker DeepRed (mitochondria); Green—Concanavalin A (endoplasmic reticulum); Blue—Hoechst33342 (nuclei). Scale bar: $100\text{ }\mu\text{m}$. TCCS, Theta Comparative Cell Scoring.

Her2-positive). Each major molecular subtype of breast cancer can be further divided into subclasses based upon genetic mutation status and protein profiles, and the diagnosis of breast cancer subtype dictates the most appropriate personalized treatment for patients.^{34–36}

In this article, we have developed a multiparametric high-content assay, data visualization tools, and a TCCS method, which support phenotypic screening of compound libraries across genetically distinct cells representing known molecular subtypes of disease. We provide proof-of-principle data applied to eight breast cancer cells representing four disease subclasses (*Table 1*), demonstrating the application of the method for quantifying distinct phenotypic response between cell types and clustering of cell-associated clinical subtypes based on similar or dissimilar phenotypic response to compound treatment.

As previously discussed, several multiparametric pathway and phenotypic profiling methods have been developed to classify drug mechanism-of-action and uncover new drug-target associations, and structure activity relationships in a more holistic and unbiased manner.^{18,20–25,27} However, the majority of these methods have been applied to single cell types amenable to high-content imaging or large-scale biochemical and proteomic analysis.^{18,21–25,27} The TCCS method described in this article was developed to provide a practical method to enable comparative multiparametric phenotypic analysis across a panel of genetically distinct cell types, which provides rapid quantification and visualization of divergent compound-induced phenotypic response between cell types. An intuitive explanation of the TCCS method would be the cosine distance in

degrees of vectors in the first two PCs; this is a variation on existing methods that largely rely on correlation or Euclidean distance between compound vectors.¹⁸

The benefits of the TCCS over previous methods are as follows: (1) use of distance from the negative control to remove poorly active or inactive compounds that might produce spurious differences in correlation of cosine similarity measures; (2) The comparison of each data point to a common reference vector enables visualizations of a single metric, which depicts the relative change in phenotypic response induced by a compound (*Fig. 3A*).

The most critical aspect of comparing results between panels of distinct cell lines regardless of downstream methods is during the data preprocessing stage, which requires careful normalization against the negative control values for each cell line to remove inherent differences in cell line morphology. Thus, the TCCS method represents a flexible approach with broad applicability to quantifying and visualizing distinct phenotypes induced by a panel of compounds within a single cell type and/or the response of a single compound across multiple cell types. The TCCS method removes compounds from the algorithm that are not sufficiently different from the negative control. While this increases the robustness of the calculation, it also creates the opportunity to miss compounds that possess differential sensitivity between cell lines. This limitation of the method arises where certain compounds that do not induce any morphological change in one cell line may still perturb cellular morphology in another cell line, thus any such compound would subsequently be removed from the calculation due to insufficient distance from the negative control centroid, despite eliciting a genuine differential response between cell lines. However, this limitation can be simply rectified by implementing an initial preanalytical stage of the algorithm by calculating the distance from DMSO for all compounds across all cell lines to assign either as “active” or “inactive” phenotypic responders. Differences in the activation state of all compounds across all cell lines are recorded and the active compounds then progress to TCCS analysis to quantify and visualize a distinct phenotype response across cell lines.

The TCCS method as outlined in this article utilized only the first two PCs produced from the PCA. These two variables

explain most of the variance of data in low dimensional data represented by majority of high-throughput high-content screens, which typically measure only small numbers of features.³⁷ In such high-throughput compound screens, TCCS applied to the first two PCs would be expected to provide a single value describing the difference in response across different cell lines for active compounds. The method as applied to the first two PCs in this article becomes less informative in higher dimensional data sets as more PCs are required to describe the data. As the calculation to define the angle between two vectors [Eq. (1)] uses the dot product of the two vectors, the vectors are not limited to the first two PCs, and it is entirely reasonable that they could contain any number of PCs. Therefore, an alternative option would be to implement the TCCS method on a number of PCs that satisfy a user-defined proportion of variance within the data.

Comparison of high dimensional vectors against one another rather than against a reference vector allows for direct calculation of a theta value in high dimensional space, an example workflow using the TCCS method applied to more than two PCs is provided in the online R scripts (github.com/swarchal/TCCS_paper) and is represented in the description of the TCCS workflow (Fig. 6). The TCCS method may also be applied to the normalized assay parameters rather than PCs as also demonstrated in the supplementary R workflow (github.com/swarchal/TCCS_paper). However, care should be taken to ensure that potentially uninformative parameters are

not included in such analysis to avoid introduction of unnecessary assay noise. Thus, the most optimal application of the TCCS method can be appropriately tailored to each study and nature of the underlying high-content data set.

Multiple concentrations are not often used in high-throughput cell-based screening assays, despite providing useful information to detect off-target effects and can be thought of as inherent replicates of individual compound data. A further approach to incorporate titration data into defining direction in PC space would be to fit a linear model to each compound using simple linear regression, forcing the y-intercept through 0. While this would lose information pertaining to the distance from the DMSO centroid at each concentration, it would provide information regarding goodness of fit, and data may be excluded from the TCCS analysis if they do not fit the linear model well or used to indicate compounds with off-target effects at higher concentrations. As the theta value is essentially a direction in PC space, another useful addition would be to relate theta back to the feature loadings that describe how the PCs were constructed. This would return the phenotypic features that best describe a certain direction in phenotypic space. However, PCA contains negatively weighted features and so methods such as nonnegative matrix factorization in which the feature loadings are all positive values, may be a potential avenue for this improvement.

Another potential use of TCCS method is in assay quality control (QC). For example, TCCS could be applied to the

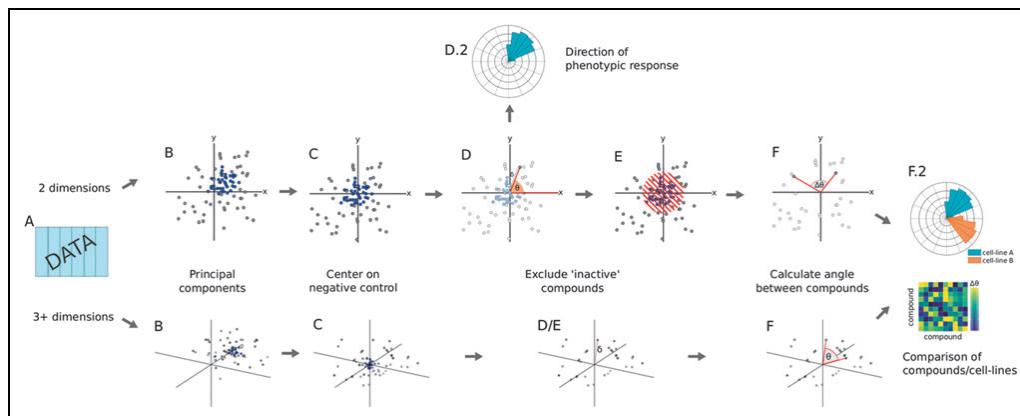


Fig. 6. TCCS workflow. (A) Normalized numerical data. (B) PC analysis, negative control values colored in blue. (C) Centering of PC values to the negative control centroid. (D) Calculation of distance from the origin to each data point, an activity cutoff is derived from the standard deviation of the distance to the negative control values. (D.2) In two-dimensional space, a directional histogram can be created by the angle of each vector against a reference vector. (E) Inactive compounds excluded based on distance from the origin. (F) Determining the angle between compounds. (F.2) Visualization or clustering of compounds based on theta values.

A METHOD TO QUANTIFY PHENOTYPIC RESPONSES BETWEEN CELL TYPES

simultaneous evaluation of two positive controls known to elicit robustly different morphologies (e.g., paclitaxel and staurosporine) along with a negative control such as DMSO to determine a theta value between the two positive controls. It would be expected that the two positive controls would have a theta value greater than a specified minimum. The variance of theta values between two positive controls per plate could therefore be used as a measure of biological assay variability during assay development and screening campaigns.

Incorporating a multiparametric QC metric that utilizes high-content analysis across two positive controls provides increased robustness and more unbiased assessment of monitoring variation in cell behavior and assay variability over current methods that use a single positive control analysis of a pre-selected parameter. Other multivariate assay QC metrics typically build on the Z'-factor using supervised machine learning techniques such as Fisher's linear discriminant analysis (LDA) to best separate the positive and negative controls.³⁸ Although more robust than single parametric analysis, a drawback of this method is that LDA is often prone to overfitting in high dimensions, which may produce overoptimistic QC values when processed to the Z'-factor calculation.

The convergence of new technologies, including next-generation sequencing, high-throughput proteomics, iPSC technology, and high-content phenotypic screening, is well placed to advance the identification of predictive biomarkers and personalized medicine approaches across a broader range of disease types and therapeutic classes.^{15,29,30,39,40}

Our study provides a broadly applicable approach for quantifying distinct phenotypic response between genetically distinct cells using high-content analysis coupled to a TCCS scoring method. The TCCS method that we describe provides a univariate metric that can be applied to any high-content assay for quantifying and visualizing a diverse phenotypic response between cell types. The TCCS metric provides a univariate score of distinct phenotypic response on a scale of 0–180° (where 0°=similar and where 180°=most dissimilar), which can be used for correlation with orthogonal genetic, epigenetic, and proteomic datasets to support the identification of biomarkers of drug phenotype and further elucidate drug mechanism-of-action at genetic and pathway levels.

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Abbreviations Used

2D	= two dimensional
3D	= three dimensional
CCLE	= Cancer Cell Line Encyclopaedia
DAPI	= 4,6-diamidino-2-phenylindole
DMSO	= dimethyl sulfoxide
EC ₅₀	= concentration of drug that produces a 50% maximal response
ER	= estrogen receptor
FITC	= fluorescein isothiocyanate
GI ₅₀	= concentration of a drug that gives half-maximal inhibition of cell proliferation
HER2	= human epidermal growth factor receptor 2
iPSC	= induced pluripotent stem cell
LDA	= linear discriminant analysis
PBS	= phosphate-buffered saline
PC	= principal component
PCA	= principal component analysis
PFA	= paraformaldehyde
PI3K	= phosphoinositide 3-kinase
PR	= progesterone receptor
PTEN	= phosphatase and tensin homolog
QC	= quality control
TCCS	= Theta Comparative Cell Scoring
TN	= triple negative
WT	= wild type

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Data-analysis strategies for image-based cell profiling

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Image-based cell profiling is a high-throughput strategy for the quantification of phenotypic differences among a variety of cell populations. It paves the way to studying biological systems on a large scale by using chemical and genetic perturbations. The general workflow for this technology involves image acquisition with high-throughput microscopy systems and subsequent image processing and analysis. Here, we introduce the steps required to create high-quality image-based (i.e., morphological) profiles from a collection of microscopy images. We recommend techniques that have proven useful in each stage of the data analysis process, on the basis of the experience of 20 laboratories worldwide that are refining their image-based cell-profiling methodologies in pursuit of biological discovery. The recommended techniques cover alternatives that may suit various biological goals, experimental designs, and laboratories' preferences.

Image analysis is heavily used to quantify phenotypes of interest to biologists, especially in high-throughput experiments^{1–3}. Recent advances in automated microscopy and image analysis allow many treatment conditions to be tested in a single day, thus enabling the systematic evaluation of particular morphologies of cells. A further revolution is currently underway: images are also being used as unbiased sources of quantitative information about cell state in an approach known as image-based profiling or morphological

profiling⁴. Herein, the term morphology will be used to refer to the full spectrum of biological phenotypes that can be observed and distinguished in images, including not only metrics of shape but also intensities, staining patterns, and spatial relationships (described in 'Feature extraction').

In image-based cell profiling, hundreds of morphological features are measured from a population of cells treated with either chemical or biological perturbagens. The effects of the treatment are quantified

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by measuring changes in those features in treated versus untreated control cells⁵. By describing a population of cells as a rich collection of measurements, termed the ‘morphological profile’, various treatment conditions can be compared to identify biologically relevant similarities for clustering samples or identifying matches or anticorrelations. This profiling strategy contrasts with image-based screening, which also involves large-scale imaging experiments but has a goal of measuring only specific predefined phenotypes and identifying outliers.

Similarly to other profiling methods that involve hundreds of measurements or more from each sample^{6,7}, the applications of image-based cell profiling are diverse and powerful. As reviewed recently^{8,9}, these applications include identifying disease-specific phenotypes, gene and allele functions, and targets or mechanisms of action of drugs.

However, the field is currently a wild frontier, including novel methods that have been proposed but not yet compared, and few methods have been used outside the laboratories in which they were developed. The scientific community would greatly benefit from sharing methods and software code at this early stage, to enable more rapid convergence on the best practices for the many steps in a typical profiling workflow (Fig. 1).

Here, we document the options at each step in the computational workflow for image-based profiling. We divide the workflow into eight main steps (Fig. 1). For each step, we describe the process, its importance, and its applicability to different experimental types and scales. We present previously published methods relevant to each step, provide guidance regarding the theoretical pros and cons for each alternative option, and refer to any prior published comparisons of methods. We do not cover the upstream steps (sample preparation and image-acquisition recommendations)^{1,2} or computational practicalities such as the necessary information-technology infrastructure to store and process images or data. The workflow’s starting point is a large set of images. The assays can be specifically designed for profiling, such as Cell Painting^{10,11}, but any image-based assays can be used, including a panel of multiple parallel image-based assays¹², or time-lapse microscopy for analyzing dynamics¹³ or even whole organisms¹⁴.

This paper is the result of a ‘hackathon’, in which the authors met to discuss and share their expertise in morphological profiling. Hands-on data-analysis challenges and the accompanying discussions helped to identify the best practices in the field and to contribute algorithms to a shared code base.

We hope to provide a valuable foundation and framework for future efforts and to lower the barrier to entry for research groups that are new to image-based profiling. The detailed workflows used by each individual laboratory contributing to this article can be found online (<https://github.com/shntnu/cytomining-hackathon-wiki/wiki/>).

Step 1: image analysis

Image analysis transforms digital images into measurements that describe the state of every single cell in an experiment. This process makes use of various algorithms to compute measurements (often called features) that can be organized in a matrix in which the rows are cells in the experiment, and the columns are extracted features.

Field-of-view illumination correction. Every image acquired by a microscope exhibits inhomogeneous illumination mainly

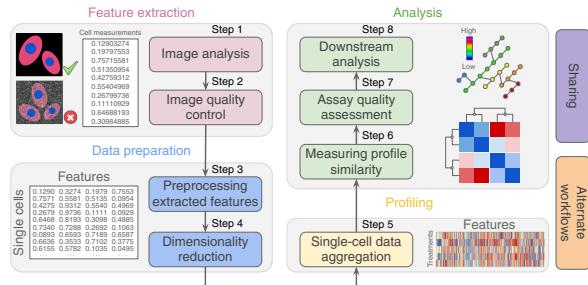


Figure 1 | Representative workflow for image-based cell profiling. Eight main steps transform images into quantitative information to support experimental conclusions.

because a nonuniform light source or optical path often yields shading around edges. This effect is often underestimated; however, intensities usually vary by 10–30%, thus corrupting accurate segmentation and intensity measurements¹⁵. Illumination correction is a process to recover the true image from a distorted one. There are three main approaches to illumination correction:

Prospective methods. These methods build correction functions from reference images, such as dark and bright images with no sample in the foreground. The approach requires careful calibration at the time of acquisition and relies on assumptions that are often inappropriate, thus yielding an incomplete correction in practice¹⁶.

Retrospective single-image methods. These methods calculate the correction model for each image individually^{17–19}. However, the result can change from image to image and thus may alter the relative intensity.

Retrospective multi-image methods. These methods build the correction function by using the images acquired in the experiment. These methods are often based on smoothing¹⁶, surface fitting²⁰, or energy-minimization models¹⁵.

Illumination correction is an important step for high-throughput quantitative profiling; the strategy of choice in most of our laboratories is a retrospective multi-image correction function. This procedure produces more robust results, particularly when separate functions are calculated for each batch of images (often with a different function for each plate and always with a different function for different imaging sessions or instruments). We recommend use of prospective and single-image methods for only qualitative experiments.

Segmentation. Typically, each cell in the image is identified and measured individually; that is, its constituent pixels are grouped to distinguish the cell from other cells and from the background. This process is called ‘segmentation’ (Fig. 2), and there are two main approaches:

Model based. The experimentalist chooses an appropriate algorithm and manually optimizes parameters on the basis of visual inspection of segmentation results. A common procedure is first to identify nuclei, as can often be done easily, and then to use the results as seeds for the identification of the cell outline. *A priori*

knowledge (i.e., a ‘model’) is needed, such as the objects’ expected size and shape²¹. Model-based approaches typically involve histogram-based methods, such as thresholding, edge detection, and watershed transformation²².

Machine learning. A classifier is trained to find the optimal segmentation solution by providing it with ground-truth data and manually indicating which pixels of an image belong to different classes of objects²³. This approach typically involves applying various transformations to the image to capture different patterns in the local pixel neighborhood. Segmentation is ultimately achieved by applying the trained model to new images to classify pixels accordingly.

Both approaches are used in profiling experiments. The model-based approach is most common (for example, in CellProfiler²⁴); it performs well for fluorescence microscopy images of cultured cells²². However, it requires manual parameter adjustment for each new experimental setup. Machine-learning-based segmentation (for example, in Ilastik²³) can perform better on difficult segmentation tasks, such as highly variable cell types or tissues. It does not require as much computational expertise, but it does require manual labeling of training pixels for each experimental setup and sometimes even for each batch of images. The creation of ground-truth data in the process of labeling allows for quantitative performance assessment.

Feature extraction. The phenotypic characteristics of each cell are measured in a step called feature extraction, which provides the raw data for profiling. The major types of features are:

Shape features. These features are computed on the boundaries of nuclei, cells, or other segmented compartments. These include standard size and shape metrics such as perimeter, area, and roundness^{25,26}.

Intensity-based features. These features are computed from the actual intensity values in each channel of the image on a single-cell basis, within each compartment (nucleus, cell, or other segmented compartments). These metrics include simple statistics (for example, mean intensity, and maximum intensity).

Texture features. These features quantify the regularity of intensities in images, and periodic changes can be detected by using mathematical functions such as cosines and correlation matrices. These features have been extensively used for single-cell analysis^{27–30}.

Microenvironment and context features. These features include counts and spatial relationships among cells in the field of view (on the basis of the number of and distance to cells in a neighborhood) as well as its position relative to a cell colony^{31–33}. Segmented regions are not limited to nuclei, and cells and may also include subcellular structures that can be quantified as measurements (for example, speckles within a nucleus or distances between the nucleus and individual cytoplasmic vesicles).

Whereas screening experiments typically measure one or two features of interest to quantify specific effects³⁴, cell profiling involves computing as many features as possible to select robust, concise, and biologically meaningful features to increase the

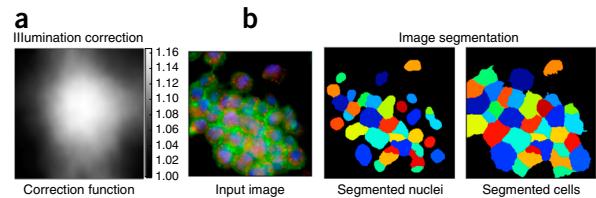


Figure 2 | Methods used for image analysis. (a) Illumination-correction function estimated with a retrospective multi-image method. Pixels in the center of the field of view are systematically brighter than pixels in the edges. (b) Image segmentation aims to classify pixels as either foreground or background, i.e. as being part of an object or not. Here, regions have been segmented with the model-based approach.

chances of detecting changes in the molecular states of cells. The most common practice is to measure hundreds or even thousands of features of many varieties; the details are typically described in the software’s documentation^{24,35,36}.

Step 2: image quality control

It is largely impossible to manually verify image quality in high-throughput experiments, so automated methods are needed to objectively flag or remove images and cells that are affected by artifacts. These methods seek to decrease the risk of contaminating the data with incorrect values.

Field-of-view quality control. Images can be corrupted by artifacts such as blurring (for example, improper autofocusing) or saturated pixels (for example, debris or aggregations that are inappropriately bright). Typically, statistical measures of image intensity are used for quality control.

Metrics can be computed to detect blurring, including the ratio of the mean and the s.d. of each image’s pixel intensities, the normalized measure of the intensity variance³⁷, and the image correlation across subregions of the image³⁸. The log–log slope of the power spectrum of pixel intensities is another effective option, because the high-frequency components of an image are lost as it becomes more blurred³⁹; this procedure has been found to be the most effective in a recent comparison for high-throughput microscopy⁴⁰. For detecting saturation artifacts, the percentage of saturated pixels has been found to be the best among all tested metrics.

We recommend computing various measures that represent a variety of artifacts that might occur in an experiment to increase the chance of artifact identification. Then, with data-analysis tools, these measurements can be reviewed to identify acceptable quality-control thresholds for each measure⁴⁰. It is also possible to use supervised machine-learning algorithms to identify problematic images^{41,42}, but these algorithms require example annotations and classifier training and validation, and thus may require more effort and introduce a risk of overfitting.

Cell-level quality control. Outlier cells may exhibit highly unusual phenotypes but may also result from errors in sample preparation, imaging, image processing, or image segmentation. Errors include incorrectly segmented cells, partly visible cells at image edges, out-of-focus cells, and staining artifacts. Although errors

are best decreased through careful techniques and protocols, there are several strategies for detecting outlier cells:

Model-free outlier detection. This strategy includes methods to define normal limits by using statistics. Data points represented with a single variable (for example, distance values or single features) can be analyzed with univariate statistical tools, including the 3- or 5-s.d. rules, Winsorizing, and the adjusted box-plot rule⁴³. Robust statistics based on estimators such as the median and the median absolute deviation⁴⁴ can also be used and extended to multivariate situations⁴⁵. Additional multivariate methods include principal component analysis (PCA) and Mahalanobis-based outlier detection⁴⁶.

Model-based outlier detection. This strategy involves training a model of normal samples to aid in detecting outlier cells⁴⁷. For instance, if a linear regression among features is suitable, outliers can be detected as data points with a large residual that does not follow the general trend⁴⁸. Alternately, a supervised-machine-learning classifier can be trained by providing examples of outliers^{49–51}.

After they are detected, outlier cells can be removed, or when the number of outliers in the sample is too high, the entire sample can be examined manually or omitted from analysis^{47,52}. Importantly, cell-outlier detection should be performed at the whole-population level; that is, it should not be separately configured per well, per replicate, or per plate. Extreme caution is recommended, to avoid removing data points that represent cells and samples with interesting phenotypes^{53,54}. Samples can be composed of various subpopulations of cells, and outlier-detection methods may incorrectly assume normality or homogenous populations (Fig. 3). For this reason, most laboratories skip outlier detection at the level of individual cells, other than to check for segmentation problems.

Step 3: preprocessing extracted features

Preparing extracted cell features for further analysis is a delicate step that can enhance the observation of useful patterns or can corrupt the information and lead to incorrect conclusions.

Missing values. Feature-extraction software may yield non-finite symbols (such as NaN and INF) representing incomputable values. In general, use of these symbols is preferred to assigning a numerical value that could be interpreted as having a phenotypic meaning. The presence of non-finite symbols poses challenges to applying statistics or machine-learning algorithms. There are three alternate solutions for handling missing values:

Removing cells. If a small proportion of cells have missing values, excluding them can be considered. However, those cells may indicate a valid and relevant phenotype, a possibility that should be assessed carefully (described in ‘Cell-level quality control’).

Removing features. If a large proportion of cells have a missing value for a particular feature, they might be removed on the grounds that the feature is insufficiently informative. Again, this removal should be assessed carefully for its effect on unexpected cell phenotypes.

Applying imputation. If the proportion of cells with missing values for certain features is relatively small, several statistical rules may

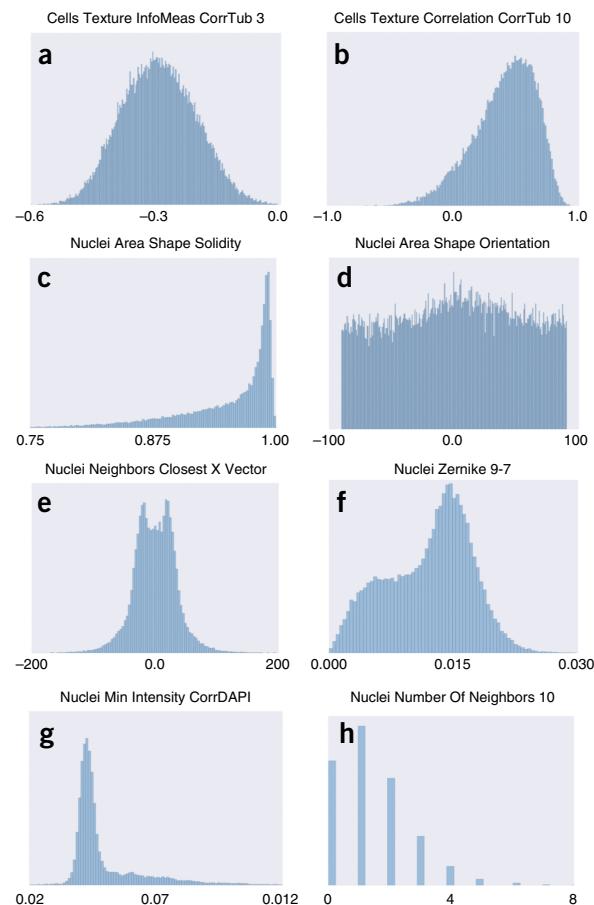


Figure 3 | Diversity of feature distributions in morphological profiling. (a–h) Morphological features display various types of distributions, including normal (a), skewed (b,c), uniform (d), multimodal (e–g), and even discrete distributions (h). The ranges in which features are represented also vary considerably. These histograms were obtained with feature values from a sample of 10,000 cells in the BBBC021 data set¹⁰⁸. The names of features correspond to conventions used in the CellProfiler software. The x axes show feature values (in different units), and the y axes show frequencies (cell counts).

be applied to complete these values. The use of zeros or the mean value is common in general statistical analysis but should not be the default option for single-cell profiling. If too many values are artificially added to the data matrix, the downstream analysis may be affected or biased by false data.

Deciding how to proceed with missing values is primarily dependent on experimental evaluations and empirical observations. Removing cells or features is more common than applying imputation. However, there is no single rule that applies in all cases, and the best practice is to collect convincing evidence supporting these decisions, especially with the use of quality measures and replicate analysis (described in ‘Downstream analysis’).

Plate-layout-effect correction. High-throughput assays use multiwell plates, which are subject to edge effects and gradient artifacts. Concerns regarding spatial effects across each plate are

not unique to imaging and have been widely discussed in both the microarray-normalization and high-throughput-screening literature^{44,55–58}. They can be decreased to some degree at the sample-preparation step⁵⁹.

We recommend checking for plate effects to determine whether any artifacts are present within plates or across multiple batches. The simplest method is a visual check, through plotting a measured variable (often cell count or cell area) as a heat map in the same spatial format as the plate; this procedure allows for easy identification of row and column effects as well as drift across multiple plates.

We recommend using a two-way median polish to correct for positional effects. This procedure involves iterative median smoothing of rows and columns to remove positional effects, then dividing each well value by the plate median absolute deviation to generate a *B* score⁶⁰. However, this procedure cannot be used on nonrandom plate layouts such as compound titration series or controls placed along an entire row or column⁵⁴. Other approaches include 2D polynomial regression and running averages, both of which correct spatial biases by using local smoothing⁶¹. Notably, image-based profiling is often sufficiently sensitive to distinguish among different well positions containing the same sample. Thus, to mitigate these positional effects, samples should be placed in random locations with respect to the plate layout. However, because such scrambling of positions is rarely practical, researchers must take special care to interpret results carefully and to consider the effects that plate-layout effects might have on the biological conclusions.

Batch-effect correction. Batch effects are subgroups of measurements that result from undesired technical variation (for example, changes in laboratory conditions, sample manipulation, or instrument calibration) rather than constituting a meaningful biological signal (Fig. 4). Batch effects pose a major challenge to high-throughput methodologies, and correction is an important preliminary step; if undetected, batch effects can lead to misinterpretation and false conclusions⁶².

We recommend identifying batch effects by inspecting correlations among profiles (described in ‘Single-cell data aggregation’). Specifically, by plotting heat maps of the correlation between all pairs of wells within an experiment, sorted by experimental repeat, batch effects can be identified as patterns of high correlation corresponding to technical artifacts (Fig. 4a). As a quantitative check, within-plate correlations should be in the same range as across-plate correlations.

When correction is needed, standardization and quantile normalization, as discussed in ‘Feature transformation and normalization’, can be applied within plates rather than to the entire screen⁶³. This procedure should be performed only if samples are relatively randomly distributed across plates. Canonical correlation analysis can also be used to transform data to maximize the similarity between technical replicates across experiments^{64,65}. Nonetheless, care should be taken to ensure that batch effects have been correctly decreased without false amplification of other sources of noise.

Feature transformation and normalization. Morphological profiles include features that display varying shapes of statistical distributions⁶⁶. It is therefore essential to transform feature values

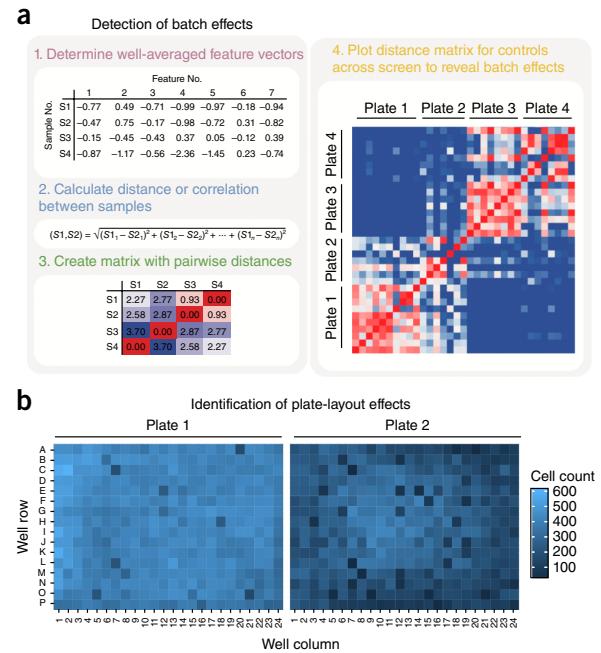


Figure 4 | Example diagnostic plots for detecting batch effects and plate-layout effects. **(a)** Process of detecting batch effects. The largest matrix on the right shows how plates 1 and 2 are more correlated to each other than to plates 3 and 4, and vice versa. This pattern suggests that plates 1 and 2, as well as 3 and 4, were prepared in batches that have noticeable differences in their experimental conditions. **(b)** Two plate layouts illustrating the cell count in each well. The visualization allows for identification of plate-layout effects, such as unfavorable edge conditions. Plate 1 shows that cells can grow normally in any well, whereas plate 2 shows markedly lower cell counts at the edges, thus indicating the presence of experimental artifacts.

with simple mathematical operations, such that the values are approximately normally distributed and mean centered and have comparable s.d. Normal distributions make it easier to work with numeric values from a mathematical, statistical, and computational point of view. We highlight three key steps in this process:

Distribution testing. The need for transforming feature values can be evaluated for each feature on the basis of diagnostic measures and plots (Fig. 3). Graphical methods such as histograms, cumulative distribution curves, and quantile–quantile plots allow for visual identification of features that deviate from symmetric distributions. Analytical tests can also be used, including the Kolmogorov–Smirnov (KS) test and the Kullback–Leibler divergence, both of which aim to compute ratios of deviation from normality.

Logarithmic transformations. These transformations are often used to obtain approximate normal distributions for features that have highly skewed values or require range correction^{67,68}. Transformations include the generalized logarithmic function⁶⁸ and other adaptations that use shrinkage terms to avoid problems with nonpositive and near-zero feature values^{69,70}, as well as the Box–Cox transformation⁶⁷.

Relative normalization. This procedure consists of computing statistics (for example, median and median absolute deviation) in one population of samples, and then centering and scaling the rest with respect to that population. Ideally, features are normalized across an entire screen in which batch effects are absent; however, normalization within plates is generally performed to correct for batch effects (described in ‘Batch-effect correction’). When choosing the normalizing population, we suggest the use of control samples (assuming that they are present in sufficient quantity), because the presence of dramatic phenotypes may confound results. This procedure is good practice regardless of the normalization being performed within plates or across the screen. Alternately, all samples on a plate can be used as the normalizing population when negative controls are unavailable, too few, or unsuitable for some reason, and when samples on each plate are expected to not be enriched in dramatic phenotypes.

We recommend applying normalization across all features. Normalization can be applied even if features are not transformed, and it is preferable to remove biases while simultaneously fixing range issues. *z*-score normalization is the most commonly used procedure in our laboratories. Normalization also aligns the range of different features, thus decreasing the effects of unbalanced scales when computing similarities (described in ‘Measuring profile similarity’) or applying analysis algorithms (described in ‘Downstream analysis’). It is advisable to compare several transformation and normalization methods, because their performance can vary significantly among assays⁷¹.

Step 4: dimensionality reduction

At this point in the workflow, it can be useful to ask which of the measured features provide the most value in answering the biological question being studied.

Dimensionality reduction aims to filter less informative features and/or merge related features in the morphological profiles, given that morphological features calculated for profiling are often relatively redundant. The resulting compact representation is computationally more tractable, and it additionally avoids overrepresentation of similar features, that is, having a subgroup of features that measure similar or redundant properties of cells. Redundant features can diminish the signals of other more complementary features that are underrepresented, thus confounding downstream analysis.

Feature selection. Feature selection reduces dimensionality by discarding individual features while leaving the remainder in their original format (and thus retaining their interpretability). Options include:

Finding correlated features. One feature is selected from a subgroup that is known to be correlated. For instance, some texture features are highly correlated; thus, not all of them are needed, because they may represent the same underlying biological property. The feature–feature correlation matrix is computed, and pairs with a correlation exceeding a given threshold are identified iteratively. At each step, the feature with the largest mean absolute correlation with the rest of the features is removed.

Filtering on the basis of replicate correlation. Features that provide the highest additional information content^{69,70} on the basis of

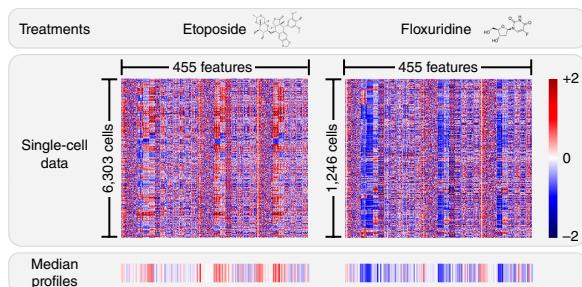


Figure 5 | Single-cell data aggregation. The feature matrices of two treatments show the measurements of their cell populations in the experiment. These measurements have been collapsed into median profiles that show very distinct signatures corresponding to two selected compounds: etoposide and floxuridine.

replicate correlation are iteratively selected as follows. An initial set of features is selected, and each of the remaining features is regressed on the selected set. The resulting residual data vector represents the additional information not already present in the selected features. The correlation of this residual vector across replicates is used to quantify information content. As a separate step, features with low replicate correlation are often excluded from analysis because they are too noisy^{69,72}.

Minimum redundancy–maximum relevance. A subset of features can have high replicate correlation without contributing substantially new information. To prevent selecting redundant features, minimum redundancy–maximum relevance⁷³ adds a constraint based on mutual information to the selection algorithm. The resulting selected features have high replicate correlation while preserving a diverse set of measurements⁷⁴.

Support-vector-machine-based recursive-feature elimination. A support vector machine is trained to implicitly weigh useful features in a classification task. Then, the features with the lowest weight are iteratively removed until the accuracy of the classification task begins to decline⁷⁵. In profiling applications, it may be desirable to select the features that best separate the treatments from the negative controls^{76,77}; the selected features would then be those that maximally differentiate phenotypes.

No previous studies have compared these options. Most groups use the filter method based on replicate correlation^{69,70,72}, and some add more powerful algorithms despite the computational cost. A combination of methods could be used, especially in tandem with the replicate-correlation strategy. There are other methodologies that may be useful, such as rescaling features in correlated groups such that their sum is one or selecting the features that contribute to most of the variance in the first two principal components.

Linear transformation. Methods of linear transformation seek lower-dimensional subspaces of higher-dimensional data that maintain information content. Linear transformation can be performed on single-cell profiles and aggregated sample-level profiles. Unlike feature selection, transformations can combine individual features, thus making the resulting features more powerful and information rich but potentially impeding their interpretability.

Linear transformation across all samples in the experiment is often needed for downstream analysis, to avoid overrepresentation of related features. Options used in morphological profiling are:

PCA. This procedure maximizes variance in successive orthogonal dimensions. PCA has been shown to outperform other dimensionality-reduction methods, such as random-forest selection for discriminating small-molecule-inhibitor effects⁷⁸, and independent component analysis and statistical image moments (Zernike/Fourier) for separating cell lines and preserving cell morphology after reconstruction from a lower-dimensional space⁷⁹.

Factor analysis and linear discriminant analysis. Factor analysis, which is closely related to PCA, finds nonorthogonal combinations of features representing frequent patterns in the data⁸⁰. Linear discriminant analysis finds a projection that maximizes the separation between positive and negative controls⁸¹. Both procedures have been successfully used in morphological profiling.

Among our laboratories, and in data science more generally, PCA is the most commonly used choice. Its simplicity and ability to retain a large amount of information in fewer dimensions probably explains its popularity. One comparative analysis using image-based profiling data has shown that factor analysis, compared with some alternate transformations, can identify a compact set of dimensions and improve downstream analysis results⁷⁷.

Step 5: single-cell data aggregation

Profiles are data representations that describe the morphological state of an individual cell or a population of cells. Population-level (also called image-level or well-level) representations are obtained by aggregating the measurements of single cells into a single vector to summarize the typical features of the population, so that populations can be compared (Fig. 5).

Simple aggregations. There are three simple and commonly used strategies for creating aggregated population-level profiles from all individual cell profiles in the sample:

Mean profile. Assuming a normal distribution of features, a profile built from the means of each feature for all cells in the population can provide a useful summary. This method has been used for compound classification^{77,82}. The profile length is sometimes doubled by also computing the s.d. of each feature.

Median profile. Taking the median for each feature over all the cells in a sample (and optionally the median absolute deviation) can be more robust to non-normal distributions and can mitigate the effects of outliers. If outliers are artifacts or errors, this procedure is useful, but the median may misrepresent populations with rare phenotypes by considering them as undesired outliers.

KS profile. This profile compares the probability distribution of a feature in a sample with respect to negative controls by using the KS nonparametric statistical test⁸³. The resulting profile is the collection of KS statistics for the features, which reveal how different the sample is with respect to the control.

There are other tests that may perform well but have not been evaluated for morphological profiling. Such tests include the

Anderson–Darling statistic and the Mann–Whitney *U* test. Other aggregation strategies can be designed by using bootstrap estimators previously used for phenotype classification⁸⁴.

The median profile has been found to have better performance than other profiling strategies in two different studies^{16,77} and is the preferred choice in most of our laboratories. One choice that varies among groups is whether to construct profiles at the level of images, fields of view, wells, or replicates. One could, for example, calculate a mean profile across all cells in a given replicate (regardless of the image or well) or instead calculate means for each image individually and then calculate means across images to create the replicate-level profile.

Subpopulation identification and aggregation. In most image-based cell-profiling workflows, it is implicitly assumed that ensemble averages of single-cell measurements reflect the dominant biological mechanism influenced by the treatment condition. However, subpopulations of cells are known to exhibit different phenotypes even within the same well^{85,86}. Classifying populations of single cells on the basis of their shape^{87–90}, cell-cycle phase^{13,88,91}, or signaling state⁹² can aid in interpretation and visualization of cell-profiling data⁹³. Cellular heterogeneity poses practical challenges for effective measurement methods that account for this variability.

Making use of subpopulations usually involves three key steps:

Subpopulation identification. Cells are clustered according to their morphological phenotypes, by using single-cell profiles (from controls or from the whole experiment). Clustering can be supervised, wherein reference phenotypes are selected^{94–96}, or unsupervised, as in *k*-means clustering^{90,97} and Gaussian mixture model fitting⁹².

Classification. Single-cell data points from all treatment conditions are then assigned to one of the subpopulations identified in the previous step. This assignment can be done by using a feature-evaluation rule, such as proximity, similarity, or feature weighting. This step is necessary because subpopulation identification is typically performed only on a subset of cells.

Aggregation. For each treatment condition, vectors are calculated and yield the number (or fraction) of cells within each subpopulation. Thus, the dimensionality of these vectors is the number of identified subpopulations.

An unproven hypothesis in the field is that profiles based on identification of phenotypically coherent subpopulations of cells should improve the accuracy of profiling, given the prevalence of heterogeneity and the existence of small subpopulations that might be ignored in mean or median profiling. In fact, to date, subpopulation-based profiling has not improved separation of treatment conditions^{77,98}. Nonetheless, defining subpopulations can assist in inferring biological meaning, by identifying over- and underrepresented subpopulations of cells under a given treatment condition⁹⁹ and by improving understanding of the dynamics of how cells transition between different phenotypes^{98,100}.

Step 6: measuring profile similarity

A key component of downstream analysis is the definition of a metric to compare treatments or experimental conditions. Similarity metrics reveal connections among morphological profiles.

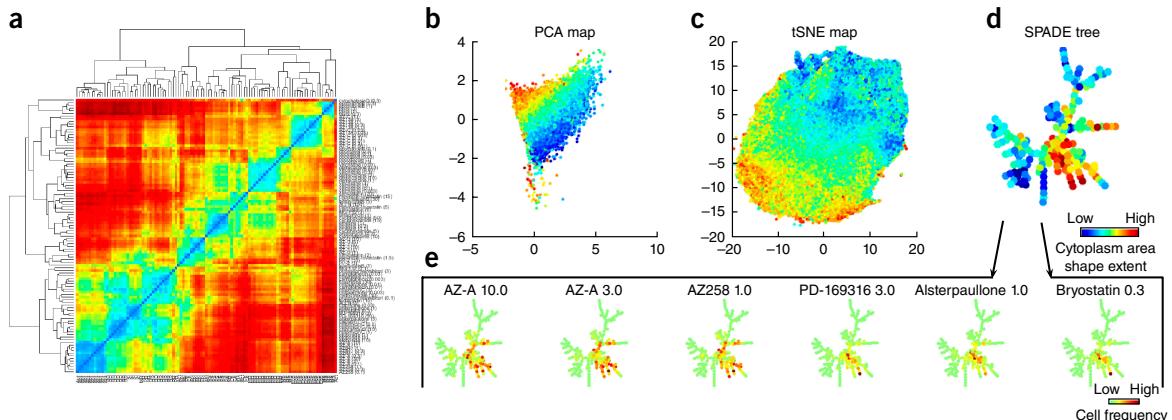


Figure 6 | Visualizations for downstream analysis. The source data are from 148,649 cells from the BBBC021 data set¹⁰⁸. (a) A heat map of the distance matrix shows the correlations between all pairs of samples, by using sample-level data (described in ‘Measuring profile similarity’). (b–d) The cellular heterogeneity landscape can be visualized from single-cell data by using PCA (b), tSNE scatter plots (c) or a SPADE tree (d). In these examples, single-cell data points are colored according to a single-cell shape feature ‘cytoplasm area shape extent’ (red, high; blue, low). (e) A separate visualization for each treatment can assist in interpreting phenotypic changes induced by sample treatments. A constant SPADE tree is shown, and treatment-induced shifts in the number of cells in each ‘node’ of the tree are shown by the color scale depicted. The first three treatments are known to have a similar functional effect (Aurora kinase inhibition), and they exhibit similar cell distributions on the SPADE tree. The remaining three treatments are known to induce protein degradation, inducing cell distributions that differ from the first three.

Similarity-metric calculation. With a suitable metric, the similarities among a collection of treatment conditions can facilitate downstream analysis and allow for direct visualization of data structure, for example in distance heat maps (Fig. 6a). Image-based cell-profiling studies use three types of metrics:

Distance measures. These measures involve calculating how far apart two points are in the high-dimensional feature space. Those used in morphological profiling include Euclidean^{72,83}, Mahalanobis¹⁰¹, and Manhattan distances. Distance measures are very useful to quantify the difference in magnitude between profiles, because they aggregate the lengths of feature variations regardless of directionality. This procedure is useful to compute estimates of phenotypic strength of treatments with respect to controls.

Similarity measures. These measures involve computing a statistical estimate of the likelihood of a relation between two profiles. Statistics used in morphological profiling include Pearson’s correlation¹⁰², Spearman’s rank correlation¹⁰³, Kendall’s rank correlation⁷⁸, and cosine similarity⁷⁷. Similarity measures quantify the proximity between profiles, because they detect deviations from one sample to another regardless of the absolute magnitude. This procedure is useful in finding relations and groups of samples that share common properties.

Learned similarity measures. These measures involve training machine-learning models that weight features differently according to prior knowledge about samples. The model can be a classifier that systematically identifies differences between two samples by using cross-validation¹⁰⁴ or by determining transformations of features that lead to maximal enrichment of groups of related samples⁸⁹. These strategies can highlight patterns that are not discriminated by regular metrics and that usually require more computational power to be calculated.

The performance of distance and similarity metrics relies on the quality of selected features (described in ‘Feature selection’). High-dimensional feature profiles are often prone to the drawback of dimensionality, which consists of a decreasing ability of metrics to discern differences between vectors when the dimensionality increases. Dimensionality reduction can mitigate this effect (described in ‘Linear transformations’). However, the choice of the metric can also be crucial, because good metrics better exploit the structure of the available features.

A comparison of metrics on one particular imaging data set has demonstrated that rank correlations (Spearman’s and Kendall’s) perform best for multiple untransformed feature vectors, whereas Euclidean and Manhattan distances are best for calculating z-prime factor values between positive and negative controls⁷⁸. A comparison of metrics in gene expression data sets has suggested that Pearson’s correlation performs best when features are ratios, whereas Euclidean distance is best on other distributions¹⁰⁵.

The consensus from our laboratories is that selecting an optimal metric is probably specific to feature-space dimensionality and distributions that result from prior steps in the pipeline. For a typical pipeline, Pearson’s correlation generally appears to be a good choice. Notably, indexes measuring clustering quality¹⁰⁶, for example the Davies–Bouldin Index, silhouette statistic, and receiver operating characteristic–area under the curve can aid in metric choice^{78,98}.

Concentration-effect handling. In experiments involving chemical perturbations, multiple concentrations are usually tested. Generally, researchers are interested in identifying phenotypic similarities among compounds even if those similarities occur at different doses. The following strategies are used to compute dose-independent similarity metrics:

Titration-invariant similarity score. First, the titration series of a compound is built by computing the similarity score between

each dose and negative controls. Then, the set of scores is sorted by increasing dose and is split into subseries by using a window of certain size (for instance, windows of three doses). Two compounds are compared by computing the correlation between their subwindows, and only the maximum value is retained⁸³.

Maximum correlation. For a set of n doses for each compound, the NxN correlation matrix is computed between all pairs of concentrations, and the maximum value is used as the dose-independent similarity score⁷².

The use of the maximum correlation is practical when a small number of concentrations are being tested. Depending on the experimental design, multiple concentrations can be treated differently. For instance, doses that do not yield a profile distinct from those of negative controls can be omitted, and the remaining doses can be combined to yield a single profile for the compound. Alternatively, if all concentrations are expected to have a phenotype, an entire compound can be left out of the analysis when its doses do not cluster together consistently¹⁰⁷. In addition, high doses can be removed if they are observed to be too toxic according to certain criteria, such as a minimum cell count^{102,107}.

Step 7: assay quality assessment

Assessing quality for morphological profiling assays can be challenging: basing the assessment on a few positive controls is not reassuring, but there are rarely a large number of controls available, nor are there other sources of ground truth. Every measured profile combines a mixture of the signal relating to the perturbation together with unintended effects such as batch effects and biological noise. Tuning the sample-preparation technique, choosing cell lines or incubation times, and choosing among alternatives within the computational pipeline all benefit from use of a quantitative indicator of whether the assay is better or worse as a result of particular design choices. Options include:

Comparison to ground truth. If the expected similarities between pairs of biological treatments are known, they can be used to validate predicted values. For instance, different concentrations of the same compound are expected to cluster together, and computed similarities should reflect that clustering. Similarly, if a subset of biological treatments is known to fall into particular classes, classification accuracy can be an appropriate metric⁷⁷. However, it is challenging to obtain ground-truth annotations at a large scale. To our knowledge, the only publicly available image data set with a large number of class annotations is for human MCF7 breast cancer cells (in this case, various classes of compound ‘mechanisms of action’)¹⁰⁸. Importantly, for proper evaluation of this data set, one complete compound set, including all concentrations, should be left out of training. A common mistake is to leave out a single dose of a single compound, inappropriately leaving the remaining doses of the same compound available to the classifier for training. Additional benchmarks beyond this data set are greatly needed.

Replicate reproducibility. This is typically measured as the similarity among the profiles of replicate pairs of the same biological treatment, which should be significantly higher than the similarity to profiles of other experimental conditions (controls and/or other biological treatments). This procedure requires at least two replicates of the experiment, a condition usually met for modern

morphological profiling experiments. To assess significance, similarity scores are compared with a suitable null distribution. A null distribution is usually built with pairs of samples that are not expected to be highly correlated, and it mainly depends on the hypothesis being tested. For instance, the use of all pairs of biological treatments can provide a diverse null distribution for measuring replicate correlation, and a null formed by random pairs of control samples can be compared against controls grouped by well location to reveal position effects. A P value can be computed nonparametrically by evaluating the probability of random pairs having greater similarity than a particular replicate pair.

Effect size. The difference between positive and negative controls, also known as the effect size, can be used as a measure of quality. This measure can be computed with a wide variety of statistical formulations, including univariate and multivariate methods, and also by assuming parametric and nonparametric models^{109,110}. The disadvantage of this approach is that maximizing effect size alone may cause a bias toward detecting only those phenotypes that distinguish the control while ignoring other phenotypes.

Exploratory approaches. Several methods have not been tested but might prove useful. Clustering can be used to ascertain the overall structure of relationships among samples in the experiment: a pipeline that produces substructures or many distinct clusters is likely to be preferable over one in which the distances between all pairs of samples are similar. The cumulative variance of the principal components is a metric not yet applied to morphological profiling experiments. Highly diverse signals from different biological treatments should require more components to explain a predefined fraction of variance (for example, 99%).

Currently, replicate reproducibility is the most commonly used method, given that ground truth is rarely available. Specifically, methods are often optimized to maximize the percentage of replicates that are reproducible relative to a null (under suitable cross validation). Using a null comprising pairwise correlations between different treatments is safer than using a null comprising correlations between treatments and negative controls; in the latter case, it is possible to optimize the assay to distinguish samples from negative controls while diminishing important differences among samples.

Step 8: downstream analysis

Downstream analysis is the process of interpreting and validating patterns in the morphological profiles. The most important readouts are the similarities and relationships among the experimental conditions tested. Visualization of the relationships and the use of machine learning can help to uncover biologically meaningful structures and connections among various treated samples. Most laboratories use a combination of these strategies; generally, unsupervised clustering is a good starting point for exploring the data. From there, the goals of the study strongly influence the combination of approaches used.

Clustering. Finding clusters is one of the most effective ways of extracting meaningful relationships from morphological profiles. Clustering algorithms can be used for identifying new associations

among treatments as well as validating known connections and ruling out batch effects. There are several ways of clustering a data set. Hierarchical clustering, the most widely adopted strategy, is used to identify groups of highly correlated experimental conditions⁸⁷ and to identify treatments with unexpected positive or negative connections⁹⁹. Although it is not discussed in detail here, examining relationships among features rather than among samples can yield useful biological insights: for example, the amount of mitochondrial material in cells is generally proportional to cell size, thus revealing stereotyped control of these parameters, but certain chemical perturbants can disrupt this relationship¹¹¹.

Hierarchical clustering is computed by using a similarity matrix that contains the similarity values for all pairs of samples (described in ‘Measuring profile similarity’). This similarity matrix can be visualized as a heat map to reveal patterns in the data for several or up to hundreds of samples. The heat maps’ rows and columns are typically sorted by using the hierarchical structure discovered by the clustering algorithm. This hierarchical structure is known as a dendrogram, which links samples together according to their proximity in the feature space, and is usually visualized together with the heat map to highlight negative and positive correlations in the data (**Fig. 6a**). Bootstrapping has been used to evaluate the statistical significance of the results obtained with hierarchical clustering, as well as other probabilistic algorithms used in the analysis of single-cell populations³². Resampling methods can generally be used to estimate variance, error bars, or other statistical properties of the data and can aid in making more accurate predictions and interpretations.

Visualization of high-dimensional data. Visualizations are useful to reveal the distribution and grouping of high-dimensional data points by using a 2D (and sometimes 3D) map layout that approximates their positions in the feature space. The relationships among points are implicitly encoded in how close together or far apart they are in the visualization. This method can be used to study cell heterogeneity by using single-cell data points, or sample relations by using aggregated profiles. Single-cell data are usually downsampled for practical reasons: to decrease data size and identify rare cell types^{112,113}. The following are the most common approaches for data visualization:

Data projections. A projection of the data matrix is displayed in a 2D (or 3D) scatter plot that approximates the geometry of the original point cloud. The most common methods include PCA (**Fig. 6b**), Isomap¹¹⁴, *t*-distributed stochastic neighbor embedding (tSNE)¹¹⁵ (**Fig. 6c**), and viSNE¹¹⁶.

Hierarchical visualizations. Plots are used to find structures in the data and reveal relationships between samples (**Fig. 6d,e**). The most commonly used choices are spanning-tree progression analysis of density-normalized events (SPADE)^{113,117} and minimum spanning trees¹¹⁸, which allow for relationships among hierarchical groups of single cells or samples to be identified by using branches that may represent phenotypes or treatments.

In many cases, data points in a visualization are colored on the basis of positive controls or otherwise known labels in the data, a common practice in analysis of single-cell flow cytometry data^{116,119,120}. The color code can also illustrate other information

in the data set, such as cell phenotypes, compound doses, values of measured features, or treatment conditions (**Fig. 6e**). Visualizations can be more effective if they are interactive, thereby allowing researchers to create and test hypotheses *ad hoc*. Software packages such as Shiny, GGobi, iPlots in R, Bokeh in Python, and D3.js in Javascript provide interactive plotting capacities, most of which can also be deployed in server-client environments for dissemination to the public.

Classification. Classification rules can be useful for transferring labels from annotated samples to unknown data points, for example, classifying the mechanism of action of new compounds in a chemical library. As such, classification strategies require prior knowledge in the form of annotations for at least some of the data points in the collection. Given examples of data points that belong to different classes of interest, supervised classification algorithms learn a rule that computes the probability of each unknown data point falling into one of the classes.

It is relatively uncommon to have a large number of annotated samples in morphological profiling, because most experiments are designed to be exploratory. However, when this information is available, a classification strategy can provide informative insights into the treatments. The most commonly used classification rule in morphological profiling experiments is the nearest-neighbors algorithm, which finds the closest data points in the collection of annotated samples and recommends a label for the new sample. For instance, this algorithm has been used for classifying the mechanism of action in a compound library⁷⁷. Other supervised prediction models can also be used to learn relations between morphological features and biological activity assays, such as Bayesian matrix factorization, neural networks, and random forests¹²¹.

The classification performance is validated in a holdout test using precision, recall, and accuracy measures. It is absolutely critical for confidence in these metrics that the holdout test set not overlap with any data points in the training set. The most recommended practice is to use samples treated in a different experimental batch to create the holdout test set (other ground-truth recommendations are described in ‘Assay quality assessment’).

Sharing

Both authors and the scientific community benefit from sharing code and data¹²². Numerous tools currently exist that address the steps outlined in this paper (**Box 1**); these tools can be useful both for beginners to experiment with and learn from and for experts to integrate into pipelines and build upon. Although data must be kept confidential for sensitive patient material, intellectual-property concerns are generally not the major issue with sharing; the primary hurdle in the process is usually the often substantial time and effort required of the authors. We do not consider code or data labeled ‘available upon request’ to qualify as being openly shared, given the poor efficacy statistics^{123,124}. We therefore recommend the following options to make code and data available publicly online.

Code sharing. Options for sharing code include:

Step-by-step narrative. For software with only a graphical user interface, a detailed walkthrough of each step of the workflow can be provided; however, this option is suboptimal.

BOX 1 SOFTWARE TOOLS

A large range of software tools and libraries currently exist that seek to address the steps outlined in this paper. For each step, the alternatives are usually several software packages or programming languages that require either parameterization or coding.

Tools for image-analysis software have been previously reviewed¹⁵⁰, and the variety in functionalities and platforms can fit a diverse range of workflows. Some of the open-source alternatives include CellProfiler²⁴ and EBImage³⁵, whereas Columbus and MetaXpress are commercial solutions.

After collection of features or measurements with image-analysis software, the next steps in the workflow may require a combination of tools and programming languages. Statistical

packages such as R have proven to be very useful for single-cell data analysis, including *cytominer*, which is specific to morphological profiling. Other programming languages such as Python, Matlab and shell scripts can be used to process data with specific algorithms, including machine learning, data transformation, or simple data filtering and selection.

Each step may require specialized methods or may be solved with off-the-shelf implementations. The field is constantly changing, and the next breakthroughs in theory and practice may require new tools not yet available. In either case, the practice of sharing code is highly valued, to ensure rapid implementation of techniques, optimization of pipelines, and reproducibility of the results by others.

Online code repository. The code should preferably be publicly hosted rather than being provided on a university website or as journal supplemental files. The options range from repositories such as Github and BitBucket to tools such as Jupyter notebooks and knitr documents¹²⁵, which allow for reproducible reports containing code, documentation, and figures to be shared within a single document.

Packaging. Researchers can capture and share the computational environment used to create the results, such as providing virtual machines or Docker containers. Doing so ensures that all code, dependencies and data are available in a single container^{126,127}, which is convenient for the user and also protects against changes in software libraries and dependencies.

Data sharing. In image-based cell profiling, publicly available data are valuable not only for reproducing results but also for identifying completely new biological findings. Options include:

Sharing processed data only. Sharing only processed data (for example, extracted features) has been common, often through supplemental data files available via the journal or via a general-purpose data repository such as Dryad (<http://datadryad.org/>).

Sharing images and data online. Few raw-image sets have been made available online, primarily because of the large size of the image data (tens of gigabytes for each 384-well plate) and therefore the high cost of maintaining the data on public servers. However, recent initiatives are decreasing this cost for authors, including the Image Data Resource (IDR; <https://idr-demo.openmicroscopy.org/>)¹²⁸, which accepts cellular images at the scale of high-throughput image profiling experiments. Generally, smaller sets of annotated images for testing image analysis methods are available in the Broad Bioimage Benchmark Collection (<https://data.broadinstitute.org/bbbc/>)¹⁰⁸ and the Cell Image Library (<http://www.cellimagelibrary.org/>). Some resources, such as IDR, support using an ontology for describing phenotypes¹²⁹. Before these public resources became available, some laboratories provided the data through their institutional servers^{13,32,52,89,103,130,131}. Tools such as OMERO¹³² and openBIS¹³³ have been used to create project-specific portals for easy

online data exploration^{32,52,130}, but bulk download of very large data sets can remain challenging.

We strongly encourage sharing of both data and images online, given how rapidly feature-extraction methods are changing, particularly via deep-learning methods (described in ‘Alternate workflows’).

Alternate workflows

The data-processing workflow and recommendations presented in this paper have evolved as a result of years of efforts in different laboratories. They have been robustly used in various studies and have proven to be successful in making biological discoveries^{8,9}. However, the field is eager to adapt as the computer-vision and machine-learning communities make progress in designing new algorithms for processing image data. Some of our laboratories are already exploring alternate workflows, such as those described below.

Segmentation-free classical-feature extraction. Instead of identifying single cells that are measured and characterized, this strategy computes classical features from whole field-of-view images or from discrete tiles within images. Examples of these include PhenoRipper^{134,135} and WND-Charm/CP-CHARM^{136–138}.

Deep-learning feature extraction. Deep learning techniques have recently and dramatically come to dominate the state-of-the-art performance in various computer vision tasks¹³⁹. The most relevant model for image analysis is currently the convolutional neural network (CNN), which learns to extract useful features directly from raw pixel data by using multiple nonlinear transformations, in contrast to the classical features described in ‘Feature extraction’. This model has been used for segmentation and classification of biomedical images^{140,141}, for phenotype discovery in single-cell images from imaging flow cytometry¹⁴², and more recently for deep-learning approaches for morphological profiling: morphological profiling^{143,144}. The following are the most relevant deep-learning approaches for morphological profiling:

Learning features from raw pixels. This approach has been used for problems in which phenotypes of interest are predefined, and a set of categorized examples is needed to train the network. This approach has been successfully used for protein-localization

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problems^{145–147} and mechanism-of-action prediction¹⁴⁴. Input images can be single cells^{146,147} or full fields of view^{144,145}.

Transferring learned features from other domains. Using a CNN trained on a large data set for other tasks different from the original is known as transfer learning. CNNs pretrained with natural images have been evaluated as feature extractors for full image profiling of compounds; its accuracy matches the results of classical features without requiring segmentation or training¹⁴³. The preprocessing steps described in ‘Field-of-view quality control’ and ‘Field-of-view illumination correction’ are still likely to be necessary for obtaining improved results. If there are few annotations available for phenotype-classification tasks, transfer learning can also be used to improve performance¹⁴⁶.

Learning transformations of classical features. Feature transformations similar to those described in ‘Linear transformations’ can be obtained with a technique known as the autoencoder. Deep autoencoders have been evaluated for high-content morphology data, thus suggesting that they may potentially have better performance for downstream analysis according to homogeneity of clusters¹⁴⁸. Another study has evaluated deep autoencoders for profiling and has also obtained competitive performance¹⁴⁹.

Using full images results in a loss of single-cell resolution but offers several advantages: the avoidance of the segmentation step eliminates the sometimes tedious manual tuning of segmentation and feature extraction algorithms, saves computation time, avoids segmentation errors, and may better capture visual patterns resulting from multiple cells. Using single-cell images explicitly captures heterogeneity and may offer improved accuracy with less training.

Although segmentation-free classical-feature extraction can be helpful for quality control, we generally consider it to be incapable of accomplishing most profiling tasks. Deep-learning techniques, although not yet proven to be more powerful than the standard workflow, are nonetheless very promising. We are actively pursuing optimized workflows based on deep learning and are gaining an understanding of how these techniques can be adapted for improving the computation and interpretation of useful image features.

We caution that it is possible to obtain excellent results on a ground-truth data set with a method that fails in realistic-use cases. This phenomenon may be especially true for machine-learning-based methods with millions of internal parameters and again reinforces the need for new and disparate sets of ground-truth data in the field.

Conclusions

It is an exciting time for the field of image-based cell profiling, as methods are rapidly evolving and applications leading to major biological discoveries are beginning to be published. We see the collection and sharing of large biologically interesting image sets, the organizing of benchmark ground-truth data sets, and the testing of new methods to be the major areas in which effort is currently most needed.

In future work, as a community, we aim to build shared codebases, namely toolboxes of algorithms in R and Python. The beginnings of this effort can be found online (<https://github.com/>

[CellProfiler/cytominer/](#)), and we welcome additional contributors as well as participants in the cytominer hackathon, which will be held annually. A shared codebase will facilitate the development and dissemination of novel methods and the comparison of alternative methods, particularly as additional ground-truth data become publicly available.

Data availability

This work did not analyze new data. The plots and figures presented in the manuscript were obtained by processing the BBBC021 image collection, which is publicly available in <https://data.broadinstitute.org/bbbc/BBBC021/>.

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Chapter 13

High-Dimensional Profiling: The Theta Comparative Cell Scoring Method

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Abstract

Principal component analysis enables dimensional reduction of multivariate datasets that are typical in high-content screening. A common analysis utilizing principal components is a distance measurement between a perturbagen—such as small-molecule treatment or shRNA knockdown—and a negative control. This method works well to identify active perturbagens, though it cannot discern between distinct phenotypic responses. Here, we describe an extension of the principal component analysis approach to multivariate high-content screening data to enable quantification of differences in direction in principal component space. The theta comparative cell scoring method can identify and quantify differential phenotypic responses between panels of cell lines to small-molecule treatment to support in vitro pharmacogenomics and drug mechanism-of-action studies.

Key words Phenotypic screening, High-content analysis, Cell-based profiling

1 Introduction

Phenotypic screening allows the identification of treatments that modify a disease model without prior knowledge of the molecular target. This re-emerging method can generate hypotheses for the etiology behind poorly understood diseases, in addition to the discovery of potential therapeutics that act through novel biological mechanisms [1].

One form of phenotypic screening is high-content image-based screening which uses multiple measurements to create a detailed multivariate profile of a perturbagen. This can make screens less biased to prenominated target or therapeutic class hypothesis and also create a phenotypic fingerprint to inform mechanism of action [2–5].

A distinct phenotypic response between cell types which represent the broad heterogeneity of human disease and/or more defined clinical subtypes can highlight differences in cellular signalling, metabolic, and biochemical transporter mechanisms that

explain the variation of drug efficacy between patients often observed in the clinic. Correlation of distinct phenotypic response and drug sensitivity across genetically distinct cell types with genomic, transcriptomic, and proteomic data can help elucidate compound mechanism of action and identify molecular biomarkers which predict drug sensitivity and clinical outcomes [6, 7]. We can also use phenotypic similarity between different perturbagens to infer mechanistic similarities. One such example is that small molecules which elicit similar cellular phenotypes are likely to have similar mechanisms of action [8]. Phenotypes can also be used to model disease biology where the underlying signaling pathways and molecular targets associated with disease progression are lacking or poorly understood [9].

In order to quantify complex phenotypes, high-content screening generates multivariate datasets in which multiple phenotypic measurements are taken from a single cell or image. These datasets are usually subjected to some form of dimensionality reduction technique in order to make analysis more manageable. A common dimensional reduction method is principal component analysis, which creates new features (principal components) through orthogonal linear combinations of the original features in order to maximize variation. As principal components are ranked in order of variation, a subset of the principal components can be taken as a replacement for the original feature measurements—with the aim of reducing the number of variables while still retaining as much information as possible. This approach helps visualize complex multivariate data points by plotting them in 2D or 3D principal component space [10, 11].

A simple method used to identify active perturbagens in multivariate datasets is a distance measurement such as Euclidean or Mahalanobis distance between the perturbagen and the negative control in principal component space. This can be used to create a threshold distance to separate the active from inactive, as well as rank perturbations on phenotypic activity [11]. However, this distance metric cannot readily discern between different active phenotypes. Two perturbations may produce very different phenotypes and coordinates in principal component space, and yet have similar distances from the negative control.

In order to discern between perturbations such as these we need a measure of directionality. The idea behind the theta comparative cell scoring (TCCS) method is that different directions in phenotypic space indicate different phenotypes. Therefore measuring the angle between perturbagen-induced phenotypes can be used as a phenotypic similarity score independent of potency. This is very similar to the use of cosine similarity, though the TCCS method centers measurements on the negative control and removes inactive perturbagens that may otherwise produce inaccurate measures of directionality.

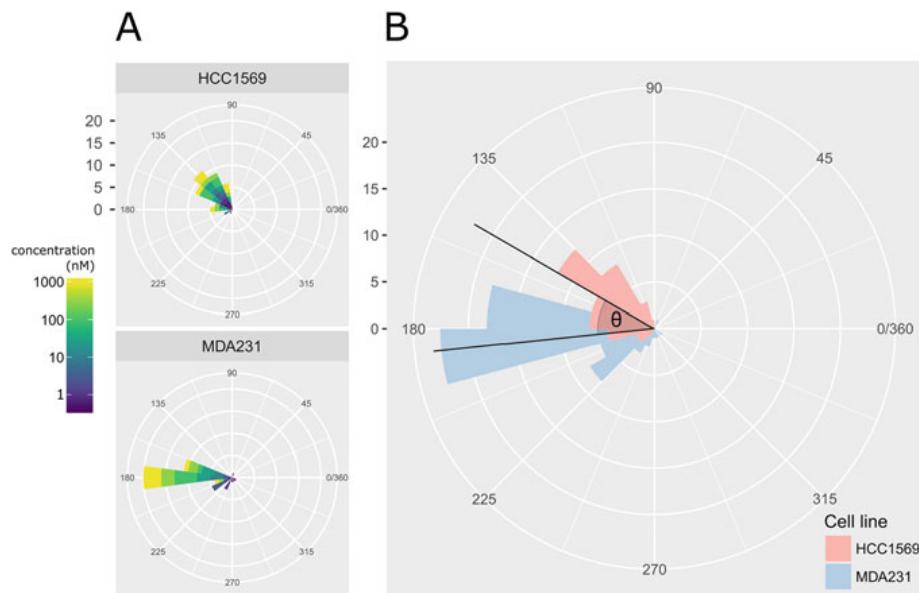


Fig. 1 Circular histograms showing the similar phenotypic direction of HCC1569 and MDA-MB-231 (MDA231) breast cancer cell lines treated with the aurora kinase inhibitor barasertib. **(a)** Theta values calculated from the first two principal components against a reference vector for both HCC1569 and MDA-MB-231 cell lines treated with barasertib at multiple concentrations. **(b)** Depiction of the θ value when calculated between a pair of cell lines representing the difference in phenotypic response

The idea of directionality can also be used to produce intuitive and quantitative figures such as circular histograms depicting the direction in phenotypic space or the difference in theta values between two perturbations or samples (Fig. 1).

2 Materials

1. Optical-bottom imaging plates (96- or 384-well).
2. Cell culture medium.
3. Trypsin.
4. Perturbagen Library.
5. Paraformaldehyde (PFA).
6. Triton X-100.
7. Wheat-germ agglutinin 594 (WGA), diluted in dH₂O.
8. SYTO14 green fluorescent nucleic acid stain.
9. Microtiter plate seals.
10. Aluminum foil.
11. Cell painting stock solution: 10 mg/mL Hoechst 33342, 1 mg/mL concanavalin A (diluted in 0.1 M NaHCO₃), 200 U/mL phalloidin-594 (diluted in methanol), 1 mg/mL WGA, 1 mM MitoTracker DeepRed.

12. Blocking buffer: 1% Bovine serum albumin (BSA) in PBS (w/v).
13. Cell painting working solution: 2 µg/mL Hoechst 33342, 11 µg/mL concanavalin A, 3 µM SYTO14, 2.5 U/mL phalloidin-594, 0.25 µg/mL WGA, 600 nM MitoTracker DeepRed.

3 Methods

3.1 Cell Seeding

Preliminary studies are required to determine the optimal number of cells to seed per well (*see Note 1*). This number is dependent on the characteristics of the cell line(s) and the well area in a given plate. Approximate values are provided in Table 1.

1. Using a sub-confluent population of cells, detach the cells by short-term incubation with trypsin and suspend to the desired concentration in cell culture medium.
2. Seed the cells into each well of an optical bottom microtiter 96- or 384-well plate. Make sure that the cells do not settle in the stock of cell suspension by frequently agitating the stock of cell suspension.
3. Incubate the plates containing cells for 24 h.

3.2 Compound Addition

1. Make up stock compound plates in DMSO at 1000× the final concentration.
2. Make an intermediate plate by diluting stock compound plate 1:50 in cell culture medium.
3. Remove cell plates from the incubator and transfer a volume from the intermediate plate to the cell plate in a 1:20 dilution.
4. Return cell plates to the humidified, 37 °C, 5% CO₂ incubator for an additional 48 h.

3.3 Fluorescent Labeling

3.3.1 Fixation

1. Make a solution of 8% paraformaldehyde (PFA) in phosphate-buffered saline (PBS).
2. Add an equal volume of PFA to each well, and incubate at room temperature for 30 min.
3. Wash wells three times with 50 µL of PBS.

Table 1
Approximate cell seeding densities for different plates

Plate	Cells/well	Volume/well (µL)
96	2000–3000	100
384	750–1500	50

3.3.2 Permeabilization

1. Add 30 µL of 0.1% Triton-X100 solution in PBS to each well, and incubate for 20 min at room temperature.
2. Wash wells three times with 50 µL of PBS.

3.3.3 Cell Labeling

Cell labeling protocol adapted from the cell painting protocol [12, 13].

1. Protect the staining solution from light sources by wrapping in aluminum foil.
2. Add 30 µL of cell painting solution and incubate in a dark place at room temperature for 30 min.
3. Wash plate three times with 50 µL of PBS. Do not aspirate the final volume.
4. Seal the plates. If the plates are not imaged immediately, then store them at 4 °C in the dark or wrapped in aluminum foil.

3.4 Imaging

1. Set up the microscope to image five channels at 20× magnification. See Table 2 for suggested filter settings.
2. Image multiple sites per well; we recommend a minimum of four.
3. Adjust the focus and exposure settings (see Note 2). These settings should be kept constant between batches and comparable experiments as intensity measurements are a function of exposure time.

3.5 Image Analysis

The following image analysis instructions use CellProfiler [14] nomenclature, though other image analysis software packages may be used to achieve similar results.

1. Extract metadata from either the image or the file path; record the date, plate number, plate name, well, site, and channel for each image.

Table 2
Cell painting reagents and suggested filters

Stain name	Filter name	Filter wavelength	
		Excitation (nm)	Emission (nm)
Hoechst 33342	DAPI	377 ± 40	447 ± 60
Con A	FITC	482 ± 35	536 ± 40
SYTO14	Cy3	531 ± 40	594 ± 40
Phalloidin & WGA	TxRed	562 ± 40	624 ± 40
MitoTracker DeepRed	Cy5	628 ± 40	692 ± 40

2. Add in external metadata from a .csv file such as compound labels or concentrations and match via plate name and well name/position.
3. Assign each image to a channel name using the extracted channel metadata.
4. Segment the nucleus using IdentifyPrimaryObjects.
5. Segment the cell body/cytoplasm using the nucleus object as a seed in the phalloidin/WGA channel with the IdentifySecondaryObjects module.
6. Measure image quality in the DAPI channel using MeasureImageQuality. Out-of-focus images and any debris can usually be detected in the DAPI channel. Image quality can also be measured in all the channels though the MeasureImageQuality module although this will increase analysis time.
7. Measure object size and shape of both the nucleus and cell body with MeasureObjectSizeShape.
8. Measure intensity of the nucleus in the DAPI channel and intensity of the cell body in the other four channels using MeasureObjectIntensity.
9. Measure texture in the channels for Golgi apparatus and actin staining (WGA channel) in the cell body objects, and the DAPI channel for the nuclei objects using MeasureTexture.
10. Measure object neighbors for both nuclei and cell bodies with MeasureObjectNeighbors.
11. Export measurement data as .csv files or to a database, excluding any feature measurements that may not be relevant such as object number or object *x*-*y* position.

3.6 Data Analysis

1. Check the data produced by the CellProfiler analysis for any missing rows or columns; these need to be removed as appropriate (*see Note 3*).
2. Using the ImageQuality measurements produced by CellProfiler, identify any images that may be out of focus or contain debris and after visually checking the images remove the data relating to that image if necessary (*see Note 4*).
3. If the data is at the object-level, i.e., measurements per cell, then aggregate this to a well median, so each measurement describes the median measurement per feature per well.
4. Remove non-informative features (any measurement columns that are not metadata) such as those with zero or very low variance.
5. Remove redundant features, such as one of a pair of features that are very highly correlated with each other. This can be performed by calculating a correlation matrix of the feature

dataset and finding groups of features that have Spearman's correlations greater than 0.95, and then removing all but one of these features from the dataset.

6. Normalize the data to the negative control values on each plate. This is performed by subtracting the median of the negative control for each feature, per plate (*see Note 5*).
7. Scale the features. For each feature: subtract the feature mean from each individual value, and then divide by the standard deviation of the feature. This standardizes the features to have a mean of zero and unit variance. This is done otherwise features with large values/small units—such as object area which is measured in pixels—will skew the subsequent statistical methods.
8. Calculate the principal components of the feature data and determine the number of principal components needed to account for a proportion of the variance in the dataset, typically 80–90% (*see Note 6*).
9. Remove those principal components that fall outside of this subset.
10. Calculate the negative control medoid, which is the median value for each feature of the negative controls.
11. Adjust the principal component values so that the negative control medoid is centered on the origin (*see Note 7*).
12. Calculate the l1-norm (AKA city-block or Manhattan distance) from the negative control medoid to each data point in principal component space.
13. Calculate the l1-norm of each negative control point from the origin and calculate a distance threshold as 2 standard deviations of these negative control distances. Any compound that has a distance less than this threshold from the medoid of the negative control can be labeled as inactive.
14. Once the inactive compounds have been removed, perturbagen similarity can be determined by the angle between perturbagen vectors (θ). In two dimensions—using the first two principal components—this can be visualized on a scatter plot. The θ value can be calculated in any number of dimensions, although visualization becomes more difficult. The similarity angle can be calculated by the cosine similarity converted to degrees (*see Eq. (1)*). Note that 180° is the value of maximum dissimilarity, where two perturbagens having completely different directions in phenotypic space, with values greater than 180° becoming increasingly similar as they approach 360° . Therefore θ values are constrained between 0 and 360 by subtracting from 360 any value greater than 180 , i.e., $\theta > 180 \rightarrow \theta := 360 - \theta$:

$$\theta = \cos^{-1} \left(\frac{\mathbf{u} \cdot \mathbf{v}}{\|\mathbf{u}\| \|\mathbf{v}\|} \right) \times \frac{180}{\pi} \quad (1)$$

where \mathbf{u} and \mathbf{v} are the vectors of principal components for each compound.

15. If two principal components capture a large proportion of the variance in the dataset then a visualization can be made by calculating θ for every perturbagen against a common reference vector, and then plotting a circular histogram of the θ values (*see Note 8*).
16. Identify cell line pairs treated with the same compound that have significantly different theta values (*see Note 9*), indicating a distinct phenotypic response between cell lines to a compound treatment.
17. *See Notes 10 and 11* for additional troubleshooting steps.

4 Notes

1. Too few cells will provide fewer replicates and may run the risk of having no cells contained in an image if a perturbagen reduces the cell number. Seeding too many cells can mean cells do not form a single monolayer which makes image analysis more difficult. We advise seeding the number of cells to result in approximately 60–70% confluence.
2. After setting the focus for the first channel (DAPI/Hoechst), all additional channel's focus settings are based on these measurements. Therefore adjusting the focus settings for the first channel will also affect all of the other channels, so it is advised to set this first and check a few different wells to ensure that the settings are robust.
3. It is recommended to remove columns containing large amounts of missing numbers. This can often be caused by missing metadata in certain samples, or some features that remain constant between samples—such as Euler number—that may be transformed to missing data entries after scaling or aggregation. Once columns of largely missing data have been removed, rows containing missing values can be removed. Without first removing the missing data columns it is often possible to erroneously remove the entire or large proportions of the dataset when using missing rows as the first step.
4. Out-of-focus images can be detected using ImageQuality_PowerLogLogSlope measurements in the nuclei channel. Images with very low values are likely to be out of focus [15]. Debris such as dust or fibers typically show up in the nuclei channel,

and can be detected by identifying images with a large percentage of saturated pixels.

5. Normalizing to the negative control is a useful step in any plate-based screen to remove any batch effects between plates that may influence the results. It is especially important when comparing effects between cell lines as this converts the values to changes from the negative control for that particular plate; as we expected to have a single cell line per plate this also removes any inherent phenotypic differences between the cell lines, and allows the compound-induced changes to be comparable.
6. The number of principal components required to capture a specified proportion of the variance in the data can be calculated in *R* (assuming that data is numeric feature data), to calculate the value for 80% of the variance:

```
threshold <- 0.8
pca_output <- prcomp(data)
pc_variance <- pca_output$sdev^2
cumulative_proportion_variance <- cumsum(pc_variance) / sum(pc_variance)
n_components <- min(which(cumulative_proportion_variance >= threshold))
```

7. To center the principal component data so that the medoid of the negative control lies on the origin, find the medoid for the negative control values, which is the median value for each feature column for the negative control values; find how much this differs from the origin for each feature; shift all values for each feature by this difference, e.g., in R:

```
centre_control <- function(df, feature_cols, cmpd_col, neg_control = "DMSO") {
  # 1. the median value for the DMSO values for each measured feature
  medioid <- apply(df[df[, cmpd_col] == neg_control, feature_cols], 2, median)
  # 2. calculate the difference from the origin for each medioid position
  delta <- 0 - medioid
  # 3. iterate along columns and adjust to centre the DMSO data
  for (i in seq_along(feature_cols)) {
    feature <- feature_cols[i]
    df[, feature] <- df[, feature] + d[i]
  }
  return(df)
}
```

8. Creating circular histograms: If the principal component vector only contains information regarding two principal components, then we can calculate a θ value for each perturbagen against a common reference such as $(0, 1)$. This generates a θ value for each perturbagen which can be plotted as a histogram. Without constraining them, the θ values are ranged between

0 and 360. As either end of this range is equivalent to the x -axis of this histogram can be wrapped round into a circle which can be used to visualize the phenotypic direction induced by a perturbagen (Fig. 1).

9. To identify distinct phenotypic responses between cell lines treated with a perturbagen, a theta value has to be calculated for each pair of cell lines per perturbagen. Cell lines that elicit a similar response to a given perturbagen will produce a low θ value, indicating that they produce similar phenotypic trajectories, whereas a θ value approaching 180 indicates opposite phenotypic directions. In our experience a histogram of all measured θ values produces a log-normal distribution, indicating that most perturbagens produce similar phenotypic response between cell lines.
10. Image analysis can take considerable time for large numbers of images. We recommended using either a computing cluster or a cloud computing service to process many images in parallel.
11. Large .csv files can also cause problems. If files exceed several GBs we recommend users switch to a database format such as SQLite.

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